



Full wwPDB EM Validation Report ⓘ

Apr 15, 2026 – 01:16 AM UTC

PDB ID : 9ZDK / pdb_00009zdk
EMDB ID : EMD-74065
Title : The cryo-EM structure of Pakpunavirus P7-1 triplex protein and sheath in contracted state
Authors : Li, F.; Cingolani, G.
Deposited on : 2025-11-25
Resolution : 5.00 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

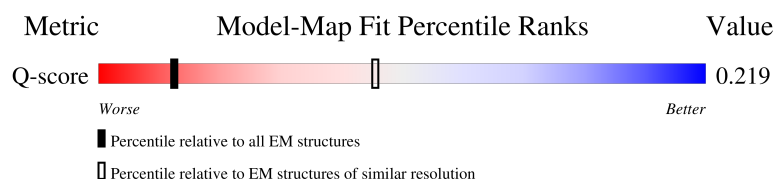
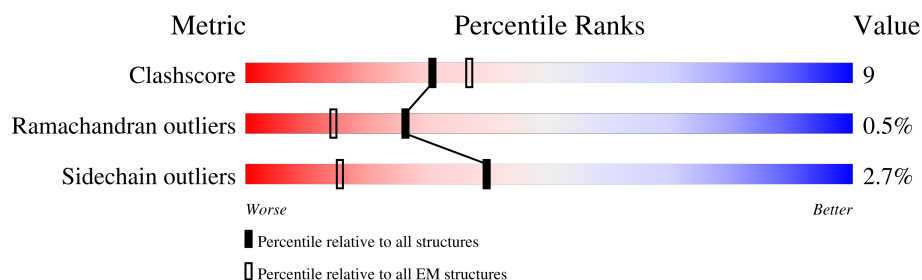
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 5.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





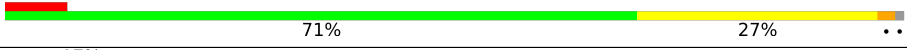



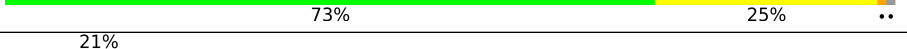
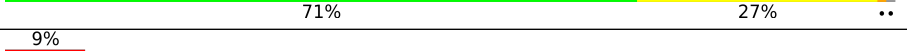
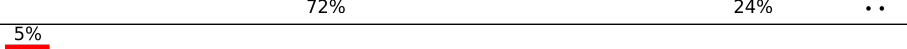
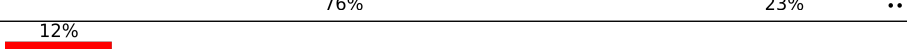
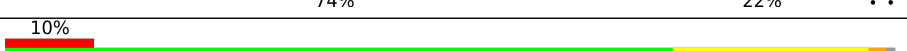



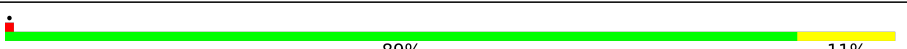





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1057 (4.50 - 5.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	487	
1	B	487	
1	D	487	
1	E	487	

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Mol	Chain	Length	Quality of chain
1	G	487	
1	H	487	
1	J	487	
1	K	487	
1	M	487	
1	N	487	
1	P	487	
1	Q	487	
2	C	243	
2	F	243	
2	I	243	
2	L	243	
2	O	243	
2	R	243	
3	S	428	
3	T	428	
3	U	428	
3	V	428	
3	W	428	
3	X	428	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 74784 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called gp88.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	484	Total	C	N	O	S	0	0
			3672	2319	616	729	8		
1	B	483	Total	C	N	O	S	0	0
			3664	2313	615	728	8		
1	D	484	Total	C	N	O	S	0	0
			3672	2319	616	729	8		
1	E	483	Total	C	N	O	S	0	0
			3664	2313	615	728	8		
1	G	484	Total	C	N	O	S	0	0
			3672	2319	616	729	8		
1	H	483	Total	C	N	O	S	0	0
			3664	2313	615	728	8		
1	J	484	Total	C	N	O	S	0	0
			3672	2319	616	729	8		
1	K	483	Total	C	N	O	S	0	0
			3664	2313	615	728	8		
1	M	484	Total	C	N	O	S	0	0
			3672	2319	616	729	8		
1	N	483	Total	C	N	O	S	0	0
			3664	2313	615	728	8		
1	P	484	Total	C	N	O	S	0	0
			3672	2319	616	729	8		
1	Q	483	Total	C	N	O	S	0	0
			3664	2313	615	728	8		

- Molecule 2 is a protein called gp89.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	241	Total	C	N	O	S	0	0
			1871	1197	314	359	1		
2	F	241	Total	C	N	O	S	0	0
			1871	1197	314	359	1		
2	I	241	Total	C	N	O	S	0	0
			1871	1197	314	359	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	241	Total	C	N	O	S	0	0
			1871	1197	314	359	1		
2	O	241	Total	C	N	O	S	0	0
			1871	1197	314	359	1		
2	R	241	Total	C	N	O	S	0	0
			1871	1197	314	359	1		

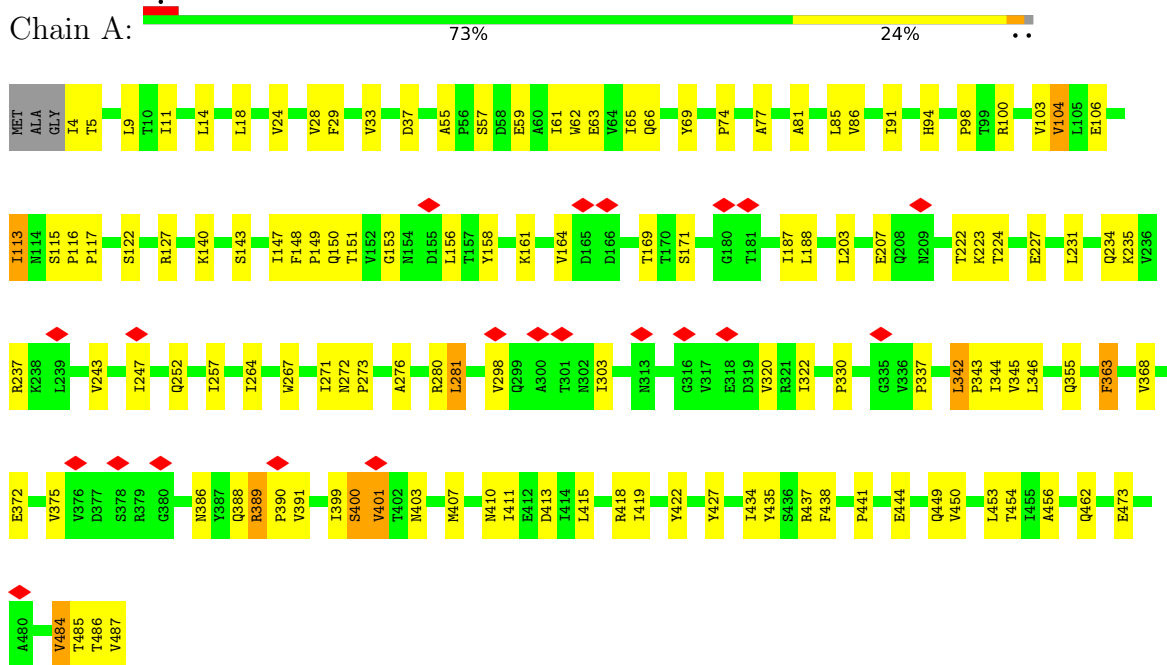
- Molecule 3 is a protein called gp76.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S	427	Total	C	N	O	S	0	0
			3257	2050	562	636	9		
3	T	427	Total	C	N	O	S	0	0
			3257	2050	562	636	9		
3	U	427	Total	C	N	O	S	0	0
			3257	2050	562	636	9		
3	V	427	Total	C	N	O	S	0	0
			3257	2050	562	636	9		
3	W	427	Total	C	N	O	S	0	0
			3257	2050	562	636	9		
3	X	427	Total	C	N	O	S	0	0
			3257	2050	562	636	9		

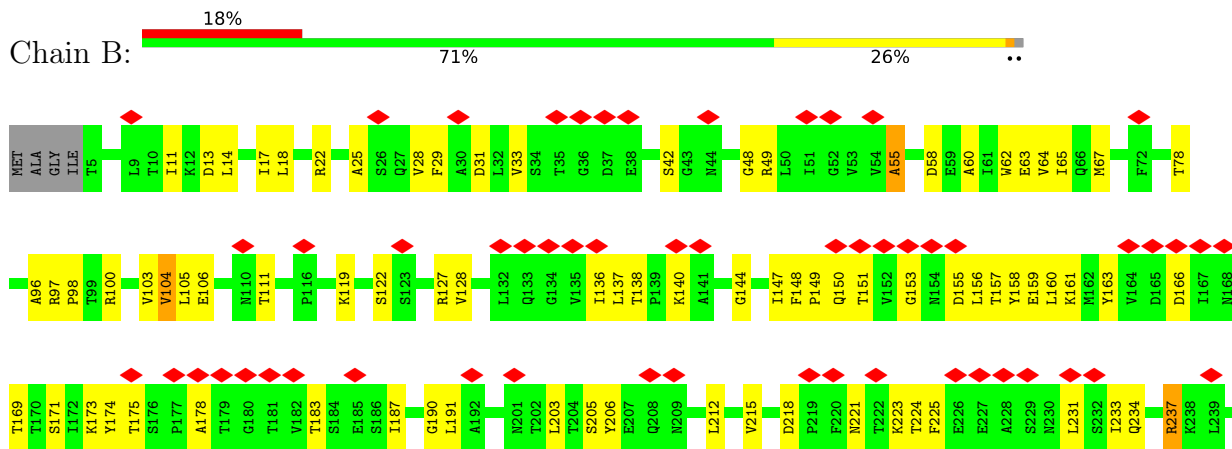
3 Residue-property plots

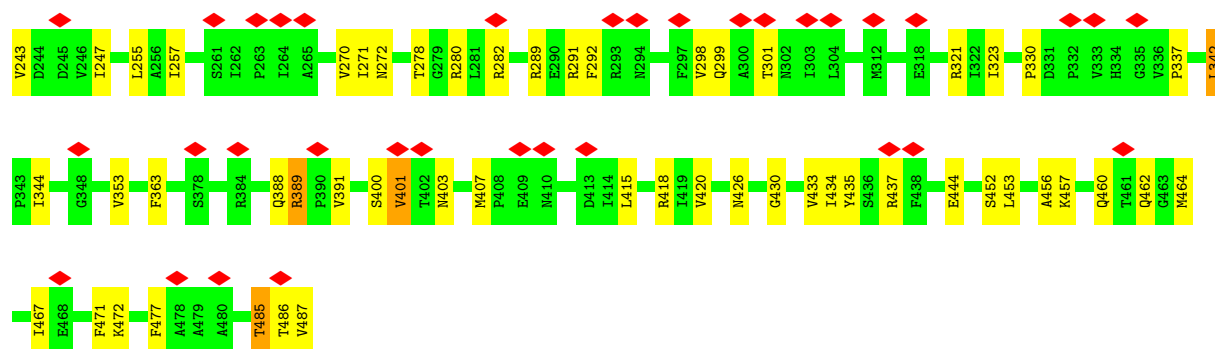
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: gp88

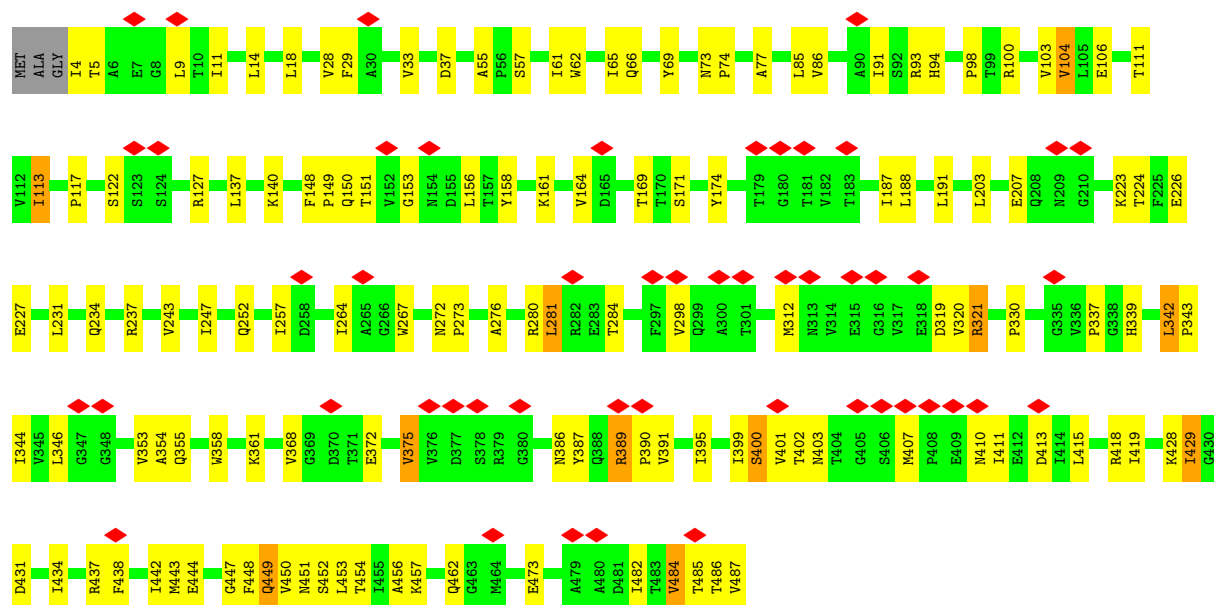


• Molecule 1: gp88

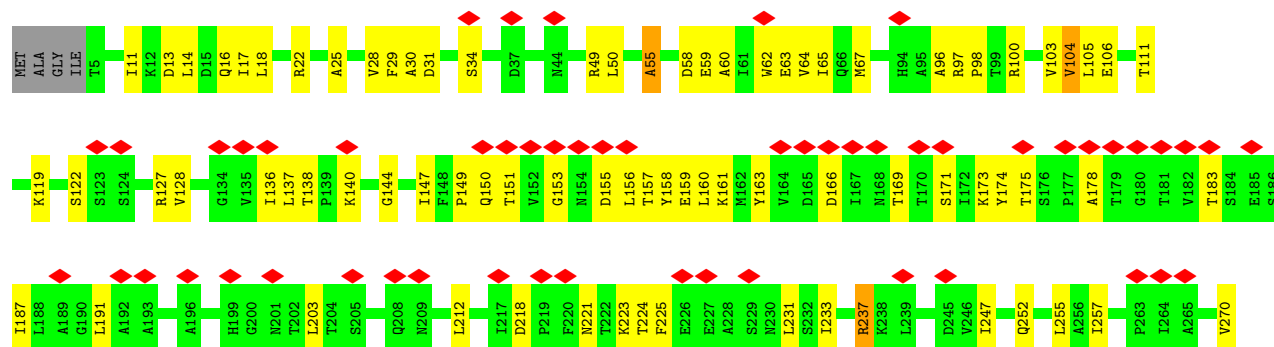


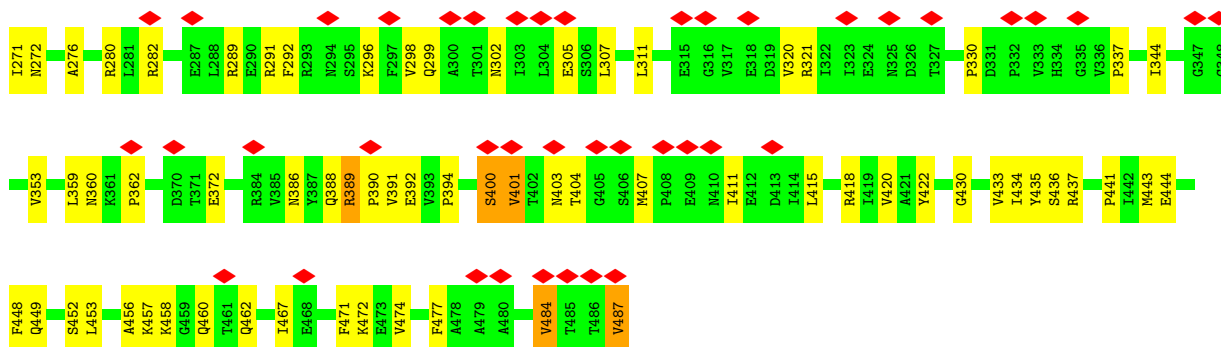


• Molecule 1: gp88



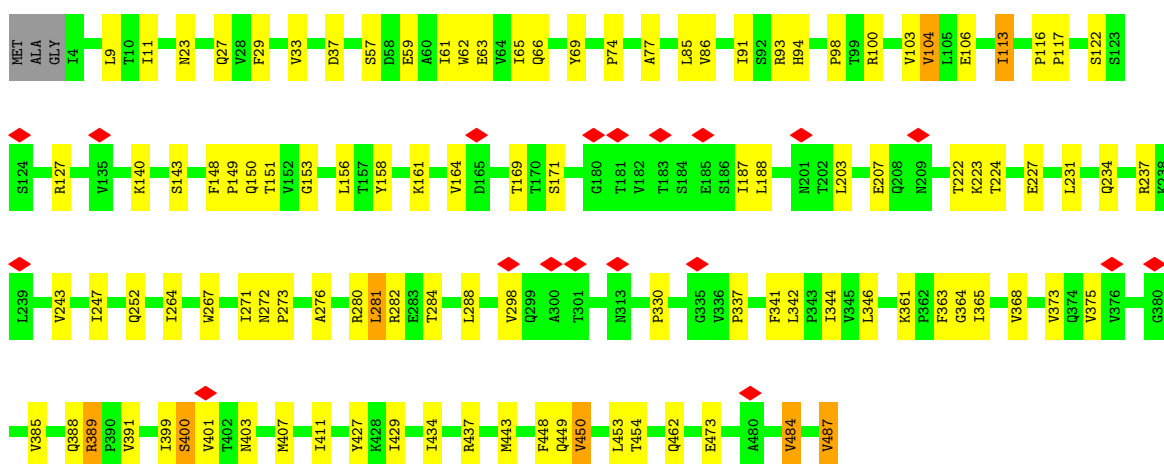
• Molecule 1: gp88





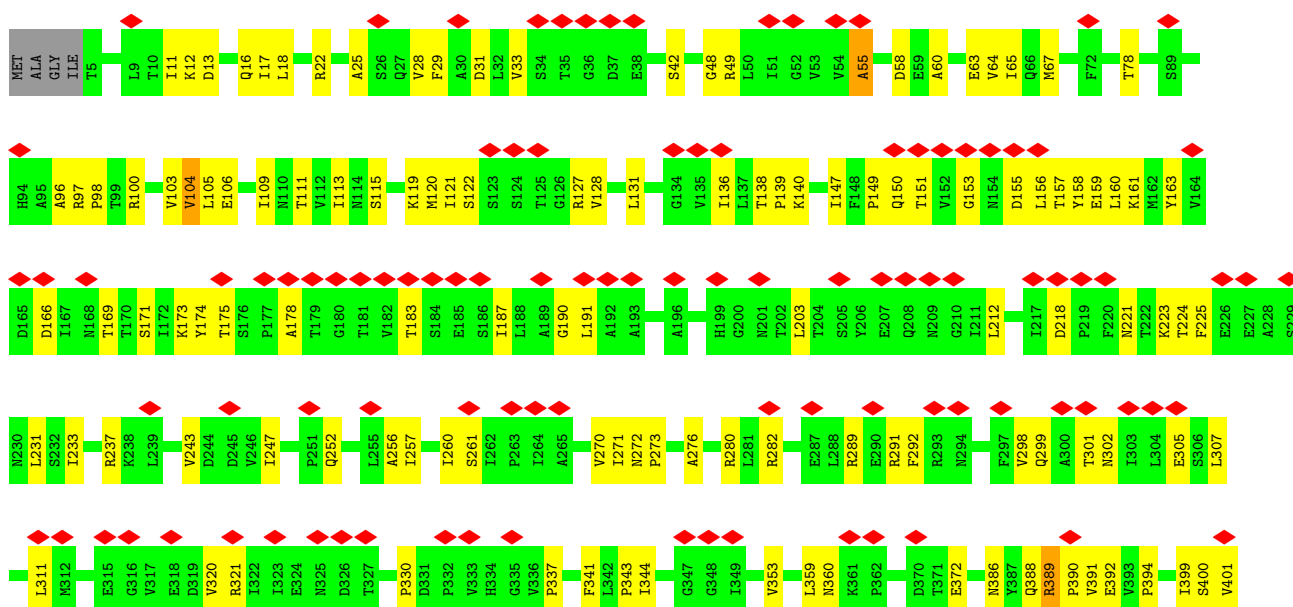
• Molecule 1: gp88

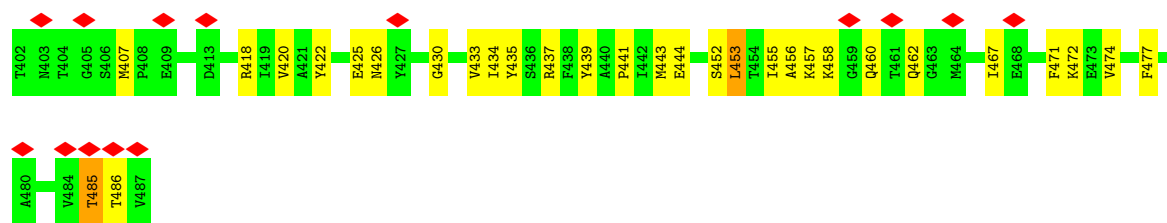
Chain G: 77% 21% ..



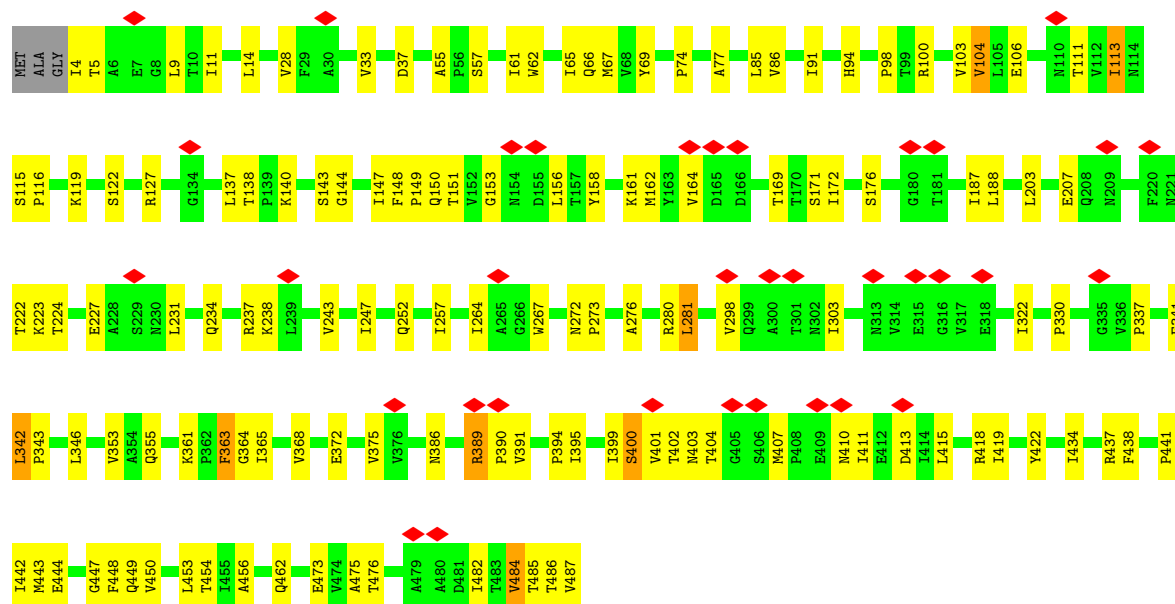
• Molecule 1: gp88

Chain H: 24% 67% 31% ..

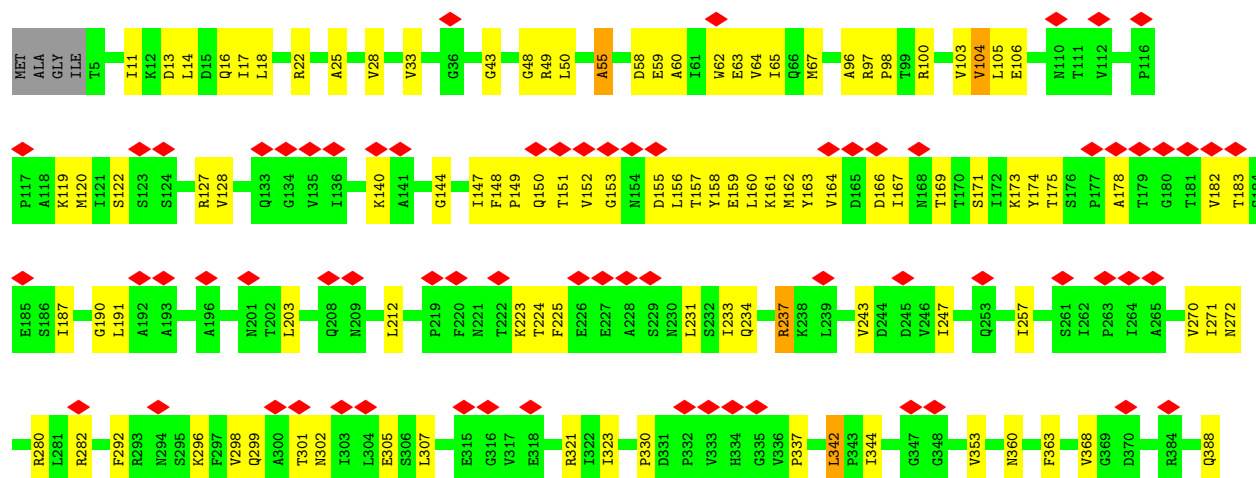


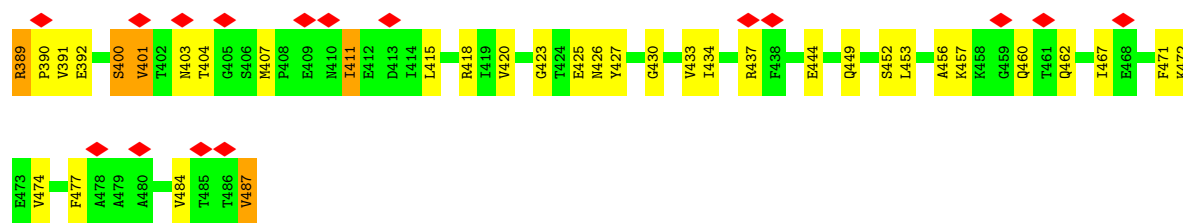


• Molecule 1: gp88

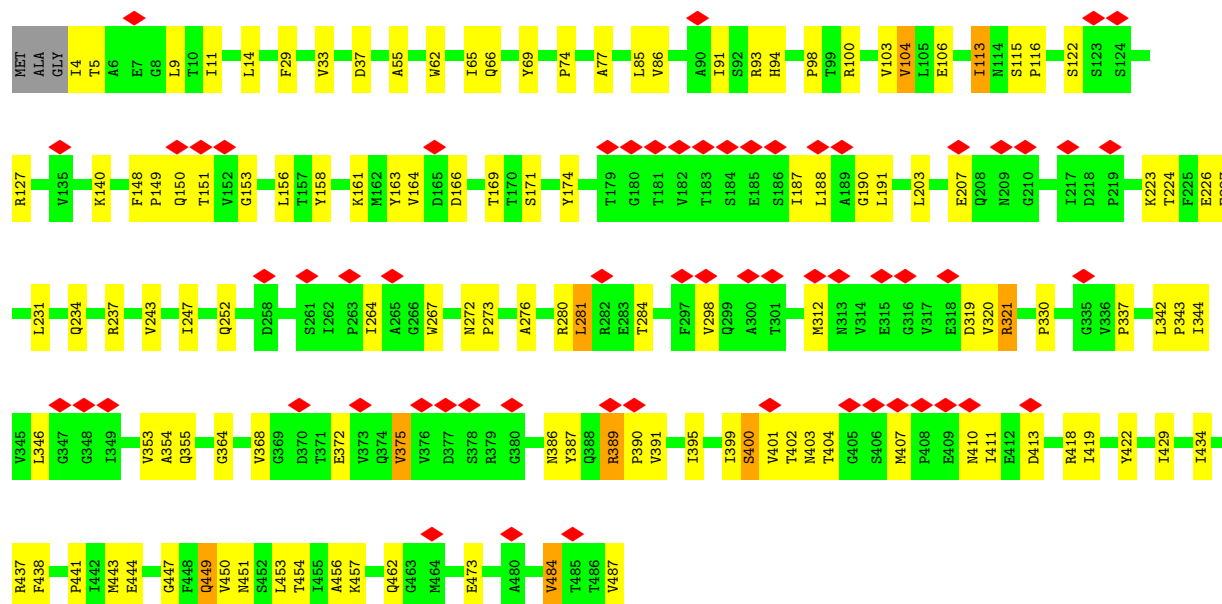
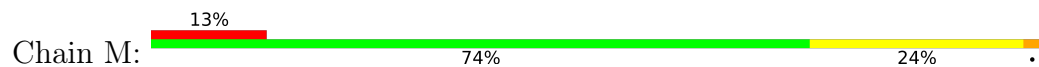


• Molecule 1: gp88

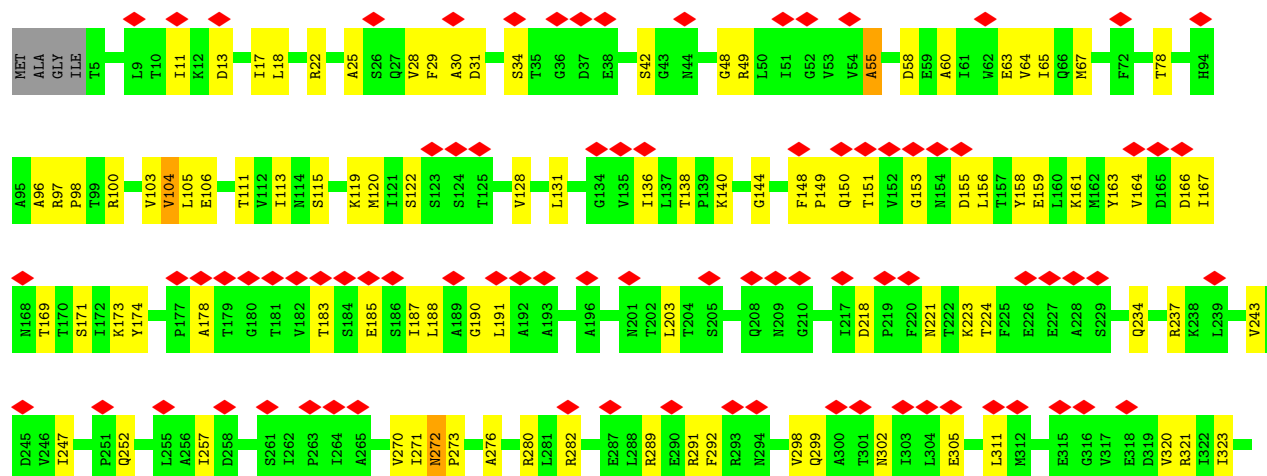


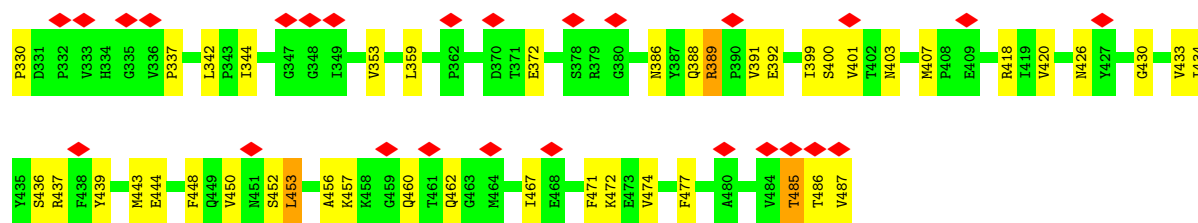


• Molecule 1: gp88

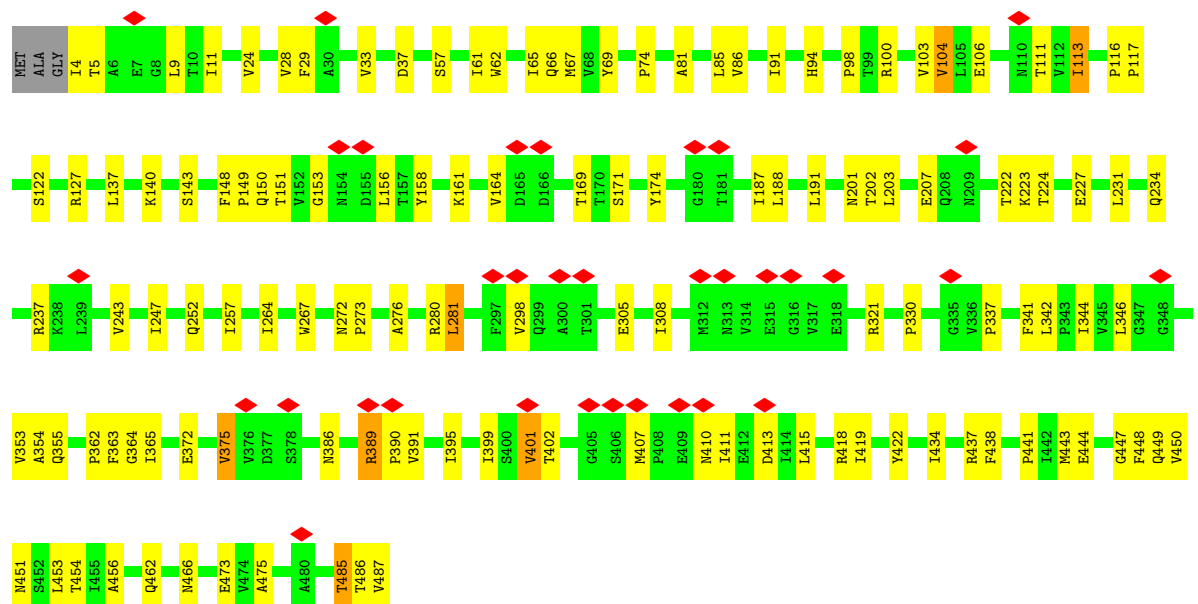
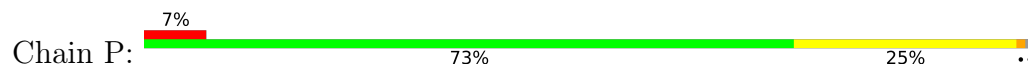


• Molecule 1: gp88

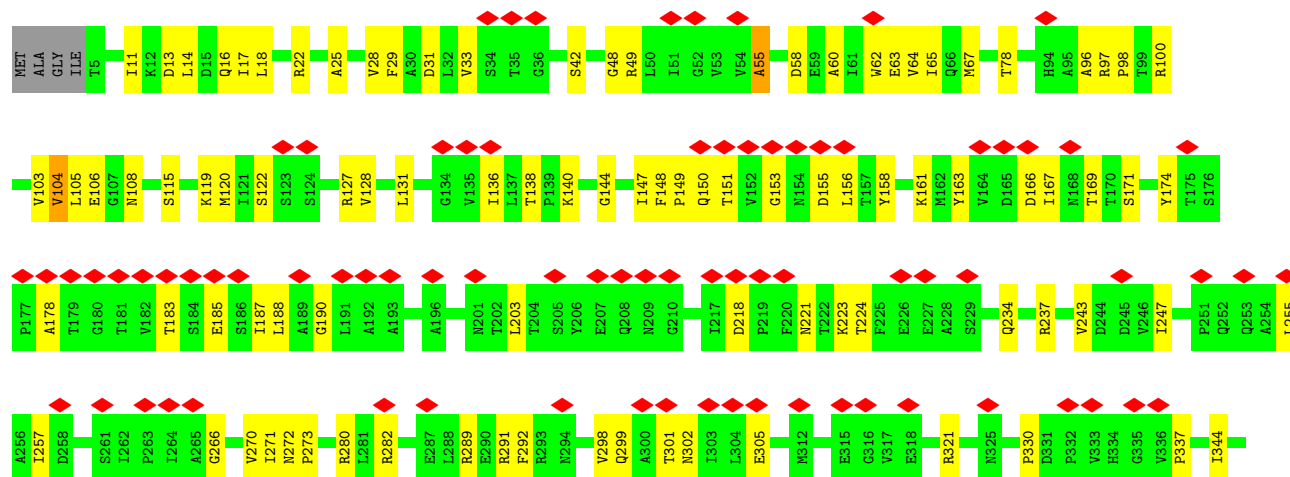


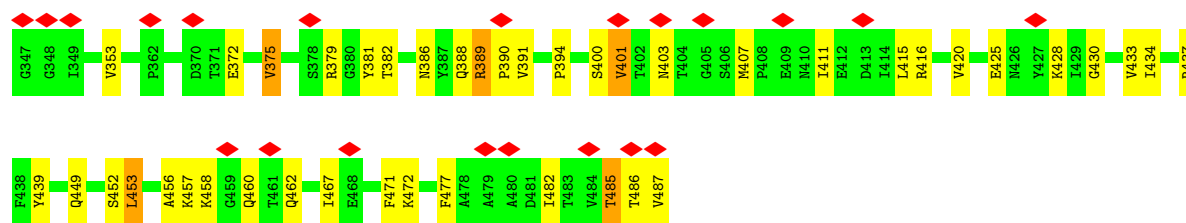


• Molecule 1: gp88

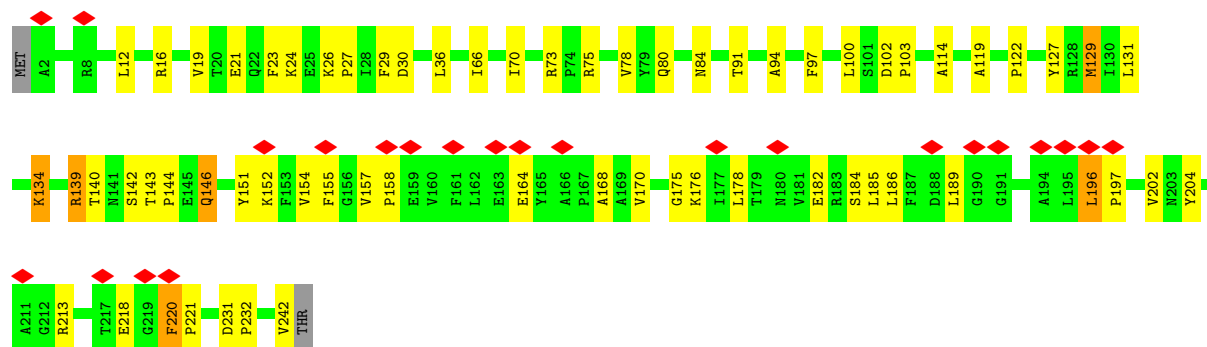
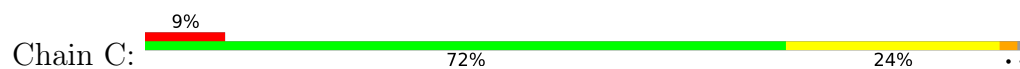


• Molecule 1: gp88

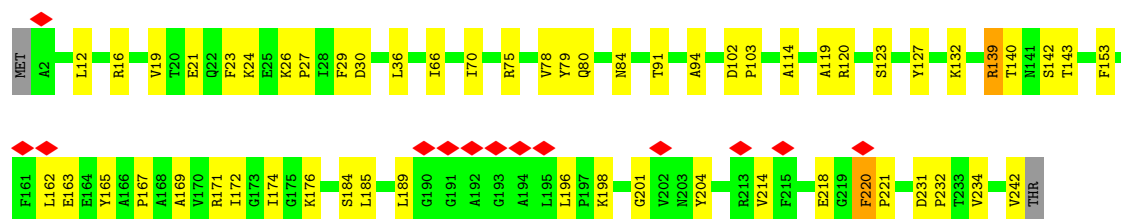
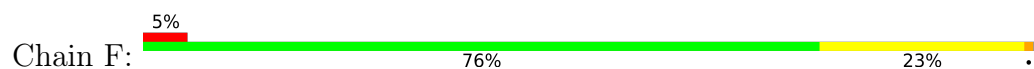




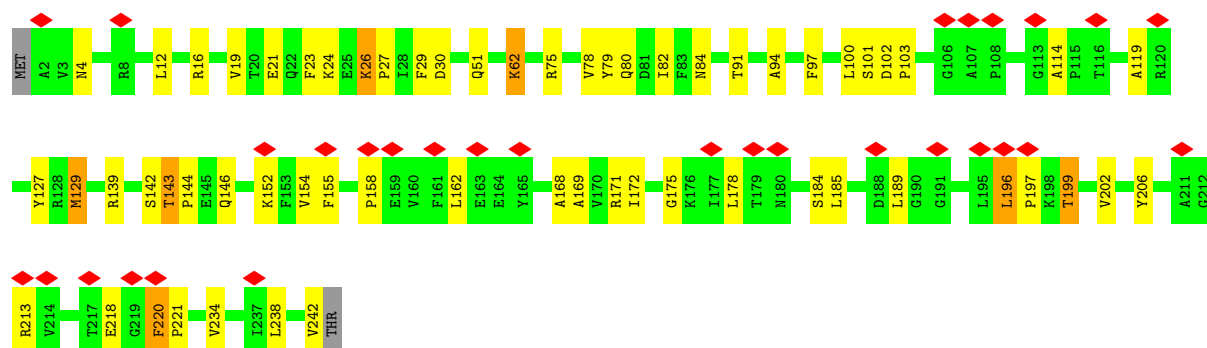
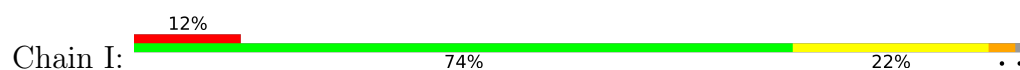
• Molecule 2: gp89




• Molecule 2: gp89

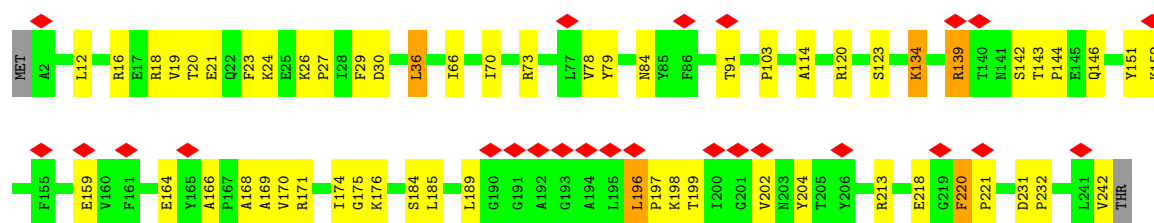


• Molecule 2: gp89




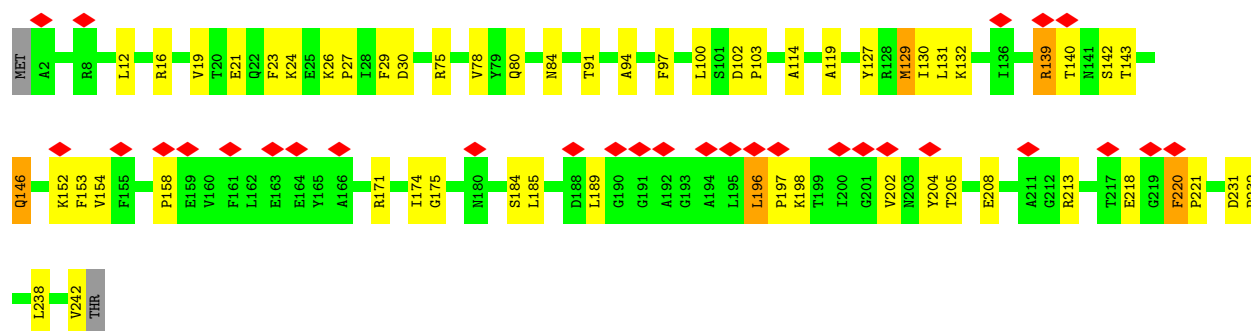
• Molecule 2: gp89

Chain L: 




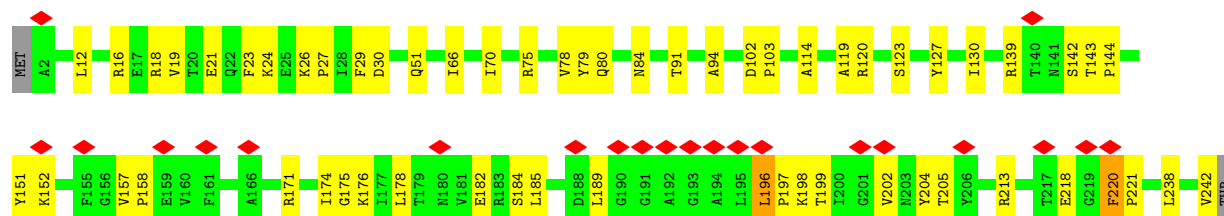
• Molecule 2: gp89

Chain O: 



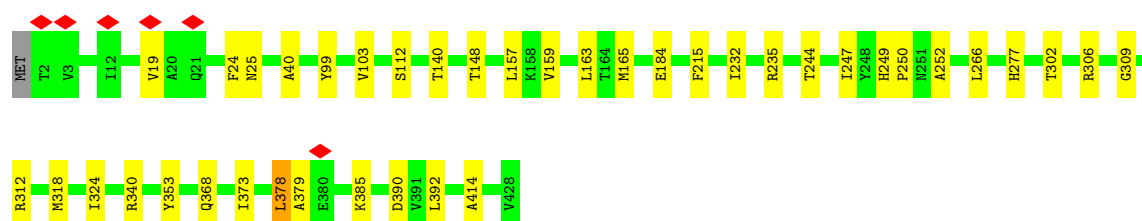
• Molecule 2: gp89

Chain R: 



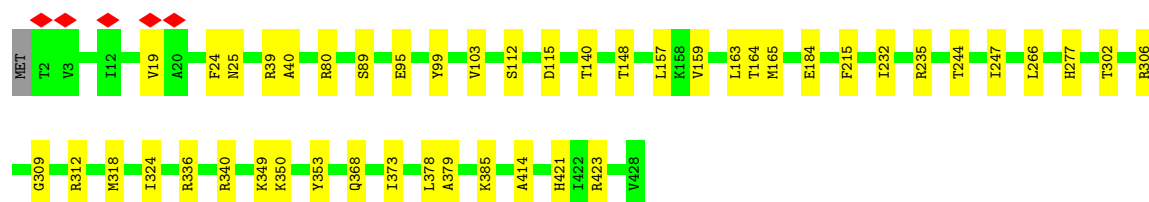
• Molecule 3: gp76

Chain S: 

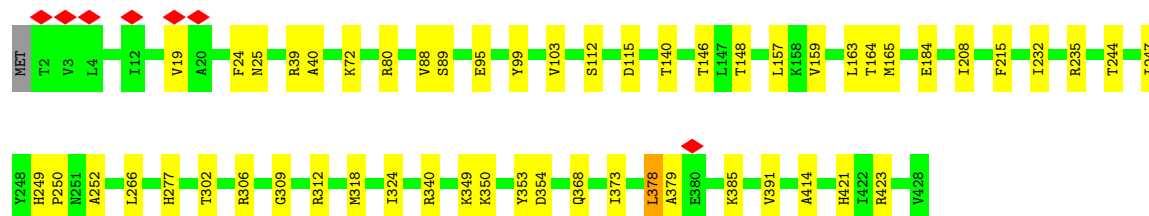


• Molecule 3: gp76

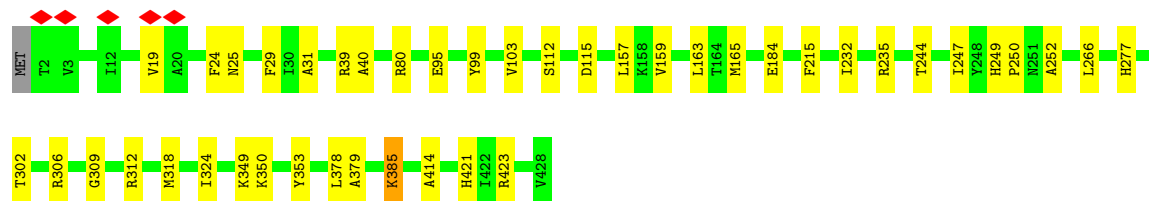
Chain T: 



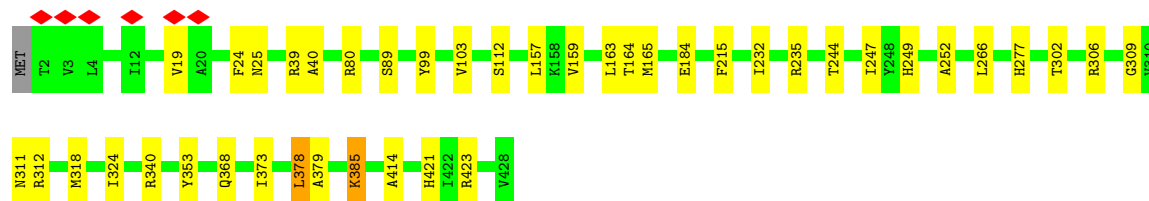
- Molecule 3: gp76



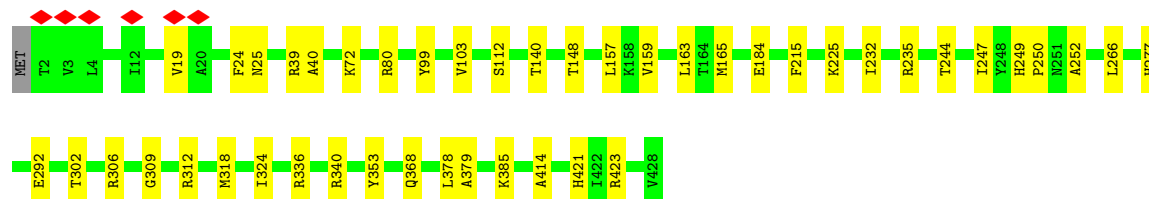
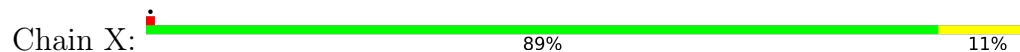
- Molecule 3: gp76



- Molecule 3: gp76



- Molecule 3: gp76



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7832	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.022	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00709	Depositor
Map size (Å)	563.2, 563.2, 563.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.13	0/3738	0.37	0/5105
1	B	0.15	0/3730	0.38	0/5094
1	D	0.13	0/3738	0.36	0/5105
1	E	0.14	0/3730	0.37	0/5094
1	G	0.13	0/3738	0.36	0/5105
1	H	0.14	0/3730	0.37	0/5094
1	J	0.13	0/3738	0.36	0/5105
1	K	0.14	0/3730	0.37	0/5094
1	M	0.13	0/3738	0.37	0/5105
1	N	0.14	0/3730	0.37	0/5094
1	P	0.13	0/3738	0.35	0/5105
1	Q	0.15	0/3730	0.38	0/5094
2	C	0.13	0/1909	0.37	0/2588
2	F	0.16	0/1909	0.39	0/2588
2	I	0.13	0/1909	0.37	0/2588
2	L	0.13	0/1909	0.37	0/2588
2	O	0.13	0/1909	0.38	0/2588
2	R	0.13	0/1909	0.36	0/2588
3	S	0.14	0/3323	0.34	0/4533
3	T	0.14	0/3323	0.34	0/4533
3	U	0.14	0/3323	0.34	0/4533
3	V	0.14	0/3323	0.34	0/4533
3	W	0.14	0/3323	0.34	0/4533
3	X	0.14	0/3323	0.34	0/4533
All	All	0.14	0/76200	0.36	0/103920

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3672	0	3670	76	0
1	B	3664	0	3659	79	0
1	D	3672	0	3670	84	0
1	E	3664	0	3659	94	0
1	G	3672	0	3670	72	0
1	H	3664	0	3659	94	0
1	J	3672	0	3670	84	0
1	K	3664	0	3659	86	0
1	M	3672	0	3670	79	0
1	N	3664	0	3659	86	0
1	P	3672	0	3670	80	0
1	Q	3664	0	3659	84	0
2	C	1871	0	1849	42	0
2	F	1871	0	1849	34	0
2	I	1871	0	1849	39	0
2	L	1871	0	1849	42	0
2	O	1871	0	1849	35	0
2	R	1871	0	1849	40	0
3	S	3257	0	3193	19	0
3	T	3257	0	3193	22	0
3	U	3257	0	3193	27	0
3	V	3257	0	3193	21	0
3	W	3257	0	3193	21	0
3	X	3257	0	3193	22	0
All	All	74784	0	74226	1322	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (1322) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:364:GLY:HA3	2:I:202:VAL:HG21	1.63	0.80
1:Q:457:LYS:HE3	1:Q:460:GLN:HG3	1.66	0.78
1:K:457:LYS:HE3	1:K:460:GLN:HG3	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:457:LYS:HE3	1:B:460:GLN:HG3	1.66	0.77
1:Q:55:ALA:HB3	1:Q:58:ASP:HB2	1.68	0.76
2:L:169:ALA:HB1	2:L:171:ARG:HH22	1.52	0.74
1:J:364:GLY:HA3	2:L:202:VAL:HG21	1.67	0.74
1:G:454:THR:HB	1:G:462:GLN:HB3	1.70	0.74
1:N:457:LYS:HE3	1:N:460:GLN:HG3	1.70	0.73
1:M:203:LEU:HD21	1:M:223:LYS:HD2	1.70	0.73
1:B:55:ALA:HB3	1:B:58:ASP:HB2	1.71	0.73
1:N:55:ALA:HB3	1:N:58:ASP:HB2	1.69	0.73
1:A:14:LEU:HD11	1:A:55:ALA:HB1	1.71	0.73
2:F:21:GLU:HA	2:F:24:LYS:HG2	1.70	0.73
1:G:403:ASN:H	1:G:487:VAL:HG13	1.54	0.72
3:S:99:TYR:HE2	3:S:112:SER:HB2	1.54	0.72
1:E:457:LYS:HE3	1:E:460:GLN:HG3	1.71	0.72
1:K:55:ALA:HB3	1:K:58:ASP:HB2	1.71	0.72
2:O:21:GLU:HA	2:O:24:LYS:HG2	1.71	0.72
1:G:33:VAL:HB	1:G:37:ASP:HB3	1.72	0.71
1:H:55:ALA:HB3	1:H:58:ASP:HB2	1.71	0.71
3:T:99:TYR:HE2	3:T:112:SER:HB2	1.56	0.71
1:E:30:ALA:HA	1:E:34:SER:HB2	1.73	0.70
1:H:344:ILE:HG12	1:H:388:GLN:HE21	1.56	0.70
1:A:454:THR:HB	1:A:462:GLN:HB3	1.73	0.70
1:M:4:ILE:HG13	1:M:5:THR:HG23	1.74	0.70
2:L:175:GLY:HA2	2:L:213:ARG:HH12	1.57	0.70
1:P:449:GLN:HB2	1:P:487:VAL:HG12	1.74	0.69
1:A:33:VAL:HB	1:A:37:ASP:HB3	1.74	0.69
1:N:353:VAL:HG21	1:N:389:ARG:HH22	1.58	0.69
1:E:55:ALA:HB3	1:E:58:ASP:HB2	1.75	0.69
1:P:454:THR:HB	1:P:462:GLN:HB3	1.74	0.69
1:H:400:SER:H	1:H:452:SER:HB2	1.57	0.69
1:D:203:LEU:HD21	1:D:223:LYS:HD2	1.76	0.68
3:X:379:ALA:HB2	3:X:414:ALA:HA	1.75	0.68
3:T:379:ALA:HB2	3:T:414:ALA:HA	1.76	0.68
1:H:457:LYS:HE3	1:H:460:GLN:HG3	1.74	0.68
2:R:21:GLU:HA	2:R:24:LYS:HG2	1.76	0.68
2:I:21:GLU:HA	2:I:24:LYS:HG2	1.74	0.68
1:K:353:VAL:HG21	1:K:389:ARG:HH22	1.58	0.67
1:B:426:ASN:HB3	1:B:437:ARG:HH12	1.59	0.67
1:J:106:GLU:HG2	1:J:237:ARG:HG2	1.75	0.67
1:M:174:TYR:HB3	1:M:191:LEU:HD23	1.76	0.67
1:N:344:ILE:HG12	1:N:388:GLN:HE21	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:X:99:TYR:HE2	3:X:112:SER:HB2	1.59	0.67
1:J:33:VAL:HB	1:J:37:ASP:HB3	1.76	0.67
1:P:33:VAL:HB	1:P:37:ASP:HB3	1.75	0.67
1:M:33:VAL:HB	1:M:37:ASP:HB3	1.77	0.67
1:Q:344:ILE:HG12	1:Q:388:GLN:HE21	1.60	0.66
1:D:161:LYS:HG2	1:D:171:SER:HB3	1.78	0.66
1:J:454:THR:HB	1:J:462:GLN:HB3	1.76	0.66
1:J:419:ILE:HG23	1:J:438:PHE:HZ	1.61	0.66
1:B:150:GLN:HG2	1:B:151:THR:HG23	1.78	0.66
1:M:153:GLY:HA3	1:M:156:LEU:HD12	1.78	0.66
2:C:21:GLU:HA	2:C:24:LYS:HG2	1.75	0.66
1:D:103:VAL:HG12	1:D:272:ASN:HB3	1.78	0.66
2:R:91:THR:H	2:R:103:PRO:HB2	1.61	0.65
1:D:454:THR:HB	1:D:462:GLN:HB3	1.77	0.65
2:F:198:LYS:HE3	2:F:204:TYR:H	1.62	0.65
1:D:4:ILE:HG13	1:D:5:THR:HG23	1.79	0.65
1:D:14:LEU:HD11	1:D:55:ALA:HB1	1.79	0.65
1:M:454:THR:HB	1:M:462:GLN:HB3	1.78	0.65
2:C:91:THR:H	2:C:103:PRO:HB2	1.62	0.65
1:M:103:VAL:HG12	1:M:272:ASN:HB3	1.78	0.65
1:P:4:ILE:HG13	1:P:5:THR:HG23	1.79	0.65
1:G:103:VAL:HG12	1:G:272:ASN:HB3	1.78	0.64
3:U:99:TYR:HE2	3:U:112:SER:HB2	1.62	0.64
3:W:99:TYR:HE2	3:W:112:SER:HB2	1.61	0.64
2:I:4:ASN:HD22	2:I:51:GLN:HG2	1.62	0.64
1:B:149:PRO:HA	1:B:231:LEU:HA	1.79	0.64
1:J:103:VAL:HG12	1:J:272:ASN:HB3	1.78	0.64
2:L:21:GLU:HA	2:L:24:LYS:HG2	1.78	0.64
1:G:93:ARG:HG3	1:G:288:LEU:HD21	1.80	0.64
1:J:363:PHE:HB2	2:L:199:THR:HG21	1.80	0.64
1:P:399:ILE:HD13	1:P:453:LEU:HD13	1.80	0.63
1:H:12:LYS:HE3	1:H:17:ILE:HG13	1.79	0.63
1:P:419:ILE:HG23	1:P:438:PHE:HZ	1.62	0.63
1:B:147:ILE:HB	1:B:231:LEU:HD21	1.80	0.63
1:H:150:GLN:HG2	1:H:151:THR:HG23	1.80	0.63
3:V:99:TYR:HE2	3:V:112:SER:HB2	1.64	0.63
1:M:419:ILE:HG23	1:M:438:PHE:HZ	1.62	0.63
3:U:373:ILE:HG12	3:U:378:LEU:HD11	1.80	0.63
1:P:103:VAL:HG12	1:P:272:ASN:HB3	1.80	0.63
1:P:363:PHE:HB2	2:R:199:THR:HG21	1.81	0.63
1:D:153:GLY:HA3	1:D:156:LEU:HD12	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:403:ASN:HD21	1:G:484:VAL:HG23	1.63	0.63
1:K:150:GLN:HG2	1:K:151:THR:HG23	1.81	0.63
1:M:161:LYS:HG2	1:M:171:SER:HB3	1.80	0.63
3:X:40:ALA:HB3	3:X:184:GLU:HG2	1.81	0.63
1:B:353:VAL:HG21	1:B:389:ARG:HH22	1.62	0.63
2:F:91:THR:H	2:F:103:PRO:HB2	1.64	0.62
1:H:434:ILE:HD13	1:H:437:ARG:HH21	1.63	0.62
1:E:50:LEU:HD11	2:F:36:LEU:HD21	1.81	0.62
2:L:220:PHE:H	2:L:221:PRO:HD2	1.64	0.62
1:A:103:VAL:HG12	1:A:272:ASN:HB3	1.80	0.62
1:H:11:ILE:HA	1:H:65:ILE:HD12	1.81	0.62
1:N:298:VAL:HG23	1:N:299:GLN:HG3	1.81	0.62
2:R:175:GLY:HA2	2:R:213:ARG:HH12	1.63	0.62
3:V:379:ALA:HB2	3:V:414:ALA:HA	1.82	0.62
1:E:362:PRO:HB3	2:F:201:GLY:HA2	1.82	0.62
1:B:401:VAL:HB	1:B:415:LEU:HD22	1.82	0.62
1:A:113:ILE:HG21	1:A:267:TRP:HB2	1.81	0.62
1:J:153:GLY:HA3	1:J:156:LEU:HD12	1.82	0.62
2:C:164:GLU:HA	2:C:170:VAL:HG22	1.81	0.62
1:D:419:ILE:HG23	1:D:438:PHE:HZ	1.65	0.61
1:J:4:ILE:HG13	1:J:5:THR:HG23	1.82	0.61
1:N:122:SER:HA	1:N:257:ILE:HA	1.82	0.61
1:E:403:ASN:HB2	1:E:487:VAL:HG13	1.81	0.61
2:L:91:THR:H	2:L:103:PRO:HB2	1.65	0.61
1:D:33:VAL:HB	1:D:37:ASP:HB3	1.82	0.61
1:D:252:GLN:HB2	1:D:276:ALA:HB3	1.82	0.61
3:S:373:ILE:HG12	3:S:378:LEU:HD11	1.81	0.61
1:A:4:ILE:HG13	1:A:5:THR:HG23	1.82	0.61
2:F:220:PHE:H	2:F:221:PRO:HD2	1.64	0.61
2:I:185:LEU:HA	2:I:189:LEU:HD22	1.82	0.61
2:O:91:THR:H	2:O:103:PRO:HB2	1.65	0.61
1:Q:161:LYS:HG2	1:Q:171:SER:HB3	1.82	0.61
2:C:175:GLY:HA2	2:C:213:ARG:HH12	1.65	0.61
2:I:91:THR:H	2:I:103:PRO:HB2	1.65	0.61
2:C:84:ASN:HB2	2:C:114:ALA:HA	1.83	0.60
2:I:84:ASN:HB2	2:I:114:ALA:HA	1.83	0.60
1:N:30:ALA:HA	1:N:34:SER:HB2	1.82	0.60
1:H:203:LEU:HD21	1:H:223:LYS:HD2	1.83	0.60
1:A:153:GLY:HA3	1:A:156:LEU:HD12	1.82	0.60
2:L:168:ALA:HA	2:L:202:VAL:HG22	1.83	0.60
1:Q:301:THR:HG23	2:R:142:SER:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:220:PHE:H	2:C:221:PRO:HD2	1.66	0.60
1:Q:401:VAL:HB	1:Q:415:LEU:HD22	1.83	0.60
1:A:122:SER:HB3	1:A:127:ARG:H	1.67	0.60
1:G:86:VAL:HB	1:G:91:ILE:HG13	1.83	0.60
1:E:401:VAL:HB	1:E:415:LEU:HD22	1.83	0.60
1:J:399:ILE:HD13	1:J:453:LEU:HD13	1.84	0.60
2:R:220:PHE:H	2:R:221:PRO:HD2	1.66	0.60
1:G:252:GLN:HB2	1:G:276:ALA:HB3	1.83	0.60
1:J:86:VAL:HB	1:J:91:ILE:HG13	1.83	0.60
1:N:321:ARG:HH12	1:N:471:PHE:HB2	1.66	0.60
1:Q:203:LEU:HD21	1:Q:223:LYS:HD2	1.84	0.60
1:A:140:LYS:HA	1:A:224:THR:HG23	1.84	0.60
1:K:403:ASN:HB2	1:K:487:VAL:HG13	1.84	0.60
1:N:400:SER:H	1:N:452:SER:HB2	1.67	0.60
3:S:379:ALA:HB2	3:S:414:ALA:HA	1.84	0.60
1:P:153:GLY:HA3	1:P:156:LEU:HD12	1.84	0.59
1:G:161:LYS:HG2	1:G:171:SER:HB3	1.84	0.59
1:M:252:GLN:HB2	1:M:276:ALA:HB3	1.84	0.59
2:O:220:PHE:H	2:O:221:PRO:HD2	1.67	0.59
2:R:185:LEU:HA	2:R:189:LEU:HD22	1.83	0.59
3:V:159:VAL:HB	3:V:163:LEU:HB2	1.84	0.59
1:B:140:LYS:HA	1:B:224:THR:HG23	1.83	0.59
1:Q:353:VAL:HG21	1:Q:389:ARG:HH22	1.67	0.59
1:D:11:ILE:HG21	1:D:66:GLN:HG2	1.85	0.59
2:O:84:ASN:HB2	2:O:114:ALA:HA	1.83	0.59
1:E:147:ILE:HB	1:E:231:LEU:HD21	1.84	0.59
1:G:122:SER:HB3	1:G:127:ARG:H	1.68	0.59
1:H:147:ILE:HB	1:H:231:LEU:HD21	1.85	0.59
1:B:344:ILE:HG12	1:B:388:GLN:HB2	1.84	0.59
1:E:150:GLN:HG2	1:E:151:THR:HG23	1.84	0.59
1:G:153:GLY:HA3	1:G:156:LEU:HD12	1.84	0.59
1:G:203:LEU:HD21	1:G:223:LYS:HD2	1.83	0.59
1:N:155:ASP:HB2	1:N:178:ALA:HB2	1.85	0.59
1:P:362:PRO:HA	2:R:144:PRO:HG2	1.84	0.59
1:H:302:ASN:HB3	1:H:305:GLU:HB2	1.85	0.59
1:K:401:VAL:HB	1:K:415:LEU:HD22	1.85	0.59
1:N:203:LEU:HD21	1:N:223:LYS:HD2	1.85	0.59
1:Q:400:SER:H	1:Q:452:SER:HB2	1.68	0.59
2:R:198:LYS:HE3	2:R:204:TYR:H	1.68	0.59
1:J:449:GLN:HB2	1:J:487:VAL:HG12	1.84	0.59
1:K:298:VAL:HG23	1:K:299:GLN:HG3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:185:LEU:HA	2:C:189:LEU:HD22	1.83	0.58
1:D:456:ALA:HB2	1:D:462:GLN:HA	1.85	0.58
1:H:104:VAL:HG13	1:H:271:ILE:HG13	1.83	0.58
1:J:122:SER:HB3	1:J:127:ARG:H	1.67	0.58
1:K:147:ILE:HB	1:K:231:LEU:HD21	1.83	0.58
1:H:161:LYS:HG2	1:H:171:SER:HB3	1.86	0.58
1:J:140:LYS:HA	1:J:224:THR:HG23	1.85	0.58
1:D:399:ILE:HD13	1:D:453:LEU:HD13	1.84	0.58
1:E:298:VAL:HG23	1:E:299:GLN:HG3	1.85	0.58
1:G:140:LYS:HA	1:G:224:THR:HG23	1.84	0.58
2:L:185:LEU:HA	2:L:189:LEU:HD22	1.85	0.58
1:B:103:VAL:HG12	1:B:272:ASN:HB3	1.85	0.58
1:K:149:PRO:HA	1:K:231:LEU:HA	1.85	0.58
1:M:372:GLU:HA	1:M:386:ASN:HB3	1.85	0.58
1:P:203:LEU:HD21	1:P:223:LYS:HD2	1.85	0.58
1:Q:155:ASP:HB2	1:Q:178:ALA:HB2	1.85	0.58
3:U:379:ALA:HB2	3:U:414:ALA:HA	1.85	0.58
1:A:399:ILE:HD13	1:A:453:LEU:HD13	1.85	0.58
3:S:277:HIS:HA	3:S:312:ARG:HB3	1.85	0.58
1:A:419:ILE:HG23	1:A:438:PHE:HZ	1.69	0.58
1:E:344:ILE:HG12	1:E:388:GLN:HB2	1.85	0.58
1:H:147:ILE:HD11	1:H:212:LEU:HD23	1.86	0.58
3:W:379:ALA:HB2	3:W:414:ALA:HA	1.84	0.58
1:E:353:VAL:HG21	1:E:389:ARG:HH22	1.68	0.58
1:H:155:ASP:HB2	1:H:178:ALA:HB2	1.85	0.58
1:M:353:VAL:HG21	1:M:389:ARG:HH22	1.69	0.58
1:N:161:LYS:HG2	1:N:171:SER:HB3	1.86	0.58
1:P:11:ILE:HG21	1:P:66:GLN:HG2	1.86	0.58
1:D:122:SER:HB3	1:D:127:ARG:H	1.69	0.58
1:G:330:PRO:HB3	1:G:337:PRO:HA	1.86	0.58
1:J:203:LEU:HD21	1:J:223:LYS:HD2	1.85	0.58
1:K:426:ASN:HB3	1:K:437:ARG:HH12	1.69	0.58
2:I:220:PHE:H	2:I:221:PRO:HD2	1.68	0.58
1:J:113:ILE:HG21	1:J:267:TRP:HB2	1.86	0.58
1:B:11:ILE:HA	1:B:65:ILE:HD12	1.86	0.57
1:J:11:ILE:HG21	1:J:66:GLN:HG2	1.86	0.57
1:P:113:ILE:HG21	1:P:267:TRP:HB2	1.85	0.57
1:Q:298:VAL:HG23	1:Q:299:GLN:HG3	1.86	0.57
3:U:40:ALA:HB3	3:U:184:GLU:HG2	1.86	0.57
1:G:391:VAL:HG12	1:G:473:GLU:HG3	1.87	0.57
1:M:150:GLN:HG2	1:M:151:THR:HG23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:LYS:HG2	1:A:171:SER:HB3	1.86	0.57
1:M:342:LEU:HD12	1:M:368:VAL:HG23	1.86	0.57
3:V:40:ALA:HB3	3:V:184:GLU:HG2	1.86	0.57
1:D:94:HIS:HD2	1:D:280:ARG:HG2	1.69	0.57
1:M:399:ILE:HD13	1:M:453:LEU:HD13	1.87	0.57
1:B:159:GLU:HA	1:B:173:LYS:HB3	1.87	0.57
1:P:161:LYS:HG2	1:P:171:SER:HB3	1.86	0.57
1:A:391:VAL:HG12	1:A:473:GLU:HG3	1.87	0.57
2:R:26:LYS:HB2	2:R:29:PHE:H	1.70	0.57
3:X:159:VAL:HB	3:X:163:LEU:HB2	1.87	0.57
1:G:113:ILE:HG21	1:G:267:TRP:HB2	1.86	0.57
1:H:353:VAL:HG21	1:H:389:ARG:HH22	1.70	0.57
1:N:433:VAL:HB	1:N:467:ILE:HB	1.87	0.57
1:P:402:THR:HG23	1:P:447:GLY:HA3	1.87	0.57
2:R:84:ASN:HB2	2:R:114:ALA:HA	1.87	0.57
3:X:277:HIS:HA	3:X:312:ARG:HB3	1.86	0.57
1:A:143:SER:HB2	1:A:222:THR:HG22	1.85	0.56
1:E:149:PRO:HA	1:E:231:LEU:HA	1.87	0.56
1:M:403:ASN:HD21	1:M:484:VAL:HG23	1.70	0.56
3:W:159:VAL:HB	3:W:163:LEU:HB2	1.87	0.56
1:D:140:LYS:HA	1:D:224:THR:HG23	1.86	0.56
1:H:159:GLU:HA	1:H:173:LYS:HB3	1.87	0.56
1:K:153:GLY:HA3	1:K:156:LEU:HD12	1.87	0.56
1:N:450:VAL:HG11	1:P:466:ASN:HD21	1.69	0.56
2:L:26:LYS:HB2	2:L:29:PHE:H	1.70	0.56
2:O:185:LEU:HA	2:O:189:LEU:HD22	1.85	0.56
1:P:122:SER:HB3	1:P:127:ARG:H	1.69	0.56
1:P:252:GLN:HB2	1:P:276:ALA:HB3	1.87	0.56
1:J:161:LYS:HG2	1:J:171:SER:HB3	1.86	0.56
1:K:400:SER:H	1:K:452:SER:HB2	1.71	0.56
1:P:140:LYS:HA	1:P:224:THR:HG23	1.86	0.56
1:B:434:ILE:HD13	1:B:437:ARG:HH21	1.70	0.56
1:G:399:ILE:HD13	1:G:453:LEU:HD13	1.88	0.56
1:K:344:ILE:HG12	1:K:388:GLN:HB2	1.86	0.56
3:T:277:HIS:HA	3:T:312:ARG:HB3	1.87	0.56
3:W:40:ALA:HB3	3:W:184:GLU:HG2	1.87	0.56
1:H:122:SER:HA	1:H:257:ILE:HA	1.87	0.56
1:A:11:ILE:HG21	1:A:66:GLN:HG2	1.88	0.56
1:K:155:ASP:HB2	1:K:178:ALA:HB2	1.88	0.56
1:E:103:VAL:HG12	1:E:272:ASN:HB3	1.88	0.56
1:E:161:LYS:HG2	1:E:171:SER:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:434:ILE:HD13	1:G:437:ARG:HH21	1.71	0.56
1:J:391:VAL:HG12	1:J:473:GLU:HG3	1.88	0.56
1:K:122:SER:HA	1:K:257:ILE:HA	1.88	0.56
1:P:330:PRO:HB3	1:P:337:PRO:HA	1.87	0.56
3:T:40:ALA:HB3	3:T:184:GLU:HG2	1.86	0.56
1:A:330:PRO:HB3	1:A:337:PRO:HA	1.88	0.56
1:D:174:TYR:HB3	1:D:191:LEU:HD23	1.88	0.56
1:K:159:GLU:HA	1:K:173:LYS:HB3	1.88	0.56
2:O:198:LYS:HE3	2:O:204:TYR:H	1.71	0.56
1:Q:321:ARG:HH12	1:Q:471:PHE:HB2	1.71	0.56
1:D:402:THR:HG23	1:D:447:GLY:HA3	1.88	0.56
1:H:103:VAL:HG12	1:H:272:ASN:HB3	1.88	0.56
1:A:252:GLN:HB2	1:A:276:ALA:HB3	1.88	0.55
1:N:104:VAL:HG13	1:N:271:ILE:HG13	1.88	0.55
3:S:159:VAL:HB	3:S:163:LEU:HB2	1.88	0.55
2:C:26:LYS:HB2	2:C:29:PHE:H	1.70	0.55
1:P:410:ASN:HB3	1:P:413:ASP:HB2	1.87	0.55
1:Q:122:SER:HA	1:Q:257:ILE:HA	1.88	0.55
1:A:104:VAL:HG13	1:A:271:ILE:HG13	1.87	0.55
1:E:122:SER:HA	1:E:257:ILE:HA	1.88	0.55
1:M:456:ALA:HB2	1:M:462:GLN:HA	1.87	0.55
1:P:391:VAL:HG12	1:P:473:GLU:HG3	1.88	0.55
3:V:277:HIS:HA	3:V:312:ARG:HB3	1.89	0.55
1:K:103:VAL:HG12	1:K:272:ASN:HB3	1.88	0.55
1:M:104:VAL:HG12	1:M:273:PRO:HD3	1.89	0.55
1:M:122:SER:HB3	1:M:127:ARG:H	1.71	0.55
1:E:147:ILE:HG22	1:E:233:ILE:HG12	1.88	0.55
1:H:104:VAL:HG12	1:H:273:PRO:HD3	1.89	0.55
1:M:113:ILE:HG21	1:M:267:TRP:HB2	1.89	0.55
1:E:96:ALA:HB2	1:E:282:ARG:HA	1.87	0.55
1:G:434:ILE:HG22	1:G:437:ARG:H	1.72	0.55
1:A:363:PHE:HB2	2:C:144:PRO:HB3	1.89	0.55
1:D:104:VAL:HG12	1:D:273:PRO:HD3	1.88	0.55
1:D:227:GLU:HB2	1:D:231:LEU:HB2	1.88	0.55
1:Q:163:TYR:HB3	1:Q:166:ASP:HA	1.89	0.55
1:H:439:TYR:HE1	1:H:453:LEU:HD21	1.72	0.55
1:M:140:LYS:HA	1:M:224:THR:HG23	1.87	0.55
3:S:249:HIS:HD1	3:S:250:PRO:HD2	1.72	0.55
3:U:249:HIS:HD1	3:U:250:PRO:HD2	1.72	0.55
1:D:312:MET:HE1	1:D:319:ASP:HA	1.88	0.54
1:G:11:ILE:HG21	1:G:66:GLN:HG2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:100:ARG:HA	1:M:100:ARG:HH11	1.73	0.54
1:D:94:HIS:CD2	1:D:280:ARG:HG2	2.42	0.54
1:M:346:LEU:HG	1:M:389:ARG:HG3	1.89	0.54
1:E:159:GLU:HA	1:E:173:LYS:HB3	1.88	0.54
1:J:143:SER:HB2	1:J:222:THR:HG22	1.89	0.54
1:P:94:HIS:HD2	1:P:280:ARG:HG2	1.72	0.54
1:P:106:GLU:HG2	1:P:237:ARG:HG2	1.87	0.54
1:Q:434:ILE:HD13	1:Q:437:ARG:HH21	1.71	0.54
1:B:161:LYS:HG2	1:B:171:SER:HB3	1.88	0.54
2:F:184:SER:HB3	2:F:189:LEU:HD13	1.89	0.54
1:G:143:SER:HB2	1:G:222:THR:HG22	1.88	0.54
1:K:96:ALA:HB2	1:K:282:ARG:HA	1.90	0.54
3:U:159:VAL:HB	3:U:163:LEU:HB2	1.88	0.54
1:N:149:PRO:HD3	1:N:188:LEU:HD21	1.90	0.54
1:B:96:ALA:HB2	1:B:282:ARG:HA	1.90	0.54
1:H:106:GLU:HG2	1:H:237:ARG:HG2	1.90	0.54
1:N:105:LEU:HB3	1:N:270:VAL:HG22	1.89	0.54
3:V:249:HIS:HD1	3:V:250:PRO:HD2	1.72	0.54
1:H:344:ILE:HG12	1:H:388:GLN:HB2	1.90	0.54
1:P:86:VAL:HB	1:P:91:ILE:HG13	1.90	0.54
1:Q:96:ALA:HB2	1:Q:282:ARG:HA	1.89	0.54
3:T:318:MET:HE2	3:T:324:ILE:HG23	1.90	0.54
1:B:122:SER:HB3	1:B:127:ARG:H	1.73	0.54
1:E:25:ALA:HA	1:E:28:VAL:HG13	1.90	0.54
2:I:169:ALA:HB1	2:I:171:ARG:HH12	1.73	0.54
2:L:84:ASN:HB2	2:L:114:ALA:HA	1.89	0.54
1:M:11:ILE:HG21	1:M:66:GLN:HG2	1.89	0.54
1:G:150:GLN:HG2	1:G:151:THR:HG23	1.88	0.54
1:G:342:LEU:HD12	1:G:368:VAL:HG23	1.89	0.54
1:H:149:PRO:HA	1:H:231:LEU:HA	1.89	0.54
3:V:249:HIS:HB3	3:V:252:ALA:HB2	1.90	0.54
1:B:122:SER:HA	1:B:257:ILE:HA	1.90	0.53
1:B:323:ILE:HB	1:B:342:LEU:HB3	1.89	0.53
2:O:26:LYS:HG2	2:O:30:ASP:HB2	1.90	0.53
1:D:449:GLN:HB2	1:D:487:VAL:HG12	1.90	0.53
2:I:196:LEU:HD22	2:I:197:PRO:HD2	1.89	0.53
1:M:94:HIS:HD2	1:M:280:ARG:HG2	1.73	0.53
1:N:103:VAL:HG12	1:N:272:ASN:HB3	1.89	0.53
1:Q:153:GLY:HA3	1:Q:156:LEU:HD12	1.90	0.53
2:F:185:LEU:HA	2:F:189:LEU:HD22	1.90	0.53
1:B:157:THR:HG22	1:B:175:THR:HA	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:372:GLU:HA	1:D:386:ASN:HB3	1.89	0.53
1:A:403:ASN:HD21	1:A:484:VAL:HG23	1.73	0.53
1:D:86:VAL:HB	1:D:91:ILE:HG13	1.91	0.53
1:B:147:ILE:HG22	1:B:233:ILE:HG12	1.90	0.53
1:D:346:LEU:HG	1:D:389:ARG:HG3	1.90	0.53
1:D:410:ASN:HB3	1:D:413:ASP:HB2	1.89	0.53
3:U:277:HIS:HA	3:U:312:ARG:HB3	1.89	0.53
1:B:106:GLU:HG2	1:B:237:ARG:HG2	1.91	0.53
1:E:449:GLN:HB3	1:E:487:VAL:HG12	1.91	0.53
2:F:84:ASN:HB2	2:F:114:ALA:HA	1.90	0.53
1:Q:106:GLU:HG2	1:Q:237:ARG:HG2	1.91	0.53
2:C:196:LEU:HD22	2:C:197:PRO:HD2	1.90	0.53
1:D:330:PRO:HB3	1:D:337:PRO:HA	1.89	0.53
1:N:163:TYR:HB3	1:N:166:ASP:HA	1.89	0.53
2:O:26:LYS:HB2	2:O:29:PHE:H	1.74	0.53
3:W:318:MET:HE2	3:W:324:ILE:HG23	1.90	0.53
2:F:139:ARG:HH22	2:F:142:SER:HA	1.73	0.53
1:J:252:GLN:HB2	1:J:276:ALA:HB3	1.90	0.53
2:L:198:LYS:HE3	2:L:204:TYR:H	1.74	0.53
1:B:420:VAL:HA	1:B:477:PHE:HD2	1.74	0.53
1:H:96:ALA:HB2	1:H:282:ARG:HA	1.91	0.53
1:H:140:LYS:HA	1:H:224:THR:HG23	1.90	0.53
1:H:153:GLY:HA3	1:H:156:LEU:HD12	1.89	0.53
1:H:321:ARG:HH12	1:H:471:PHE:HB2	1.74	0.53
1:J:280:ARG:HH11	1:J:281:LEU:H	1.56	0.53
1:J:415:LEU:HD11	1:J:442:ILE:HG12	1.89	0.53
1:D:391:VAL:HG12	1:D:473:GLU:HG3	1.91	0.52
1:G:227:GLU:HB2	1:G:231:LEU:HB2	1.91	0.52
1:J:330:PRO:HB3	1:J:337:PRO:HA	1.89	0.52
3:T:159:VAL:HB	3:T:163:LEU:HB2	1.90	0.52
1:E:104:VAL:HG13	1:E:271:ILE:HG13	1.91	0.52
1:N:153:GLY:HA3	1:N:156:LEU:HD12	1.91	0.52
3:X:249:HIS:HD1	3:X:250:PRO:HD2	1.74	0.52
1:A:280:ARG:HH11	1:A:281:LEU:H	1.56	0.52
1:H:298:VAL:HG23	1:H:299:GLN:HG3	1.90	0.52
1:A:203:LEU:HD21	1:A:223:LYS:HD2	1.90	0.52
1:N:344:ILE:HG12	1:N:388:GLN:HB2	1.91	0.52
1:Q:103:VAL:HG12	1:Q:272:ASN:HB3	1.91	0.52
1:A:322:ILE:HG12	1:A:343:PRO:HA	1.92	0.52
1:K:161:LYS:HG2	1:K:171:SER:HB3	1.91	0.52
1:A:150:GLN:HG2	1:A:151:THR:HG23	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:LEU:HD21	1:B:223:LYS:HD2	1.92	0.52
1:H:163:TYR:HB3	1:H:166:ASP:HA	1.91	0.52
1:Q:104:VAL:HG13	1:Q:271:ILE:HG13	1.92	0.52
1:Q:430:GLY:HA2	1:Q:471:PHE:HA	1.92	0.52
1:D:113:ILE:HG21	1:D:267:TRP:HB2	1.90	0.52
1:E:14:LEU:HB2	1:E:62:TRP:HZ2	1.75	0.52
1:E:330:PRO:HB3	1:E:337:PRO:HA	1.92	0.52
2:F:26:LYS:HG2	2:F:30:ASP:HB2	1.92	0.52
2:I:26:LYS:HG2	2:I:30:ASP:HB2	1.91	0.52
1:M:410:ASN:HB3	1:M:413:ASP:HB2	1.91	0.52
1:Q:149:PRO:HD3	1:Q:188:LEU:HD21	1.92	0.52
1:H:127:ARG:HH12	1:H:128:VAL:HG22	1.75	0.52
1:N:11:ILE:HA	1:N:65:ILE:HD12	1.92	0.52
1:D:100:ARG:HA	1:D:100:ARG:HH11	1.75	0.52
1:M:62:TRP:CE3	1:M:65:ILE:HD11	2.45	0.52
1:M:312:MET:HE1	1:M:319:ASP:HA	1.92	0.52
1:M:449:GLN:HG3	1:M:451:ASN:H	1.75	0.52
3:X:318:MET:HE2	3:X:324:ILE:HG23	1.91	0.52
1:A:227:GLU:HB2	1:A:231:LEU:HB2	1.92	0.52
1:E:163:TYR:HB3	1:E:166:ASP:HA	1.91	0.52
1:G:346:LEU:HA	1:G:389:ARG:HG3	1.92	0.52
1:G:427:TYR:HE1	1:G:437:ARG:HH22	1.56	0.52
1:P:62:TRP:CE3	1:P:65:ILE:HD11	2.45	0.52
1:E:430:GLY:HA2	1:E:471:PHE:HA	1.90	0.51
1:H:119:LYS:HD3	1:H:128:VAL:HB	1.92	0.51
1:B:155:ASP:HB2	1:B:178:ALA:HB2	1.92	0.51
1:J:410:ASN:HB3	1:J:413:ASP:HB2	1.91	0.51
1:K:14:LEU:HB2	1:K:62:TRP:HZ2	1.75	0.51
3:S:340:ARG:HH21	3:S:368:GLN:HB2	1.75	0.51
1:E:18:LEU:O	1:E:22:ARG:HG2	2.10	0.51
1:E:155:ASP:HB2	1:E:178:ALA:HB2	1.93	0.51
1:H:311:LEU:HD12	1:H:320:VAL:HG21	1.92	0.51
1:H:434:ILE:HG22	1:H:437:ARG:H	1.75	0.51
1:K:119:LYS:HD3	1:K:128:VAL:HB	1.93	0.51
1:M:94:HIS:CD2	1:M:280:ARG:HG2	2.45	0.51
1:M:391:VAL:HG12	1:M:473:GLU:HG3	1.92	0.51
1:N:106:GLU:HG2	1:N:237:ARG:HG2	1.93	0.51
1:A:86:VAL:HB	1:A:91:ILE:HG13	1.91	0.51
1:D:150:GLN:HG2	1:D:151:THR:HG23	1.92	0.51
1:D:312:MET:HE2	1:D:320:VAL:HG12	1.92	0.51
1:H:330:PRO:HB3	1:H:337:PRO:HA	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:140:LYS:HA	1:Q:224:THR:HG23	1.93	0.51
3:S:40:ALA:HB3	3:S:184:GLU:HG2	1.93	0.51
3:S:306:ARG:HE	3:S:309:GLY:C	2.19	0.51
1:K:100:ARG:HA	1:K:100:ARG:HH11	1.76	0.51
1:N:330:PRO:HB3	1:N:337:PRO:HA	1.92	0.51
1:P:280:ARG:HH11	1:P:281:LEU:H	1.57	0.51
1:P:354:ALA:HB1	1:P:375:VAL:HB	1.92	0.51
2:C:157:VAL:HG21	2:C:176:LYS:HD3	1.93	0.51
1:E:119:LYS:HD3	1:E:128:VAL:HB	1.93	0.51
1:K:122:SER:HB3	1:K:127:ARG:H	1.76	0.51
1:N:96:ALA:HB2	1:N:282:ARG:HA	1.92	0.51
1:Q:119:LYS:HD3	1:Q:128:VAL:HB	1.93	0.51
1:G:363:PHE:CG	2:I:144:PRO:HB3	2.46	0.51
1:P:150:GLN:HG2	1:P:151:THR:HG23	1.93	0.51
3:S:215:PHE:HD2	3:S:244:THR:HG23	1.75	0.51
1:A:106:GLU:HG2	1:A:237:ARG:HG2	1.93	0.51
1:B:78:THR:HG23	1:B:289:ARG:HH22	1.76	0.51
1:E:100:ARG:HH11	1:E:100:ARG:HA	1.76	0.51
1:E:140:LYS:HA	1:E:224:THR:HG23	1.92	0.51
1:K:147:ILE:HG22	1:K:233:ILE:HG12	1.93	0.51
1:M:264:ILE:HB	1:M:267:TRP:HB3	1.93	0.51
1:N:140:LYS:HA	1:N:224:THR:HG23	1.93	0.51
3:U:249:HIS:HB3	3:U:252:ALA:HB2	1.93	0.51
1:A:403:ASN:H	1:A:487:VAL:HG13	1.76	0.51
1:A:449:GLN:HB2	1:A:487:VAL:HG12	1.92	0.51
1:B:119:LYS:HD3	1:B:128:VAL:HB	1.93	0.51
1:G:400:SER:HB2	1:G:449:GLN:NE2	2.26	0.51
3:W:277:HIS:HA	3:W:312:ARG:HB3	1.92	0.51
1:G:449:GLN:HB2	1:G:487:VAL:HG12	1.93	0.51
1:M:149:PRO:HD3	1:M:188:LEU:HD21	1.93	0.51
3:T:215:PHE:HD2	3:T:244:THR:HG23	1.76	0.51
1:B:485:THR:HG22	1:B:486:THR:H	1.76	0.50
1:H:372:GLU:HA	1:H:386:ASN:HB3	1.93	0.50
1:N:485:THR:HG22	1:N:486:THR:H	1.76	0.50
1:Q:104:VAL:HG12	1:Q:273:PRO:HD3	1.92	0.50
3:T:157:LEU:HD23	3:T:165:MET:HE3	1.93	0.50
1:E:153:GLY:HA3	1:E:156:LEU:HD12	1.92	0.50
1:K:18:LEU:O	1:K:22:ARG:HG2	2.11	0.50
1:M:106:GLU:HG2	1:M:237:ARG:HG2	1.92	0.50
3:S:318:MET:HE2	3:S:324:ILE:HG23	1.91	0.50
1:A:342:LEU:HD12	1:A:368:VAL:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:62:TRP:CE3	1:D:65:ILE:HD11	2.45	0.50
1:D:280:ARG:HH11	1:D:281:LEU:H	1.59	0.50
1:E:400:SER:H	1:E:452:SER:HB2	1.76	0.50
1:J:353:VAL:HG21	1:J:389:ARG:HH22	1.76	0.50
1:M:330:PRO:HB3	1:M:337:PRO:HA	1.93	0.50
1:N:100:ARG:HA	1:N:100:ARG:HH11	1.75	0.50
1:P:264:ILE:HB	1:P:267:TRP:HB3	1.93	0.50
1:Q:18:LEU:O	1:Q:22:ARG:HG2	2.11	0.50
1:B:301:THR:HG23	2:C:142:SER:HB3	1.92	0.50
2:F:162:LEU:HG	2:F:172:ILE:HG12	1.93	0.50
1:H:100:ARG:HA	1:H:100:ARG:HH11	1.76	0.50
2:I:143:THR:HG23	2:I:146:GLN:HB2	1.93	0.50
1:K:420:VAL:HA	1:K:477:PHE:HD2	1.77	0.50
2:L:26:LYS:HG2	2:L:30:ASP:HB2	1.93	0.50
2:L:139:ARG:HE	2:L:146:GLN:HG3	1.77	0.50
1:M:29:PHE:CE1	1:N:49:ARG:HG3	2.46	0.50
2:O:171:ARG:HD3	2:O:205:THR:HB	1.94	0.50
1:K:163:TYR:HB3	1:K:166:ASP:HA	1.93	0.50
1:B:14:LEU:HB2	1:B:62:TRP:HZ2	1.77	0.50
1:G:62:TRP:CE3	1:G:65:ILE:HD11	2.46	0.50
1:N:420:VAL:HA	1:N:477:PHE:HD2	1.77	0.50
1:N:426:ASN:HB3	1:N:437:ARG:HH12	1.76	0.50
1:P:29:PHE:CE1	1:Q:49:ARG:HG3	2.47	0.50
1:Q:420:VAL:HA	1:Q:477:PHE:HD2	1.76	0.50
2:R:196:LEU:HD22	2:R:197:PRO:HD2	1.94	0.50
1:E:105:LEU:HB3	1:E:270:VAL:HG22	1.92	0.50
1:H:256:ALA:H	1:H:272:ASN:HD21	1.60	0.50
1:J:62:TRP:CE3	1:J:65:ILE:HD11	2.46	0.50
1:J:138:THR:H	1:J:238:LYS:HE3	1.76	0.50
1:Q:485:THR:HG22	1:Q:486:THR:H	1.77	0.50
1:B:153:GLY:HA3	1:B:156:LEU:HD12	1.92	0.50
2:C:80:GLN:HB2	2:C:119:ALA:HB2	1.93	0.50
1:K:147:ILE:HD11	1:K:212:LEU:HD23	1.92	0.50
1:K:152:VAL:HB	1:K:182:VAL:HG23	1.92	0.50
1:K:174:TYR:CZ	1:K:190:GLY:HA3	2.47	0.50
1:Q:100:ARG:HH11	1:Q:100:ARG:HA	1.76	0.50
1:Q:122:SER:HB3	1:Q:127:ARG:H	1.77	0.50
2:C:26:LYS:HG2	2:C:30:ASP:HB2	1.93	0.50
1:E:437:ARG:HG2	1:G:448:PHE:CD2	2.47	0.50
1:G:106:GLU:HG2	1:G:237:ARG:HG2	1.93	0.50
1:H:485:THR:HG22	1:H:486:THR:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:400:SER:HB2	1:M:449:GLN:NE2	2.26	0.50
1:P:401:VAL:HB	1:P:415:LEU:HD22	1.93	0.50
3:V:306:ARG:HE	3:V:309:GLY:C	2.19	0.50
1:A:62:TRP:CE3	1:A:65:ILE:HD11	2.47	0.49
1:B:174:TYR:CZ	1:B:190:GLY:HA3	2.47	0.49
1:G:373:VAL:HG23	1:G:385:VAL:HG23	1.94	0.49
2:R:26:LYS:HG2	2:R:30:ASP:HB2	1.94	0.49
2:R:184:SER:HB3	2:R:189:LEU:HD13	1.94	0.49
3:U:318:MET:HE2	3:U:324:ILE:HG23	1.94	0.49
1:B:98:PRO:HB3	1:B:247:ILE:HD13	1.93	0.49
1:E:434:ILE:HD13	1:E:437:ARG:HE	1.77	0.49
1:G:104:VAL:HG12	1:G:273:PRO:HD3	1.94	0.49
3:V:215:PHE:HD2	3:V:244:THR:HG23	1.77	0.49
1:D:358:TRP:HE3	1:D:361:LYS:HD3	1.77	0.49
1:E:218:ASP:HB3	1:E:221:ASN:ND2	2.26	0.49
1:E:420:VAL:HA	1:E:477:PHE:HD2	1.76	0.49
1:K:174:TYR:HB3	1:K:191:LEU:HD23	1.94	0.49
1:N:18:LEU:O	1:N:22:ARG:HG2	2.13	0.49
1:N:119:LYS:HD3	1:N:128:VAL:HB	1.94	0.49
1:D:149:PRO:HD3	1:D:188:LEU:HD21	1.95	0.49
1:E:157:THR:HG22	1:E:175:THR:HA	1.94	0.49
1:P:364:GLY:HA3	2:R:202:VAL:HG21	1.94	0.49
3:X:306:ARG:HE	3:X:309:GLY:C	2.20	0.49
1:B:298:VAL:HG23	1:B:299:GLN:HG3	1.92	0.49
1:H:13:ASP:HB3	1:H:16:GLN:HG3	1.94	0.49
1:K:292:PHE:O	1:K:296:LYS:HG2	2.12	0.49
1:E:147:ILE:HD11	1:E:212:LEU:HD23	1.94	0.49
1:K:430:GLY:HA2	1:K:471:PHE:HA	1.95	0.49
1:Q:375:VAL:O	1:Q:382:THR:HA	2.13	0.49
1:D:353:VAL:HG21	1:D:389:ARG:HH22	1.77	0.49
1:D:485:THR:HG22	1:D:486:THR:HG22	1.95	0.49
1:E:449:GLN:HE21	1:E:452:SER:H	1.61	0.49
1:M:402:THR:HG23	1:M:447:GLY:HA3	1.95	0.49
1:N:63:GLU:HB3	1:N:67:MET:HE2	1.94	0.49
1:N:323:ILE:HB	1:N:342:LEU:HB3	1.93	0.49
3:U:232:ILE:HA	3:U:235:ARG:HD3	1.95	0.49
3:U:306:ARG:HE	3:U:309:GLY:C	2.20	0.49
3:V:157:LEU:HD23	3:V:165:MET:HE3	1.95	0.49
3:V:318:MET:HE2	3:V:324:ILE:HG23	1.94	0.49
3:W:232:ILE:HA	3:W:235:ARG:HD3	1.95	0.49
3:W:249:HIS:HB3	3:W:252:ALA:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:W:340:ARG:HH21	3:W:368:GLN:HB2	1.78	0.49
1:A:164:VAL:HA	1:A:223:LYS:HB2	1.95	0.49
1:A:427:TYR:HE1	1:A:437:ARG:HH22	1.61	0.49
1:E:203:LEU:HD21	1:E:223:LYS:HD2	1.95	0.49
1:E:344:ILE:HG12	1:E:388:GLN:HE21	1.77	0.49
1:G:280:ARG:HH11	1:G:281:LEU:H	1.61	0.49
1:M:227:GLU:HB2	1:M:231:LEU:HB2	1.93	0.49
2:O:139:ARG:HE	2:O:146:GLN:HG3	1.77	0.49
1:P:143:SER:HB2	1:P:222:THR:HG22	1.95	0.49
1:Q:330:PRO:HB3	1:Q:337:PRO:HA	1.93	0.49
1:Q:344:ILE:HG12	1:Q:388:GLN:HB2	1.93	0.49
3:T:247:ILE:HG13	3:T:302:THR:HB	1.95	0.49
1:N:430:GLY:HA2	1:N:471:PHE:HA	1.94	0.49
1:B:218:ASP:HB3	1:B:221:ASN:ND2	2.28	0.49
1:E:433:VAL:HB	1:E:467:ILE:HB	1.94	0.49
1:G:113:ILE:HG22	1:G:264:ILE:HG21	1.94	0.49
1:H:63:GLU:O	1:H:67:MET:HG2	2.13	0.49
2:L:184:SER:HB3	2:L:189:LEU:HD13	1.94	0.49
1:N:104:VAL:HG12	1:N:273:PRO:HD3	1.93	0.49
3:X:249:HIS:HB3	3:X:252:ALA:HB2	1.95	0.49
1:A:400:SER:HB2	1:A:449:GLN:NE2	2.28	0.48
3:S:247:ILE:HG13	3:S:302:THR:HB	1.94	0.48
1:B:148:PHE:HB3	1:B:234:GLN:HE22	1.79	0.48
1:B:330:PRO:HB3	1:B:337:PRO:HA	1.94	0.48
1:J:322:ILE:HG12	1:J:343:PRO:HA	1.95	0.48
1:K:63:GLU:O	1:K:67:MET:HG2	2.12	0.48
1:K:157:THR:HG22	1:K:175:THR:HA	1.94	0.48
1:M:312:MET:HE2	1:M:320:VAL:HG12	1.95	0.48
1:Q:379:ARG:HG3	1:Q:381:TYR:HD1	1.78	0.48
2:F:26:LYS:HB2	2:F:29:PHE:H	1.77	0.48
2:F:132:LYS:HD3	2:F:153:PHE:HZ	1.78	0.48
1:G:363:PHE:HB2	2:I:199:THR:HG21	1.95	0.48
1:H:218:ASP:HB3	1:H:221:ASN:ND2	2.29	0.48
2:L:78:VAL:HB	2:L:189:LEU:HG	1.96	0.48
2:O:80:GLN:HB2	2:O:119:ALA:HB2	1.95	0.48
3:S:157:LEU:HD23	3:S:165:MET:HE3	1.95	0.48
3:W:215:PHE:HD2	3:W:244:THR:HG23	1.78	0.48
3:X:25:ASN:HA	3:X:266:LEU:HG	1.94	0.48
3:X:215:PHE:HD2	3:X:244:THR:HG23	1.78	0.48
3:X:247:ILE:HG13	3:X:302:THR:HB	1.95	0.48
1:H:174:TYR:HB3	1:H:191:LEU:HD23	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:164:GLU:HG2	2:L:170:VAL:HG22	1.95	0.48
2:O:196:LEU:HD22	2:O:197:PRO:HD2	1.94	0.48
1:B:63:GLU:O	1:B:67:MET:HG2	2.13	0.48
1:B:147:ILE:HG13	1:B:212:LEU:O	2.13	0.48
2:F:169:ALA:HB1	2:F:171:ARG:HH22	1.78	0.48
1:J:164:VAL:HA	1:J:223:LYS:HB2	1.96	0.48
1:K:144:GLY:HA3	1:K:237:ARG:HD3	1.95	0.48
1:G:93:ARG:HH21	1:G:284:THR:HA	1.78	0.48
1:Q:63:GLU:O	1:Q:67:MET:HG2	2.14	0.48
1:A:149:PRO:HD3	1:A:188:LEU:HD21	1.96	0.48
1:B:418:ARG:HH11	1:B:444:GLU:HB2	1.78	0.48
1:H:430:GLY:HA2	1:H:471:PHE:HA	1.96	0.48
1:M:86:VAL:HB	1:M:91:ILE:HG13	1.95	0.48
3:U:215:PHE:HD2	3:U:244:THR:HG23	1.77	0.48
1:A:434:ILE:HG22	1:A:437:ARG:H	1.78	0.48
1:D:400:SER:HB2	1:D:449:GLN:NE2	2.29	0.48
1:D:418:ARG:NH1	1:D:444:GLU:HB2	2.28	0.48
1:E:434:ILE:HG22	1:E:437:ARG:H	1.78	0.48
2:F:120:ARG:HH22	2:F:123:SER:HB3	1.79	0.48
1:G:149:PRO:HD3	1:G:188:LEU:HD21	1.94	0.48
3:T:306:ARG:HE	3:T:309:GLY:C	2.22	0.48
1:J:149:PRO:HD3	1:J:188:LEU:HD21	1.96	0.48
1:K:434:ILE:HD13	1:K:437:ARG:HE	1.79	0.48
1:N:63:GLU:O	1:N:67:MET:HG2	2.13	0.48
1:P:149:PRO:HD3	1:P:188:LEU:HD21	1.96	0.48
1:Q:25:ALA:HA	1:Q:28:VAL:HG13	1.95	0.48
1:E:63:GLU:O	1:E:67:MET:HG2	2.13	0.48
1:E:144:GLY:HA3	1:E:237:ARG:HD3	1.96	0.48
2:I:152:LYS:HD2	2:I:158:PRO:HA	1.96	0.48
1:K:301:THR:HG23	2:L:142:SER:HB3	1.96	0.48
2:L:73:ARG:HB2	2:L:134:LYS:HG2	1.96	0.48
1:M:98:PRO:HB3	1:M:247:ILE:HD13	1.96	0.48
1:M:403:ASN:H	1:M:487:VAL:HG13	1.78	0.48
1:N:391:VAL:HG11	1:N:472:LYS:HD3	1.96	0.48
1:P:104:VAL:HG12	1:P:273:PRO:HD3	1.96	0.48
1:B:13:ASP:O	1:B:17:ILE:HG12	2.14	0.47
1:H:29:PHE:HE2	1:H:31:ASP:HB2	1.79	0.47
2:L:120:ARG:HH22	2:L:123:SER:HB3	1.79	0.47
1:M:418:ARG:NH1	1:M:444:GLU:HB2	2.29	0.47
1:N:311:LEU:HD12	1:N:320:VAL:HG21	1.96	0.47
1:N:439:TYR:HE1	1:N:453:LEU:HD21	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:LEU:O	1:B:22:ARG:HG2	2.13	0.47
1:E:302:ASN:HB3	1:E:305:GLU:HB2	1.96	0.47
1:G:403:ASN:HD22	1:G:449:GLN:HE22	1.62	0.47
1:H:105:LEU:HB3	1:H:270:VAL:HG22	1.96	0.47
1:H:420:VAL:HA	1:H:477:PHE:HD2	1.78	0.47
2:I:238:LEU:H	2:I:238:LEU:HD23	1.78	0.47
1:K:98:PRO:HB3	1:K:247:ILE:HD13	1.96	0.47
1:K:140:LYS:HA	1:K:224:THR:HG23	1.96	0.47
1:K:434:ILE:HD13	1:K:437:ARG:HH21	1.79	0.47
2:L:79:TYR:CE1	2:L:189:LEU:HD12	2.49	0.47
1:M:343:PRO:HG2	1:M:387:TYR:HB3	1.96	0.47
1:Q:183:THR:HG22	1:Q:185:GLU:H	1.80	0.47
3:V:232:ILE:HA	3:V:235:ARG:HD3	1.95	0.47
3:W:306:ARG:HE	3:W:309:GLY:C	2.21	0.47
1:E:174:TYR:HB3	1:E:191:LEU:HD23	1.95	0.47
1:E:434:ILE:HG21	1:E:437:ARG:HG3	1.97	0.47
1:J:14:LEU:HD11	1:J:55:ALA:HB1	1.96	0.47
1:K:391:VAL:HG11	1:K:472:LYS:HD3	1.97	0.47
2:O:19:VAL:HG13	2:O:23:PHE:HE1	1.80	0.47
1:H:63:GLU:HB3	1:H:67:MET:HE2	1.96	0.47
1:P:100:ARG:HA	1:P:100:ARG:HH11	1.79	0.47
1:P:372:GLU:HA	1:P:386:ASN:HB3	1.95	0.47
2:R:80:GLN:HB2	2:R:119:ALA:HB2	1.97	0.47
1:J:150:GLN:HG2	1:J:151:THR:HG23	1.96	0.47
1:K:342:LEU:HD12	1:K:368:VAL:HG23	1.96	0.47
1:K:456:ALA:HB2	1:K:462:GLN:HA	1.96	0.47
1:P:227:GLU:HB2	1:P:231:LEU:HB2	1.97	0.47
3:U:340:ARG:HH21	3:U:368:GLN:HB2	1.79	0.47
1:D:395:ILE:HA	1:D:457:LYS:HA	1.96	0.47
1:E:111:THR:HB	1:E:137:LEU:HB2	1.95	0.47
1:J:94:HIS:HD2	1:J:280:ARG:HG2	1.79	0.47
1:J:372:GLU:HA	1:J:386:ASN:HB3	1.97	0.47
1:M:395:ILE:HA	1:M:457:LYS:HA	1.96	0.47
1:N:22:ARG:HA	1:N:22:ARG:HD3	1.74	0.47
1:N:434:ILE:HD13	1:N:437:ARG:HH21	1.79	0.47
1:A:346:LEU:HA	1:A:389:ARG:HG3	1.96	0.47
1:J:418:ARG:NH1	1:J:444:GLU:HB2	2.30	0.47
2:O:174:ILE:HB	2:O:208:GLU:HG2	1.95	0.47
2:R:238:LEU:H	2:R:238:LEU:HD23	1.80	0.47
3:U:247:ILE:HG13	3:U:302:THR:HB	1.97	0.47
1:D:127:ARG:HA	1:D:127:ARG:NH1	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:13:ASP:O	1:E:17:ILE:HG12	2.15	0.47
2:I:27:PRO:HD2	2:I:29:PHE:CD2	2.50	0.47
1:N:399:ILE:HD13	1:N:453:LEU:HD22	1.97	0.47
1:P:9:LEU:HB2	1:P:69:TYR:CE2	2.50	0.47
1:P:353:VAL:HG21	1:P:389:ARG:HH22	1.80	0.47
1:P:419:ILE:HG23	1:P:438:PHE:CZ	2.47	0.47
2:R:78:VAL:HB	2:R:189:LEU:HG	1.96	0.47
3:S:249:HIS:HB3	3:S:252:ALA:HB2	1.97	0.47
2:C:139:ARG:HE	2:C:146:GLN:HG3	1.79	0.47
1:D:321:ARG:HG3	1:D:344:ILE:HB	1.96	0.47
2:F:19:VAL:HG13	2:F:23:PHE:HE1	1.79	0.47
1:H:136:ILE:HG22	1:H:138:THR:HG23	1.97	0.47
1:M:113:ILE:HG22	1:M:264:ILE:HG21	1.96	0.47
1:M:419:ILE:HG23	1:M:438:PHE:CZ	2.47	0.47
1:P:422:TYR:CE1	1:P:441:PRO:HD3	2.50	0.47
3:S:25:ASN:HA	3:S:266:LEU:HG	1.97	0.47
1:E:311:LEU:HD12	1:E:320:VAL:HG21	1.97	0.46
1:E:321:ARG:HH12	1:E:471:PHE:HB2	1.80	0.46
1:G:29:PHE:CE1	1:H:49:ARG:HG3	2.50	0.46
1:K:330:PRO:HB3	1:K:337:PRO:HA	1.97	0.46
1:N:136:ILE:HG22	1:N:138:THR:HG23	1.96	0.46
2:O:184:SER:O	2:O:189:LEU:HB2	2.15	0.46
1:Q:150:GLN:HG2	1:Q:151:THR:HG23	1.98	0.46
1:Q:372:GLU:HA	1:Q:386:ASN:HB3	1.97	0.46
3:X:232:ILE:HA	3:X:235:ARG:HD3	1.98	0.46
2:C:27:PRO:HD2	2:C:29:PHE:CD2	2.50	0.46
2:C:73:ARG:HD3	2:C:134:LYS:HE3	1.97	0.46
1:G:264:ILE:HB	1:G:267:TRP:HB3	1.96	0.46
1:H:78:THR:HG23	1:H:289:ARG:HH22	1.80	0.46
1:H:291:ARG:HH11	1:H:292:PHE:HA	1.80	0.46
1:M:280:ARG:HH11	1:M:281:LEU:H	1.63	0.46
1:N:218:ASP:HB3	1:N:221:ASN:ND2	2.30	0.46
1:N:434:ILE:HD13	1:N:437:ARG:HE	1.80	0.46
1:Q:136:ILE:HG22	1:Q:138:THR:HG23	1.97	0.46
1:E:456:ALA:HB2	1:E:462:GLN:HA	1.97	0.46
1:G:361:LYS:O	2:I:144:PRO:HG2	2.15	0.46
1:Q:11:ILE:HA	1:Q:65:ILE:HD12	1.98	0.46
2:R:151:TYR:HD2	2:R:152:LYS:HD2	1.80	0.46
3:V:25:ASN:HA	3:V:266:LEU:HG	1.97	0.46
1:A:485:THR:HG22	1:A:486:THR:HG22	1.96	0.46
1:B:456:ALA:HB2	1:B:462:GLN:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:77:ALA:HB3	1:D:85:LEU:HD11	1.98	0.46
1:D:403:ASN:HB2	1:D:487:VAL:HG13	1.97	0.46
1:D:428:LYS:H	1:D:431:ASP:HB2	1.81	0.46
1:H:121:ILE:HD11	1:H:261:SER:HB3	1.97	0.46
1:M:163:TYR:HB3	1:M:166:ASP:HA	1.97	0.46
1:N:321:ARG:NH1	1:N:471:PHE:HB2	2.30	0.46
1:N:372:GLU:HA	1:N:386:ASN:HB3	1.97	0.46
1:Q:22:ARG:HA	1:Q:22:ARG:HD3	1.76	0.46
1:Q:302:ASN:HB3	1:Q:305:GLU:HB2	1.98	0.46
3:T:25:ASN:HA	3:T:266:LEU:HG	1.98	0.46
1:A:127:ARG:NH1	1:A:127:ARG:HA	2.31	0.46
2:C:184:SER:O	2:C:189:LEU:HB2	2.15	0.46
1:E:160:LEU:HD11	1:E:225:PHE:HD2	1.80	0.46
2:L:196:LEU:HD22	2:L:197:PRO:HD2	1.98	0.46
1:M:422:TYR:CE1	1:M:441:PRO:HD3	2.50	0.46
1:P:346:LEU:HA	1:P:389:ARG:HG3	1.96	0.46
3:W:25:ASN:HA	3:W:266:LEU:HG	1.97	0.46
1:B:206:TYR:HE1	1:B:215:VAL:HG22	1.81	0.46
1:D:343:PRO:HG2	1:D:387:TYR:HB3	1.97	0.46
2:F:66:ILE:O	2:F:70:ILE:HG12	2.16	0.46
2:F:78:VAL:HB	2:F:189:LEU:HG	1.96	0.46
2:I:175:GLY:HA2	2:I:213:ARG:HH12	1.80	0.46
1:J:9:LEU:HB2	1:J:69:TYR:CE2	2.50	0.46
2:L:231:ASP:HB2	2:L:232:PRO:HD3	1.96	0.46
1:M:77:ALA:HB3	1:M:85:LEU:HD11	1.98	0.46
2:O:139:ARG:HH22	2:O:142:SER:HA	1.79	0.46
1:P:113:ILE:HG22	1:P:264:ILE:HG21	1.97	0.46
3:U:25:ASN:HA	3:U:266:LEU:HG	1.97	0.46
1:B:163:TYR:HB3	1:B:166:ASP:HA	1.97	0.46
1:G:11:ILE:HD13	1:G:66:GLN:HE21	1.81	0.46
1:J:227:GLU:HB2	1:J:231:LEU:HB2	1.97	0.46
1:J:403:ASN:HD21	1:J:484:VAL:HG23	1.80	0.46
1:M:127:ARG:HA	1:M:127:ARG:NH1	2.30	0.46
1:N:392:GLU:HA	1:N:474:VAL:H	1.80	0.46
1:G:344:ILE:HG12	1:G:388:GLN:HB2	1.97	0.46
1:J:456:ALA:HB2	1:J:462:GLN:HA	1.97	0.46
1:Q:433:VAL:HB	1:Q:467:ILE:HB	1.96	0.46
1:B:400:SER:H	1:B:452:SER:HB2	1.80	0.46
2:I:12:LEU:O	2:I:16:ARG:HD3	2.16	0.46
1:M:321:ARG:HG3	1:M:344:ILE:HB	1.98	0.46
1:N:13:ASP:O	1:N:17:ILE:HG12	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:184:SER:HB3	2:O:189:LEU:HD13	1.98	0.46
1:Q:105:LEU:HB3	1:Q:270:VAL:HG22	1.97	0.46
1:Q:403:ASN:HB2	1:Q:487:VAL:HG13	1.98	0.46
3:T:421:HIS:HB3	3:T:423:ARG:HH22	1.81	0.46
3:V:247:ILE:HG13	3:V:302:THR:HB	1.98	0.46
3:X:336:ARG:HG3	3:X:368:GLN:HE22	1.81	0.46
1:A:410:ASN:HB3	1:A:413:ASP:HB2	1.97	0.46
1:K:13:ASP:O	1:K:17:ILE:HG12	2.16	0.46
1:K:423:GLY:HA2	1:K:427:TYR:HD2	1.81	0.46
1:M:11:ILE:HD13	1:M:66:GLN:HE21	1.81	0.46
3:X:340:ARG:HH21	3:X:368:GLN:HB2	1.81	0.46
1:A:104:VAL:HG12	1:A:273:PRO:HD3	1.97	0.45
1:B:100:ARG:HA	1:B:100:ARG:HH11	1.80	0.45
1:D:9:LEU:HB2	1:D:69:TYR:CE2	2.51	0.45
1:D:106:GLU:HG2	1:D:237:ARG:HG2	1.97	0.45
2:I:19:VAL:HG13	2:I:23:PHE:HE1	1.81	0.45
1:Q:13:ASP:O	1:Q:17:ILE:HG12	2.16	0.45
2:R:27:PRO:HD2	2:R:29:PHE:CD2	2.51	0.45
3:W:157:LEU:HD23	3:W:165:MET:HE3	1.98	0.45
1:A:435:TYR:CE1	1:A:453:LEU:HD12	2.51	0.45
2:C:139:ARG:HH22	2:C:142:SER:HA	1.82	0.45
1:D:113:ILE:HG22	1:D:264:ILE:HG21	1.97	0.45
1:E:403:ASN:HD21	1:E:484:VAL:HG23	1.82	0.45
1:H:391:VAL:HG11	1:H:472:LYS:HD3	1.98	0.45
2:L:12:LEU:O	2:L:16:ARG:HD3	2.17	0.45
1:N:42:SER:O	1:N:48:GLY:HA3	2.17	0.45
1:A:11:ILE:HD13	1:A:66:GLN:HE21	1.81	0.45
1:A:401:VAL:HB	1:A:415:LEU:HD22	1.98	0.45
2:C:155:PHE:HE2	2:C:178:LEU:HD11	1.82	0.45
1:D:321:ARG:HD3	1:D:429:ILE:HD12	1.99	0.45
1:G:98:PRO:HB3	1:G:247:ILE:HD13	1.98	0.45
1:H:78:THR:HA	1:H:289:ARG:HH12	1.80	0.45
1:H:120:MET:HA	1:H:260:ILE:HA	1.98	0.45
1:K:302:ASN:HB3	1:K:305:GLU:HB2	1.99	0.45
2:O:152:LYS:HD2	2:O:158:PRO:HA	1.99	0.45
1:Q:456:ALA:HB2	1:Q:462:GLN:HA	1.98	0.45
3:U:157:LEU:HD23	3:U:165:MET:HE3	1.99	0.45
3:W:247:ILE:HG13	3:W:302:THR:HB	1.99	0.45
1:A:264:ILE:HB	1:A:267:TRP:HB3	1.98	0.45
1:E:404:THR:HA	1:E:487:VAL:HG21	1.98	0.45
2:F:231:ASP:HB2	2:F:232:PRO:HD3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:203:LEU:HD21	1:K:223:LYS:HD2	1.98	0.45
1:K:321:ARG:HH12	1:K:471:PHE:HB2	1.80	0.45
3:T:349:LYS:HG3	3:T:350:LYS:HG2	1.98	0.45
3:V:39:ARG:HD3	3:V:80:ARG:HH21	1.81	0.45
3:X:421:HIS:HB3	3:X:423:ARG:HH12	1.81	0.45
2:C:78:VAL:HB	2:C:189:LEU:HG	1.99	0.45
1:K:392:GLU:HA	1:K:474:VAL:H	1.82	0.45
1:N:120:MET:HG2	1:N:270:VAL:HB	1.98	0.45
1:N:122:SER:HB2	1:N:257:ILE:HG12	1.99	0.45
1:P:98:PRO:HB3	1:P:247:ILE:HD13	1.98	0.45
1:P:485:THR:HG22	1:P:486:THR:H	1.81	0.45
1:Q:471:PHE:HE1	1:Q:472:LYS:HE3	1.80	0.45
1:B:105:LEU:HB3	1:B:270:VAL:HG22	1.98	0.45
1:D:117:PRO:HB2	1:D:264:ILE:HD11	1.98	0.45
1:G:93:ARG:HH12	1:G:282:ARG:CZ	2.29	0.45
2:L:151:TYR:HD2	2:L:152:LYS:HD2	1.82	0.45
2:C:19:VAL:HG13	2:C:23:PHE:HE1	1.81	0.45
2:C:94:ALA:C	2:C:102:ASP:HB3	2.42	0.45
1:D:98:PRO:HB3	1:D:247:ILE:HD13	1.98	0.45
1:H:120:MET:HG2	1:H:270:VAL:HB	1.97	0.45
1:K:25:ALA:HA	1:K:28:VAL:HG13	1.99	0.45
1:M:449:GLN:HB2	1:M:487:VAL:HG12	1.99	0.45
1:A:98:PRO:HB3	1:A:247:ILE:HD13	1.98	0.45
2:C:146:GLN:HE21	2:C:146:GLN:HB3	1.62	0.45
1:D:264:ILE:HB	1:D:267:TRP:HB3	1.99	0.45
1:E:136:ILE:HG22	1:E:138:THR:HG23	1.99	0.45
1:H:160:LEU:HD11	1:H:225:PHE:HD2	1.82	0.45
1:H:443:MET:HE2	1:M:437:ARG:HA	1.99	0.45
1:J:127:ARG:NH1	1:J:127:ARG:HA	2.31	0.45
1:K:147:ILE:HG13	1:K:212:LEU:O	2.16	0.45
1:P:127:ARG:NH1	1:P:127:ARG:HA	2.31	0.45
1:Q:42:SER:O	1:Q:48:GLY:HA3	2.16	0.45
1:E:98:PRO:HB3	1:E:247:ILE:HD13	1.97	0.45
2:I:62:LYS:HA	2:I:62:LYS:HD3	1.77	0.45
2:I:168:ALA:HA	2:I:202:VAL:HG22	1.97	0.45
1:J:400:SER:HB2	1:J:449:GLN:NE2	2.32	0.45
1:K:149:PRO:HB3	1:K:158:TYR:CE2	2.52	0.45
1:K:418:ARG:HH11	1:K:444:GLU:HB2	1.81	0.45
1:M:434:ILE:HB	1:M:437:ARG:HE	1.82	0.45
1:M:449:GLN:HB2	1:M:487:VAL:HA	1.99	0.45
1:P:164:VAL:HA	1:P:223:LYS:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:TYR:HB3	1:B:191:LEU:HD23	1.99	0.45
1:G:127:ARG:NH1	1:G:127:ARG:HA	2.32	0.45
1:H:147:ILE:HG13	1:H:212:LEU:O	2.17	0.45
1:J:422:TYR:CE1	1:J:441:PRO:HD3	2.52	0.45
2:L:19:VAL:HG13	2:L:23:PHE:HE1	1.82	0.45
1:N:291:ARG:HH11	1:N:292:PHE:HA	1.82	0.45
1:N:418:ARG:NH1	1:N:444:GLU:HB2	2.32	0.45
1:N:456:ALA:HB2	1:N:462:GLN:HA	1.99	0.45
1:A:100:ARG:HA	1:A:100:ARG:HH11	1.82	0.44
1:D:158:TYR:CZ	1:D:187:ILE:HG21	2.53	0.44
1:D:339:HIS:ND1	2:F:167:PRO:HB3	2.32	0.44
2:O:132:LYS:HD3	2:O:153:PHE:HZ	1.82	0.44
1:Q:98:PRO:HB3	1:Q:247:ILE:HD13	1.99	0.44
1:B:391:VAL:HG11	1:B:472:LYS:HD3	1.99	0.44
1:E:434:ILE:HD13	1:E:437:ARG:HH21	1.82	0.44
1:H:399:ILE:HD13	1:H:453:LEU:HD22	1.99	0.44
1:J:104:VAL:HG12	1:J:273:PRO:HD3	1.99	0.44
1:J:363:PHE:CD2	2:L:144:PRO:HB3	2.52	0.44
1:K:433:VAL:HB	1:K:467:ILE:HB	1.99	0.44
1:Q:14:LEU:HB2	1:Q:62:TRP:HZ2	1.82	0.44
2:R:12:LEU:O	2:R:16:ARG:HD3	2.18	0.44
2:R:26:LYS:HE2	2:R:30:ASP:HB3	2.00	0.44
2:R:79:TYR:CE1	2:R:189:LEU:HD12	2.53	0.44
1:A:303:ILE:HB	1:B:363:PHE:HE2	1.82	0.44
1:A:372:GLU:HA	1:A:386:ASN:HB3	1.98	0.44
1:H:174:TYR:CZ	1:H:190:GLY:HA3	2.51	0.44
1:H:394:PRO:HG2	1:H:458:LYS:HB3	1.99	0.44
1:K:148:PHE:HB3	1:K:234:GLN:HE22	1.82	0.44
1:M:164:VAL:HG13	1:M:223:LYS:HE3	1.99	0.44
1:Q:63:GLU:HB3	1:Q:67:MET:HE2	1.98	0.44
1:Q:120:MET:HG2	1:Q:270:VAL:HB	2.00	0.44
1:Q:434:ILE:HG22	1:Q:437:ARG:H	1.82	0.44
3:T:340:ARG:HH21	3:T:368:GLN:HB2	1.82	0.44
1:B:434:ILE:HG21	1:B:437:ARG:HG3	2.00	0.44
1:H:149:PRO:HB3	1:H:158:TYR:CE2	2.53	0.44
2:R:157:VAL:HG21	2:R:176:LYS:HD3	1.99	0.44
1:A:29:PHE:CE1	1:B:49:ARG:HG3	2.53	0.44
1:A:113:ILE:HG22	1:A:264:ILE:HG21	1.99	0.44
1:D:419:ILE:HD13	1:D:419:ILE:HA	1.88	0.44
2:F:184:SER:O	2:F:189:LEU:HB2	2.17	0.44
2:I:26:LYS:HB2	2:I:29:PHE:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:264:ILE:HB	1:J:267:TRP:HB3	1.99	0.44
1:J:443:MET:HE3	1:J:443:MET:HB3	1.85	0.44
2:O:94:ALA:C	2:O:102:ASP:HB3	2.43	0.44
3:X:157:LEU:HD23	3:X:165:MET:HE3	2.00	0.44
2:C:12:LEU:O	2:C:16:ARG:HD3	2.17	0.44
1:E:147:ILE:HG13	1:E:212:LEU:O	2.18	0.44
1:N:29:PHE:CE2	1:N:31:ASP:HB2	2.53	0.44
1:P:449:GLN:HG2	1:P:451:ASN:H	1.83	0.44
1:Q:13:ASP:HB3	1:Q:16:GLN:HG3	2.00	0.44
2:R:19:VAL:HG13	2:R:23:PHE:HE1	1.81	0.44
3:T:232:ILE:HA	3:T:235:ARG:HD3	1.99	0.44
3:V:349:LYS:HG3	3:V:350:LYS:HG2	2.00	0.44
1:D:164:VAL:HG13	1:D:223:LYS:HE3	2.00	0.44
1:G:100:ARG:NH1	1:G:243:VAL:HG22	2.33	0.44
1:J:341:PHE:HD1	1:J:365:ILE:HG22	1.82	0.44
1:N:174:TYR:CZ	1:N:190:GLY:HA3	2.53	0.44
1:Q:255:LEU:HD12	1:Q:255:LEU:HA	1.88	0.44
2:R:120:ARG:HH22	2:R:123:SER:HB3	1.83	0.44
3:T:336:ARG:HG3	3:T:368:GLN:HE22	1.82	0.44
1:B:144:GLY:HA3	1:B:237:ARG:HD3	1.99	0.44
1:D:403:ASN:HD21	1:D:484:VAL:HG23	1.83	0.44
1:E:29:PHE:CE2	1:E:31:ASP:HB2	2.53	0.44
1:G:9:LEU:HB2	1:G:69:TYR:CE2	2.53	0.44
1:G:104:VAL:HG13	1:G:271:ILE:HG13	2.00	0.44
2:I:97:PHE:CD2	2:I:100:LEU:HB2	2.52	0.44
1:J:164:VAL:HG13	1:J:223:LYS:HE3	2.00	0.44
1:N:78:THR:HG23	1:N:289:ARG:HH22	1.83	0.44
1:N:183:THR:O	1:N:187:ILE:HG12	2.18	0.44
1:N:403:ASN:HB2	1:N:487:VAL:HG13	2.00	0.44
1:N:434:ILE:HG22	1:N:436:SER:H	1.82	0.44
2:R:184:SER:O	2:R:189:LEU:HB2	2.18	0.44
3:S:140:THR:HB	3:S:148:THR:OG1	2.18	0.44
1:A:94:HIS:HD2	1:A:280:ARG:HG2	1.82	0.44
1:D:419:ILE:HG23	1:D:438:PHE:CZ	2.49	0.44
1:E:372:GLU:HA	1:E:386:ASN:HB3	2.00	0.44
2:F:80:GLN:HB2	2:F:119:ALA:HB2	1.99	0.44
1:H:321:ARG:NH1	1:H:471:PHE:HB2	2.33	0.44
2:I:184:SER:O	2:I:189:LEU:HB2	2.16	0.44
1:K:160:LEU:HD11	1:K:225:PHE:HD2	1.83	0.44
1:N:115:SER:HA	1:N:131:LEU:HB2	1.99	0.44
3:U:354:ASP:HA	3:U:391:VAL:HG11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:PRO:HB2	1:A:117:PRO:HD3	1.99	0.43
1:B:344:ILE:HG12	1:B:388:GLN:HE21	1.82	0.43
1:B:433:VAL:HB	1:B:467:ILE:HB	1.98	0.43
1:D:399:ILE:O	1:D:482:ILE:HG23	2.18	0.43
1:J:98:PRO:HB3	1:J:247:ILE:HD13	1.99	0.43
1:J:419:ILE:HG23	1:J:438:PHE:CZ	2.46	0.43
1:K:13:ASP:HB3	1:K:16:GLN:HG3	2.00	0.43
1:N:302:ASN:HB3	1:N:305:GLU:HB2	2.00	0.43
2:O:27:PRO:HD2	2:O:29:PHE:CD2	2.52	0.43
2:O:139:ARG:HG2	2:O:140:THR:H	1.83	0.43
1:A:456:ALA:HB2	1:A:462:GLN:HA	2.00	0.43
1:B:321:ARG:HG2	1:B:344:ILE:HB	1.99	0.43
1:E:11:ILE:HA	1:E:65:ILE:HD12	2.00	0.43
2:F:27:PRO:HD2	2:F:29:PHE:CD2	2.53	0.43
2:F:79:TYR:CE1	2:F:189:LEU:HD12	2.53	0.43
2:F:139:ARG:HG2	2:F:140:THR:H	1.83	0.43
1:K:100:ARG:NH1	1:K:243:VAL:HG22	2.33	0.43
2:O:238:LEU:HD23	2:O:238:LEU:H	1.82	0.43
1:P:399:ILE:HG23	1:P:453:LEU:HD22	2.00	0.43
1:B:149:PRO:HB3	1:B:158:TYR:CE2	2.52	0.43
2:C:75:ARG:HD3	2:C:127:TYR:CD1	2.53	0.43
1:G:100:ARG:HH11	1:G:100:ARG:HA	1.83	0.43
1:H:147:ILE:HG22	1:H:233:ILE:HG12	2.00	0.43
1:J:113:ILE:HG22	1:J:264:ILE:HG21	1.99	0.43
1:J:389:ARG:HB3	1:J:390:PRO:HD3	2.01	0.43
1:K:106:GLU:HG2	1:K:237:ARG:HG2	2.00	0.43
2:L:27:PRO:HD2	2:L:29:PHE:CD2	2.53	0.43
1:M:9:LEU:HB2	1:M:69:TYR:CE2	2.53	0.43
1:M:158:TYR:CZ	1:M:187:ILE:HG21	2.53	0.43
1:N:97:ARG:HG2	1:N:280:ARG:HB3	2.01	0.43
1:P:434:ILE:HG22	1:P:437:ARG:H	1.82	0.43
1:Q:449:GLN:HB3	1:Q:487:VAL:HG12	2.00	0.43
1:A:422:TYR:CE1	1:A:441:PRO:HD3	2.53	0.43
1:B:42:SER:O	1:B:48:GLY:HA3	2.19	0.43
1:B:100:ARG:NH1	1:B:243:VAL:HG22	2.34	0.43
1:B:136:ILE:HG22	1:B:138:THR:HG23	1.99	0.43
1:B:147:ILE:HD11	1:B:212:LEU:HD23	1.99	0.43
1:D:399:ILE:HA	1:D:452:SER:O	2.19	0.43
1:E:391:VAL:HG11	1:E:472:LYS:HD3	2.01	0.43
2:O:231:ASP:HB2	2:O:232:PRO:HD3	2.00	0.43
1:Q:218:ASP:HB3	1:Q:221:ASN:OD1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:425:GLU:C	1:Q:428:LYS:HZ1	2.27	0.43
2:C:66:ILE:O	2:C:70:ILE:HG12	2.18	0.43
1:D:449:GLN:HG3	1:D:451:ASN:H	1.83	0.43
1:G:77:ALA:HB3	1:G:85:LEU:HD11	2.00	0.43
1:G:94:HIS:HD2	1:G:280:ARG:HG2	1.83	0.43
2:I:129:MET:HE1	2:I:154:VAL:HA	1.99	0.43
1:J:403:ASN:HB2	1:J:487:VAL:HG13	2.00	0.43
1:K:404:THR:HA	1:K:487:VAL:HG21	1.99	0.43
1:M:148:PHE:HB3	1:M:234:GLN:NE2	2.33	0.43
1:N:144:GLY:HA3	1:N:237:ARG:HD3	2.01	0.43
2:O:12:LEU:O	2:O:16:ARG:HD3	2.17	0.43
2:O:26:LYS:HB2	2:O:29:PHE:HB2	2.01	0.43
2:O:127:TYR:HD1	2:O:130:ILE:HD11	1.84	0.43
1:Q:174:TYR:CZ	1:Q:190:GLY:HA3	2.54	0.43
3:S:277:HIS:C	3:S:312:ARG:HD2	2.43	0.43
3:W:373:ILE:HG12	3:W:378:LEU:HD11	1.99	0.43
1:A:9:LEU:HB2	1:A:69:TYR:CE2	2.53	0.43
1:E:22:ARG:HA	1:E:22:ARG:HD3	1.75	0.43
1:E:443:MET:HB2	1:G:443:MET:HE2	1.99	0.43
1:J:111:THR:HB	1:J:137:LEU:HD13	2.01	0.43
2:L:184:SER:O	2:L:189:LEU:HB2	2.17	0.43
1:M:14:LEU:HD11	1:M:55:ALA:HB1	2.00	0.43
1:N:98:PRO:HB3	1:N:247:ILE:HD13	2.00	0.43
1:N:150:GLN:HG2	1:N:151:THR:HG23	2.00	0.43
2:R:178:LEU:HD22	2:R:182:GLU:HG2	2.01	0.43
3:U:349:LYS:HG3	3:U:350:LYS:HG2	2.00	0.43
1:B:111:THR:HB	1:B:137:LEU:HB2	1.99	0.43
1:D:342:LEU:HD12	1:D:368:VAL:HG23	2.00	0.43
1:E:291:ARG:HH11	1:E:292:PHE:HA	1.83	0.43
1:G:93:ARG:NH2	1:G:284:THR:HA	2.34	0.43
1:M:434:ILE:HD13	1:M:437:ARG:HE	1.83	0.43
1:N:25:ALA:HA	1:N:28:VAL:HG13	2.00	0.43
1:Q:144:GLY:HA3	1:Q:237:ARG:HD3	2.00	0.43
3:T:39:ARG:HD3	3:T:80:ARG:HH21	1.84	0.43
1:B:403:ASN:HB2	1:B:487:VAL:HG13	2.01	0.43
2:L:166:ALA:HB3	2:L:169:ALA:HB3	2.01	0.43
1:M:364:GLY:HA3	2:O:202:VAL:HG21	2.01	0.43
1:N:148:PHE:HB3	1:N:234:GLN:HE22	1.84	0.43
2:O:129:MET:HE1	2:O:154:VAL:HA	2.01	0.43
1:P:389:ARG:HB3	1:P:390:PRO:HD3	2.00	0.43
1:P:434:ILE:HD13	1:P:437:ARG:HE	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:205:SER:HB3	1:B:212:LEU:HD11	2.00	0.43
2:C:152:LYS:HE3	2:C:158:PRO:HA	2.01	0.43
1:E:59:GLU:CD	1:E:59:GLU:H	2.27	0.43
1:E:292:PHE:O	1:E:296:LYS:HG2	2.19	0.43
1:G:74:PRO:HG3	1:G:85:LEU:HD22	2.00	0.43
1:H:307:LEU:HA	1:H:360:ASN:HD21	1.84	0.43
2:I:146:GLN:HE21	2:I:146:GLN:HB3	1.66	0.43
1:J:74:PRO:HG3	1:J:85:LEU:HB3	2.01	0.43
1:J:100:ARG:NH1	1:J:243:VAL:HG22	2.34	0.43
1:P:305:GLU:HA	1:P:308:ILE:HD12	2.00	0.43
1:Q:321:ARG:NH1	1:Q:471:PHE:HB2	2.34	0.43
1:Q:439:TYR:HE1	1:Q:453:LEU:HD21	1.84	0.43
1:D:74:PRO:HG3	1:D:85:LEU:HD22	2.00	0.43
1:H:98:PRO:HB3	1:H:247:ILE:HD13	1.99	0.43
1:K:164:VAL:HA	1:K:223:LYS:HB2	2.00	0.43
1:N:183:THR:HG22	1:N:185:GLU:H	1.83	0.43
1:P:100:ARG:NH1	1:P:243:VAL:HG22	2.33	0.43
1:P:158:TYR:CZ	1:P:187:ILE:HG21	2.54	0.43
3:S:232:ILE:HA	3:S:235:ARG:HD3	2.01	0.43
1:A:164:VAL:HG13	1:A:223:LYS:HE3	2.01	0.42
1:B:25:ALA:HA	1:B:28:VAL:HG13	2.01	0.42
2:C:184:SER:HB3	2:C:189:LEU:HD13	2.01	0.42
1:M:74:PRO:HG3	1:M:85:LEU:HB3	2.00	0.42
1:N:60:ALA:O	1:N:64:VAL:HG23	2.18	0.42
1:N:100:ARG:NH1	1:N:243:VAL:HG22	2.34	0.42
3:W:39:ARG:HD3	3:W:80:ARG:HH21	1.83	0.42
1:E:296:LYS:HD2	1:E:296:LYS:HA	1.87	0.42
2:F:26:LYS:HD3	2:F:30:ASP:H	1.83	0.42
1:J:28:VAL:HG21	1:K:49:ARG:HD3	2.01	0.42
1:J:342:LEU:HD12	1:J:368:VAL:HG23	2.01	0.42
1:P:418:ARG:NH1	1:P:444:GLU:HB2	2.33	0.42
2:R:127:TYR:HD1	2:R:130:ILE:HD11	1.84	0.42
2:R:171:ARG:HH11	2:R:205:THR:HB	1.84	0.42
3:U:277:HIS:C	3:U:312:ARG:HD2	2.44	0.42
1:B:434:ILE:HG22	1:B:437:ARG:H	1.84	0.42
1:B:435:TYR:OH	1:B:464:MET:HB2	2.18	0.42
1:E:13:ASP:HB3	1:E:16:GLN:HG3	2.00	0.42
1:E:183:THR:O	1:E:187:ILE:HG12	2.19	0.42
1:G:400:SER:HB2	1:G:449:GLN:HE22	1.83	0.42
1:H:42:SER:O	1:H:48:GLY:HA3	2.19	0.42
1:H:183:THR:O	1:H:187:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:97:PHE:HB3	2:I:101:SER:H	1.84	0.42
1:J:346:LEU:HA	1:J:389:ARG:HG3	2.00	0.42
1:J:395:ILE:HG13	1:J:475:ALA:HB1	2.00	0.42
1:J:434:ILE:HG22	1:J:437:ARG:H	1.83	0.42
2:L:26:LYS:HB2	2:L:29:PHE:HB2	2.00	0.42
1:M:74:PRO:HG3	1:M:85:LEU:HD22	2.01	0.42
2:O:175:GLY:HA2	2:O:213:ARG:HH12	1.85	0.42
1:P:443:MET:HE3	1:P:443:MET:HB3	1.95	0.42
1:Q:100:ARG:NH1	1:Q:243:VAL:HG22	2.34	0.42
3:T:140:THR:HB	3:T:148:THR:OG1	2.19	0.42
3:T:277:HIS:C	3:T:312:ARG:HD2	2.44	0.42
1:H:109:ILE:HG13	1:H:139:PRO:HD3	2.00	0.42
1:J:119:LYS:HE2	1:J:119:LYS:HB2	1.90	0.42
1:K:43:GLY:HA2	1:K:48:GLY:HA3	2.01	0.42
1:K:59:GLU:CD	1:K:59:GLU:H	2.27	0.42
1:K:105:LEU:HB3	1:K:270:VAL:HG22	2.01	0.42
2:L:139:ARG:HH22	2:L:142:SER:HA	1.85	0.42
2:R:26:LYS:HB2	2:R:29:PHE:HB2	2.00	0.42
1:A:158:TYR:CZ	1:A:187:ILE:HG21	2.55	0.42
1:B:430:GLY:HA2	1:B:471:PHE:HA	2.02	0.42
2:C:168:ALA:HB1	2:C:202:VAL:HG22	1.99	0.42
1:D:434:ILE:HB	1:D:437:ARG:HE	1.84	0.42
1:D:434:ILE:HD13	1:D:437:ARG:HE	1.84	0.42
1:K:120:MET:HE2	1:K:120:MET:HB2	1.92	0.42
1:N:78:THR:HA	1:N:289:ARG:HH12	1.84	0.42
1:P:355:GLN:HG3	1:P:375:VAL:HG23	2.01	0.42
1:Q:60:ALA:O	1:Q:64:VAL:HG23	2.19	0.42
2:R:152:LYS:HE3	2:R:158:PRO:HA	2.02	0.42
3:U:72:LYS:HE3	3:U:72:LYS:HB2	1.91	0.42
1:A:435:TYR:HE1	1:A:453:LEU:HD12	1.84	0.42
2:C:139:ARG:HG2	2:C:140:THR:H	1.84	0.42
1:E:149:PRO:HB3	1:E:158:TYR:CE2	2.55	0.42
1:E:255:LEU:HD12	1:E:255:LEU:HA	1.88	0.42
1:H:18:LEU:O	1:H:22:ARG:HG2	2.19	0.42
2:I:79:TYR:CD2	2:I:82:ILE:HG23	2.54	0.42
1:J:443:MET:HA	1:J:448:PHE:HE1	1.84	0.42
1:J:485:THR:HG22	1:J:486:THR:HG22	2.01	0.42
1:P:74:PRO:HG3	1:P:85:LEU:HD22	2.00	0.42
1:Q:391:VAL:HG11	1:Q:472:LYS:HG3	2.02	0.42
1:Q:416:ARG:HE	1:Q:482:ILE:HB	1.84	0.42
2:R:94:ALA:C	2:R:102:ASP:HB3	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:421:HIS:HB3	3:V:423:ARG:HH12	1.84	0.42
1:A:100:ARG:NH1	1:A:243:VAL:HG22	2.34	0.42
1:A:389:ARG:HB3	1:A:390:PRO:HD3	2.02	0.42
2:C:231:ASP:HB2	2:C:232:PRO:HD3	2.01	0.42
1:D:57:SER:O	1:D:61:ILE:HG12	2.20	0.42
1:D:389:ARG:HB3	1:D:390:PRO:HD3	2.01	0.42
2:F:26:LYS:HB2	2:F:29:PHE:HB2	2.02	0.42
1:G:148:PHE:HB3	1:G:234:GLN:NE2	2.34	0.42
1:J:144:GLY:HA3	1:J:237:ARG:HD3	2.02	0.42
1:K:167:ILE:HD12	1:K:167:ILE:HA	1.89	0.42
1:K:307:LEU:HA	1:K:360:ASN:HD21	1.84	0.42
1:K:400:SER:HB2	1:K:449:GLN:NE2	2.34	0.42
1:Q:115:SER:HA	1:Q:131:LEU:HB2	2.02	0.42
3:W:277:HIS:C	3:W:312:ARG:HD2	2.45	0.42
3:W:385:LYS:HB3	3:W:385:LYS:HE3	1.84	0.42
3:W:421:HIS:HB3	3:W:423:ARG:HH22	1.85	0.42
1:B:291:ARG:HH11	1:B:292:PHE:HA	1.85	0.42
1:D:93:ARG:NH1	1:D:284:THR:HA	2.34	0.42
1:H:22:ARG:HA	1:H:22:ARG:HD3	1.84	0.42
1:H:122:SER:HB2	1:H:257:ILE:HG12	2.01	0.42
1:H:392:GLU:HA	1:H:474:VAL:H	1.84	0.42
2:I:172:ILE:HB	2:I:206:TYR:HD1	1.85	0.42
1:J:361:LYS:O	2:L:144:PRO:HG2	2.20	0.42
1:J:394:PRO:HA	1:J:476:THR:HB	2.01	0.42
2:O:97:PHE:CD2	2:O:100:LEU:HB2	2.55	0.42
1:P:399:ILE:HG12	1:P:453:LEU:HA	2.02	0.42
1:Q:183:THR:O	1:Q:187:ILE:HG12	2.19	0.42
1:A:74:PRO:HG3	1:A:85:LEU:HD22	2.02	0.42
1:A:77:ALA:HB3	1:A:85:LEU:HD11	2.00	0.42
1:B:29:PHE:HE2	1:B:31:ASP:HB2	1.84	0.42
2:C:26:LYS:HB2	2:C:29:PHE:HB2	2.01	0.42
1:E:282:ARG:HA	1:E:282:ARG:HD2	1.88	0.42
1:G:158:TYR:CZ	1:G:187:ILE:HG21	2.55	0.42
1:H:456:ALA:HB2	1:H:462:GLN:HA	2.01	0.42
1:J:148:PHE:HB3	1:J:234:GLN:NE2	2.35	0.42
1:J:399:ILE:O	1:J:482:ILE:HG23	2.20	0.42
1:K:183:THR:O	1:K:187:ILE:HG12	2.19	0.42
1:K:323:ILE:HB	1:K:342:LEU:HB3	2.02	0.42
1:M:93:ARG:NH1	1:M:284:THR:HA	2.35	0.42
1:M:100:ARG:NH1	1:M:243:VAL:HG22	2.35	0.42
1:P:11:ILE:HD13	1:P:66:GLN:HE21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:321:ARG:HG3	1:P:344:ILE:HD12	2.01	0.42
1:Q:29:PHE:HE2	1:Q:31:ASP:HB2	1.85	0.42
1:A:234:GLN:HB3	1:A:235:LYS:HZ2	1.85	0.42
2:C:26:LYS:HD3	2:C:30:ASP:H	1.85	0.42
2:C:97:PHE:CD2	2:C:100:LEU:HB2	2.55	0.42
2:C:151:TYR:HD2	2:C:152:LYS:HD2	1.85	0.42
1:D:415:LEU:HD11	1:D:442:ILE:HG12	2.01	0.42
2:I:80:GLN:HB2	2:I:119:ALA:HB2	2.01	0.42
1:J:402:THR:HG23	1:J:447:GLY:HA3	2.02	0.42
1:K:50:LEU:HD11	2:L:36:LEU:HD11	2.01	0.42
2:R:66:ILE:O	2:R:70:ILE:HG12	2.20	0.42
1:A:148:PHE:HB3	1:A:234:GLN:NE2	2.35	0.41
1:D:11:ILE:HD13	1:D:66:GLN:HE21	1.85	0.41
1:E:97:ARG:HG2	1:E:280:ARG:HB3	2.01	0.41
1:H:97:ARG:HG2	1:H:280:ARG:HB3	2.01	0.41
1:H:115:SER:HA	1:H:131:LEU:HB2	2.01	0.41
1:H:301:THR:HG23	2:I:142:SER:HB3	2.02	0.41
1:K:434:ILE:HG22	1:K:437:ARG:H	1.84	0.41
1:M:115:SER:HB3	1:M:116:PRO:HD3	2.02	0.41
1:N:164:VAL:HG13	1:N:223:LYS:HE3	2.01	0.41
2:O:78:VAL:HB	2:O:189:LEU:HG	2.01	0.41
1:P:116:PRO:HB2	1:P:117:PRO:HD3	2.01	0.41
1:Q:97:ARG:HG2	1:Q:280:ARG:HB3	2.02	0.41
1:Q:148:PHE:HB3	1:Q:234:GLN:HE22	1.85	0.41
1:D:148:PHE:HB3	1:D:234:GLN:NE2	2.35	0.41
1:E:122:SER:HB3	1:E:127:ARG:H	1.85	0.41
1:G:164:VAL:HA	1:G:223:LYS:HB2	2.03	0.41
1:G:400:SER:HB3	1:G:484:VAL:HA	2.02	0.41
1:K:63:GLU:HB3	1:K:67:MET:HE2	2.03	0.41
1:K:411:ILE:H	1:K:411:ILE:HG12	1.61	0.41
2:L:66:ILE:O	2:L:70:ILE:HG12	2.21	0.41
1:P:164:VAL:HG13	1:P:223:LYS:HE3	2.01	0.41
1:Q:120:MET:HE2	1:Q:120:MET:HB2	1.92	0.41
3:S:390:ASP:OD2	3:S:392:LEU:HB3	2.19	0.41
3:U:88:VAL:O	3:U:146:THR:HA	2.20	0.41
3:V:385:LYS:HB3	3:V:385:LYS:HE3	1.84	0.41
1:D:100:ARG:NH1	1:D:243:VAL:HG22	2.34	0.41
2:I:155:PHE:CE2	2:I:178:LEU:HD11	2.56	0.41
1:J:115:SER:HB3	1:J:116:PRO:HD3	2.02	0.41
1:K:97:ARG:HG2	1:K:280:ARG:HB3	2.01	0.41
1:Q:158:TYR:CZ	1:Q:187:ILE:HG21	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:SER:HB3	1:A:484:VAL:HA	2.02	0.41
2:C:75:ARG:HB2	2:C:122:PRO:HG2	2.00	0.41
1:D:28:VAL:HG21	1:E:49:ARG:HD3	2.02	0.41
1:G:59:GLU:O	1:G:63:GLU:HG2	2.21	0.41
1:J:94:HIS:CD2	1:J:280:ARG:HG2	2.54	0.41
2:L:79:TYR:HE1	2:L:189:LEU:HD12	1.84	0.41
1:N:453:LEU:HD22	1:N:453:LEU:HA	1.95	0.41
2:O:127:TYR:O	2:O:131:LEU:HG	2.20	0.41
1:Q:291:ARG:HH11	1:Q:292:PHE:HA	1.85	0.41
3:T:89:SER:HB3	3:T:164:THR:HB	2.02	0.41
3:X:39:ARG:HD3	3:X:80:ARG:HH21	1.85	0.41
3:X:225:LYS:HB3	3:X:292:GLU:HB3	2.02	0.41
1:A:74:PRO:HG3	1:A:85:LEU:HB3	2.02	0.41
1:A:320:VAL:HG23	1:A:345:VAL:HG22	2.03	0.41
1:E:394:PRO:HG2	1:E:458:LYS:HB3	2.01	0.41
1:H:433:VAL:HB	1:H:467:ILE:HB	2.02	0.41
2:I:75:ARG:HD3	2:I:127:TYR:CD1	2.55	0.41
1:J:158:TYR:CZ	1:J:187:ILE:HG21	2.55	0.41
2:L:159:GLU:HG3	2:L:175:GLY:HA3	2.02	0.41
1:M:321:ARG:HD3	1:M:429:ILE:HD12	2.01	0.41
1:M:389:ARG:HB3	1:M:390:PRO:HD3	2.02	0.41
1:N:167:ILE:HD12	1:N:167:ILE:HA	1.89	0.41
1:P:81:ALA:O	1:P:85:LEU:HG	2.20	0.41
1:P:94:HIS:CD2	1:P:280:ARG:HG2	2.52	0.41
1:P:148:PHE:HB3	1:P:234:GLN:NE2	2.35	0.41
1:P:201:ASN:ND2	1:P:202:THR:HG23	2.36	0.41
1:D:354:ALA:HB1	1:D:375:VAL:HB	2.03	0.41
1:E:418:ARG:HH11	1:E:444:GLU:HB2	1.85	0.41
2:F:12:LEU:O	2:F:16:ARG:HD3	2.20	0.41
1:J:67:MET:HE3	1:J:67:MET:HB3	1.99	0.41
1:P:28:VAL:HG21	1:Q:49:ARG:HD3	2.01	0.41
1:Q:167:ILE:HD12	1:Q:167:ILE:HA	1.90	0.41
3:V:277:HIS:C	3:V:312:ARG:HD2	2.45	0.41
1:A:418:ARG:NH1	1:A:444:GLU:HB2	2.35	0.41
1:B:160:LEU:HD11	1:B:225:PHE:HD2	1.85	0.41
1:E:289:ARG:H	1:E:289:ARG:HG3	1.64	0.41
2:I:78:VAL:HB	2:I:189:LEU:HG	2.03	0.41
1:J:147:ILE:H	1:J:147:ILE:HG13	1.71	0.41
1:K:282:ARG:HA	1:K:282:ARG:HD2	1.88	0.41
1:M:443:MET:HE3	1:M:443:MET:HB3	1.99	0.41
1:N:158:TYR:CZ	1:N:187:ILE:HG21	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:174:TYR:HB3	1:N:191:LEU:HD23	2.03	0.41
2:O:26:LYS:HD3	2:O:30:ASP:H	1.86	0.41
1:P:67:MET:HE1	2:R:51:GLN:HE22	1.86	0.41
1:Q:78:THR:HG23	1:Q:289:ARG:HH22	1.86	0.41
3:U:39:ARG:HD3	3:U:80:ARG:HH21	1.84	0.41
3:V:95:GLU:CD	3:V:115:ASP:H	2.28	0.41
3:X:277:HIS:C	3:X:312:ARG:HD2	2.45	0.41
1:A:147:ILE:H	1:A:147:ILE:HG13	1.75	0.41
2:C:155:PHE:CE2	2:C:178:LEU:HD11	2.56	0.41
1:D:29:PHE:CE1	1:E:49:ARG:HG3	2.56	0.41
1:D:443:MET:HA	1:D:448:PHE:HE1	1.86	0.41
1:E:436:SER:HB3	1:G:450:VAL:HG13	2.02	0.41
1:E:443:MET:HA	1:E:448:PHE:CE1	2.56	0.41
2:F:163:GLU:HB2	2:F:165:TYR:CZ	2.56	0.41
1:G:57:SER:O	1:G:61:ILE:HG12	2.21	0.41
1:G:363:PHE:CD2	2:I:144:PRO:HB3	2.56	0.41
1:G:429:ILE:HA	1:G:473:GLU:O	2.20	0.41
1:H:422:TYR:CE1	1:H:441:PRO:HD3	2.56	0.41
1:J:77:ALA:HB3	1:J:85:LEU:HD11	2.03	0.41
1:J:162:MET:HE1	1:J:172:ILE:HG13	2.03	0.41
1:J:303:ILE:HB	1:K:363:PHE:HE2	1.86	0.41
2:L:174:ILE:HG22	2:L:176:LYS:H	1.86	0.41
1:N:111:THR:HG22	1:N:113:ILE:HG23	2.03	0.41
3:U:95:GLU:CD	3:U:115:ASP:H	2.29	0.41
3:U:208:ILE:HD13	3:U:208:ILE:HA	1.95	0.41
1:A:57:SER:O	1:A:61:ILE:HG12	2.21	0.41
1:A:81:ALA:O	1:A:85:LEU:HG	2.21	0.41
1:A:115:SER:HB3	1:A:116:PRO:HD3	2.03	0.41
1:B:60:ALA:O	1:B:64:VAL:HG23	2.21	0.41
2:C:170:VAL:HB	2:C:204:TYR:CZ	2.56	0.41
1:D:161:LYS:O	1:D:226:GLU:HB2	2.21	0.41
1:E:60:ALA:O	1:E:64:VAL:HG23	2.20	0.41
1:E:307:LEU:HA	1:E:360:ASN:HD21	1.86	0.41
2:F:75:ARG:HD3	2:F:127:TYR:CD1	2.56	0.41
1:H:252:GLN:HB2	1:H:276:ALA:HB3	2.01	0.41
1:H:341:PHE:CD2	1:H:343:PRO:HD3	2.56	0.41
1:H:434:ILE:HG21	1:H:437:ARG:HG3	2.03	0.41
1:J:57:SER:O	1:J:61:ILE:HG12	2.21	0.41
1:K:22:ARG:HA	1:K:22:ARG:HD3	1.74	0.41
1:K:425:GLU:HG3	1:K:426:ASN:OD1	2.21	0.41
2:L:18:ARG:HA	2:L:18:ARG:HD2	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:139:ARG:NE	2:L:146:GLN:HG3	2.36	0.41
1:M:174:TYR:CZ	1:M:190:GLY:HA3	2.55	0.41
1:M:354:ALA:HB1	1:M:375:VAL:HB	2.01	0.41
1:N:148:PHE:HA	1:N:149:PRO:HD3	1.98	0.41
1:N:282:ARG:HA	1:N:282:ARG:HD2	1.91	0.41
2:O:75:ARG:HD3	2:O:127:TYR:CD1	2.55	0.41
1:P:24:VAL:O	1:P:28:VAL:HG13	2.21	0.41
1:P:456:ALA:HB2	1:P:462:GLN:HA	2.02	0.41
1:Q:389:ARG:HB3	1:Q:390:PRO:HD3	2.02	0.41
1:Q:394:PRO:HG2	1:Q:458:LYS:HB3	2.03	0.41
2:R:18:ARG:HA	2:R:18:ARG:HD2	1.90	0.41
3:T:373:ILE:H	3:T:373:ILE:HG13	1.74	0.41
3:U:89:SER:HB3	3:U:164:THR:HB	2.03	0.41
1:B:183:THR:O	1:B:187:ILE:HG12	2.21	0.41
2:F:94:ALA:C	2:F:102:ASP:HB3	2.46	0.41
1:H:100:ARG:NH1	1:H:243:VAL:HG22	2.36	0.41
1:H:111:THR:HG22	1:H:113:ILE:HG23	2.03	0.41
1:H:453:LEU:HD22	1:H:453:LEU:HA	1.92	0.41
2:I:94:ALA:C	2:I:102:ASP:HB3	2.45	0.41
1:K:104:VAL:HG13	1:K:271:ILE:HG13	2.03	0.41
2:L:139:ARG:NH2	2:L:142:SER:HA	2.36	0.41
1:Q:147:ILE:H	1:Q:147:ILE:HG13	1.79	0.41
3:X:140:THR:HB	3:X:148:THR:OG1	2.21	0.41
1:A:344:ILE:HG12	1:A:388:GLN:HB2	2.03	0.40
1:B:22:ARG:HA	1:B:22:ARG:HD3	1.72	0.40
1:D:111:THR:HB	1:D:137:LEU:HD13	2.04	0.40
1:D:164:VAL:HA	1:D:223:LYS:HB2	2.02	0.40
1:E:389:ARG:HB3	1:E:390:PRO:HD3	2.03	0.40
2:F:174:ILE:HG22	2:F:176:LYS:H	1.87	0.40
1:H:435:TYR:CE1	1:H:455:ILE:HD12	2.56	0.40
1:J:11:ILE:HD13	1:J:66:GLN:HE21	1.85	0.40
1:K:11:ILE:HG13	1:K:65:ILE:HD12	2.03	0.40
1:M:404:THR:HA	1:M:487:VAL:HG21	2.03	0.40
1:N:252:GLN:HB2	1:N:276:ALA:HB3	2.02	0.40
1:P:111:THR:HB	1:P:137:LEU:HD13	2.04	0.40
1:P:395:ILE:HG13	1:P:475:ALA:HB1	2.02	0.40
2:R:24:LYS:HD3	2:R:24:LYS:HA	1.96	0.40
3:T:95:GLU:CD	3:T:115:ASP:H	2.28	0.40
3:U:421:HIS:HB3	3:U:423:ARG:HH22	1.87	0.40
1:D:449:GLN:HB2	1:D:487:VAL:HA	2.02	0.40
1:E:422:TYR:CE1	1:E:441:PRO:HD3	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:79:TYR:HE1	2:F:189:LEU:HD12	1.86	0.40
1:G:23:ASN:O	1:G:27:GLN:HG2	2.21	0.40
1:G:341:PHE:HD1	1:G:365:ILE:HG22	1.85	0.40
1:H:425:GLU:HG3	1:H:426:ASN:OD1	2.21	0.40
1:J:156:LEU:H	1:J:176:SER:HB2	1.85	0.40
1:P:341:PHE:HD1	1:P:365:ILE:HG22	1.85	0.40
1:P:443:MET:HA	1:P:448:PHE:HE1	1.85	0.40
1:Q:108:ASN:HB2	1:Q:266:GLY:HA2	2.03	0.40
2:R:174:ILE:HG22	2:R:176:LYS:H	1.86	0.40
3:W:89:SER:HB3	3:W:164:THR:HB	2.03	0.40
1:A:24:VAL:O	1:A:28:VAL:HG13	2.22	0.40
1:B:97:ARG:HG2	1:B:280:ARG:HB3	2.03	0.40
1:B:149:PRO:HG3	1:B:231:LEU:HD12	2.02	0.40
1:B:255:LEU:HD12	1:B:255:LEU:HA	1.90	0.40
2:C:127:TYR:O	2:C:131:LEU:HG	2.21	0.40
1:D:74:PRO:HG3	1:D:85:LEU:HB3	2.03	0.40
1:E:106:GLU:HG2	1:E:237:ARG:HG2	2.03	0.40
1:G:116:PRO:HB2	1:G:117:PRO:HD3	2.03	0.40
1:H:60:ALA:O	1:H:64:VAL:HG23	2.20	0.40
1:H:157:THR:HG22	1:H:175:THR:HA	2.03	0.40
1:H:389:ARG:HB3	1:H:390:PRO:HD3	2.02	0.40
2:I:162:LEU:HG	2:I:172:ILE:HG12	2.01	0.40
1:J:363:PHE:CG	2:L:144:PRO:HB3	2.56	0.40
1:K:60:ALA:O	1:K:64:VAL:HG23	2.21	0.40
3:U:140:THR:HB	3:U:148:THR:OG1	2.20	0.40
1:A:59:GLU:O	1:A:63:GLU:HG2	2.21	0.40
1:B:104:VAL:HG13	1:B:271:ILE:HG13	2.03	0.40
2:C:182:GLU:O	2:C:186:LEU:HG	2.22	0.40
1:H:418:ARG:NH1	1:H:444:GLU:HB2	2.36	0.40
1:M:403:ASN:HB2	1:M:487:VAL:HG13	2.02	0.40
1:N:159:GLU:HA	1:N:173:LYS:HB3	2.02	0.40
1:N:443:MET:HA	1:N:448:PHE:HE1	1.86	0.40
1:P:174:TYR:HB3	1:P:191:LEU:HD23	2.02	0.40
2:R:75:ARG:HD3	2:R:127:TYR:CD1	2.56	0.40
2:R:79:TYR:HE1	2:R:189:LEU:HD12	1.85	0.40
3:V:29:PHE:HE2	3:V:31:ALA:HB2	1.86	0.40
3:W:306:ARG:HA	3:W:311:ASN:HA	2.04	0.40
3:X:72:LYS:HB2	3:X:72:LYS:HE3	1.90	0.40
2:C:129:MET:HE1	2:C:154:VAL:HA	2.04	0.40
1:E:252:GLN:HB2	1:E:276:ALA:HB3	2.03	0.40
1:E:392:GLU:HA	1:E:474:VAL:H	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:435:TYR:HD2	1:G:450:VAL:HG21	1.85	0.40
1:H:25:ALA:HA	1:H:28:VAL:HG13	2.04	0.40
2:I:26:LYS:HB2	2:I:29:PHE:HB2	2.04	0.40
1:J:404:THR:HA	1:J:487:VAL:HG21	2.04	0.40
1:K:389:ARG:HB3	1:K:390:PRO:HD3	2.04	0.40
1:M:161:LYS:O	1:M:226:GLU:HB2	2.21	0.40
1:P:57:SER:O	1:P:61:ILE:HG12	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	482/487 (99%)	456 (95%)	23 (5%)	3 (1%)	21	58
1	B	481/487 (99%)	454 (94%)	24 (5%)	3 (1%)	21	58
1	D	482/487 (99%)	458 (95%)	21 (4%)	3 (1%)	21	58
1	E	481/487 (99%)	453 (94%)	25 (5%)	3 (1%)	21	58
1	G	482/487 (99%)	456 (95%)	23 (5%)	3 (1%)	21	58
1	H	481/487 (99%)	457 (95%)	21 (4%)	3 (1%)	21	58
1	J	482/487 (99%)	455 (94%)	24 (5%)	3 (1%)	21	58
1	K	481/487 (99%)	451 (94%)	27 (6%)	3 (1%)	21	58
1	M	482/487 (99%)	459 (95%)	20 (4%)	3 (1%)	21	58
1	N	481/487 (99%)	455 (95%)	23 (5%)	3 (1%)	21	58
1	P	482/487 (99%)	459 (95%)	20 (4%)	3 (1%)	21	58
1	Q	481/487 (99%)	456 (95%)	22 (5%)	3 (1%)	21	58
2	C	239/243 (98%)	218 (91%)	20 (8%)	1 (0%)	30	67
2	F	239/243 (98%)	215 (90%)	23 (10%)	1 (0%)	30	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	I	239/243 (98%)	213 (89%)	25 (10%)	1 (0%)	30	67
2	L	239/243 (98%)	218 (91%)	20 (8%)	1 (0%)	30	67
2	O	239/243 (98%)	212 (89%)	26 (11%)	1 (0%)	30	67
2	R	239/243 (98%)	214 (90%)	24 (10%)	1 (0%)	30	67
3	S	425/428 (99%)	412 (97%)	12 (3%)	1 (0%)	43	77
3	T	425/428 (99%)	412 (97%)	12 (3%)	1 (0%)	43	77
3	U	425/428 (99%)	410 (96%)	14 (3%)	1 (0%)	43	77
3	V	425/428 (99%)	414 (97%)	10 (2%)	1 (0%)	43	77
3	W	425/428 (99%)	415 (98%)	9 (2%)	1 (0%)	43	77
3	X	425/428 (99%)	414 (97%)	10 (2%)	1 (0%)	43	77
All	All	9762/9870 (99%)	9236 (95%)	478 (5%)	48 (0%)	26	63

All (48) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	298	VAL
1	A	389	ARG
1	B	389	ARG
1	D	298	VAL
1	D	389	ARG
1	E	389	ARG
1	G	298	VAL
1	G	389	ARG
1	H	389	ARG
1	J	298	VAL
1	J	389	ARG
1	M	298	VAL
1	M	389	ARG
1	N	389	ARG
1	P	298	VAL
1	P	389	ARG
1	Q	389	ARG
2	C	220	PHE
2	F	220	PHE
2	I	220	PHE
1	K	389	ARG
2	L	220	PHE
2	O	220	PHE

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Mol	Chain	Res	Type
2	R	220	PHE
3	S	19	VAL
3	T	19	VAL
3	U	19	VAL
3	V	19	VAL
3	W	19	VAL
3	X	19	VAL
1	A	169	THR
1	D	169	THR
1	E	169	THR
1	G	169	THR
1	J	169	THR
1	N	169	THR
1	P	169	THR
1	Q	169	THR
1	B	169	THR
1	H	169	THR
1	K	169	THR
1	M	169	THR
1	N	55	ALA
1	H	55	ALA
1	E	55	ALA
1	B	55	ALA
1	K	55	ALA
1	Q	55	ALA

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	410/411 (100%)	394 (96%)	16 (4%)	28	50
1	B	409/411 (100%)	400 (98%)	9 (2%)	45	64
1	D	410/411 (100%)	391 (95%)	19 (5%)	24	46
1	E	409/411 (100%)	399 (98%)	10 (2%)	43	63
1	G	410/411 (100%)	398 (97%)	12 (3%)	37	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	409/411 (100%)	402 (98%)	7 (2%)	53	68
1	J	410/411 (100%)	395 (96%)	15 (4%)	30	51
1	K	409/411 (100%)	397 (97%)	12 (3%)	37	58
1	M	410/411 (100%)	396 (97%)	14 (3%)	32	54
1	N	409/411 (100%)	402 (98%)	7 (2%)	53	68
1	P	410/411 (100%)	398 (97%)	12 (3%)	37	58
1	Q	409/411 (100%)	401 (98%)	8 (2%)	48	66
2	C	196/198 (99%)	187 (95%)	9 (5%)	24	46
2	F	196/198 (99%)	189 (96%)	7 (4%)	31	52
2	I	196/198 (99%)	186 (95%)	10 (5%)	21	43
2	L	196/198 (99%)	188 (96%)	8 (4%)	27	49
2	O	196/198 (99%)	189 (96%)	7 (4%)	31	52
2	R	196/198 (99%)	191 (97%)	5 (3%)	40	61
3	S	343/344 (100%)	338 (98%)	5 (2%)	57	71
3	T	343/344 (100%)	338 (98%)	5 (2%)	57	71
3	U	343/344 (100%)	338 (98%)	5 (2%)	57	71
3	V	343/344 (100%)	338 (98%)	5 (2%)	57	71
3	W	343/344 (100%)	338 (98%)	5 (2%)	57	71
3	X	343/344 (100%)	338 (98%)	5 (2%)	57	71
All	All	8148/8184 (100%)	7931 (97%)	217 (3%)	40	60

All (217) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	LEU
1	A	104	VAL
1	A	113	ILE
1	A	207	GLU
1	A	257	ILE
1	A	281	LEU
1	A	342	LEU
1	A	355	GLN
1	A	363	PHE
1	A	375	VAL
1	A	400	SER

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Mol	Chain	Res	Type
1	A	401	VAL
1	A	407	MET
1	A	411	ILE
1	A	450	VAL
1	A	484	VAL
1	B	33	VAL
1	B	104	VAL
1	B	237	ARG
1	B	278	THR
1	B	342	LEU
1	B	401	VAL
1	B	407	MET
1	B	453	LEU
1	B	485	THR
2	C	36	LEU
2	C	129	MET
2	C	134	LYS
2	C	139	ARG
2	C	143	THR
2	C	146	GLN
2	C	196	LEU
2	C	218	GLU
2	C	242	VAL
1	D	18	LEU
1	D	73	ASN
1	D	104	VAL
1	D	113	ILE
1	D	207	GLU
1	D	257	ILE
1	D	281	LEU
1	D	321	ARG
1	D	342	LEU
1	D	355	GLN
1	D	375	VAL
1	D	400	SER
1	D	401	VAL
1	D	407	MET
1	D	411	ILE
1	D	429	ILE
1	D	449	GLN
1	D	450	VAL
1	D	484	VAL

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Mol	Chain	Res	Type
1	E	104	VAL
1	E	237	ARG
1	E	359	LEU
1	E	400	SER
1	E	401	VAL
1	E	407	MET
1	E	411	ILE
1	E	453	LEU
1	E	484	VAL
1	E	487	VAL
2	F	139	ARG
2	F	143	THR
2	F	196	LEU
2	F	214	VAL
2	F	218	GLU
2	F	234	VAL
2	F	242	VAL
1	G	104	VAL
1	G	113	ILE
1	G	207	GLU
1	G	281	LEU
1	G	375	VAL
1	G	400	SER
1	G	401	VAL
1	G	407	MET
1	G	411	ILE
1	G	450	VAL
1	G	484	VAL
1	G	487	VAL
1	H	33	VAL
1	H	104	VAL
1	H	359	LEU
1	H	401	VAL
1	H	407	MET
1	H	453	LEU
1	H	485	THR
2	I	26	LYS
2	I	62	LYS
2	I	129	MET
2	I	139	ARG
2	I	143	THR
2	I	196	LEU

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Mol	Chain	Res	Type
2	I	199	THR
2	I	218	GLU
2	I	234	VAL
2	I	242	VAL
1	J	104	VAL
1	J	113	ILE
1	J	207	GLU
1	J	257	ILE
1	J	281	LEU
1	J	342	LEU
1	J	355	GLN
1	J	363	PHE
1	J	375	VAL
1	J	400	SER
1	J	401	VAL
1	J	407	MET
1	J	411	ILE
1	J	450	VAL
1	J	484	VAL
1	K	33	VAL
1	K	104	VAL
1	K	162	MET
1	K	237	ARG
1	K	342	LEU
1	K	400	SER
1	K	401	VAL
1	K	407	MET
1	K	411	ILE
1	K	453	LEU
1	K	484	VAL
1	K	487	VAL
2	L	20	THR
2	L	36	LEU
2	L	134	LYS
2	L	139	ARG
2	L	143	THR
2	L	196	LEU
2	L	218	GLU
2	L	242	VAL
1	M	104	VAL
1	M	113	ILE
1	M	207	GLU

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Mol	Chain	Res	Type
1	M	281	LEU
1	M	321	ARG
1	M	355	GLN
1	M	375	VAL
1	M	400	SER
1	M	401	VAL
1	M	407	MET
1	M	411	ILE
1	M	449	GLN
1	M	450	VAL
1	M	484	VAL
1	N	104	VAL
1	N	272	ASN
1	N	359	LEU
1	N	401	VAL
1	N	407	MET
1	N	453	LEU
1	N	485	THR
2	O	129	MET
2	O	139	ARG
2	O	143	THR
2	O	146	GLN
2	O	196	LEU
2	O	218	GLU
2	O	242	VAL
1	P	104	VAL
1	P	113	ILE
1	P	207	GLU
1	P	257	ILE
1	P	281	LEU
1	P	342	LEU
1	P	375	VAL
1	P	401	VAL
1	P	407	MET
1	P	411	ILE
1	P	450	VAL
1	P	485	THR
1	Q	33	VAL
1	Q	104	VAL
1	Q	375	VAL
1	Q	401	VAL
1	Q	407	MET

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Mol	Chain	Res	Type
1	Q	411	ILE
1	Q	453	LEU
1	Q	485	THR
2	R	139	ARG
2	R	143	THR
2	R	196	LEU
2	R	218	GLU
2	R	242	VAL
3	S	24	PHE
3	S	103	VAL
3	S	353	TYR
3	S	378	LEU
3	S	385	LYS
3	T	24	PHE
3	T	103	VAL
3	T	353	TYR
3	T	378	LEU
3	T	385	LYS
3	U	24	PHE
3	U	103	VAL
3	U	353	TYR
3	U	378	LEU
3	U	385	LYS
3	V	24	PHE
3	V	103	VAL
3	V	353	TYR
3	V	378	LEU
3	V	385	LYS
3	W	24	PHE
3	W	103	VAL
3	W	353	TYR
3	W	378	LEU
3	W	385	LYS
3	X	24	PHE
3	X	103	VAL
3	X	353	TYR
3	X	378	LEU
3	X	385	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (88) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	168	ASN
1	A	234	GLN
1	A	325	ASN
1	A	403	ASN
1	A	410	ASN
1	B	73	ASN
1	B	221	ASN
1	B	252	GLN
1	B	325	ASN
2	C	5	GLN
2	C	210	GLN
1	D	234	GLN
1	D	313	ASN
1	E	73	ASN
1	E	221	ASN
1	E	325	ASN
1	E	355	GLN
1	E	388	GLN
1	E	403	ASN
1	E	449	GLN
1	G	70	ASN
1	G	84	ASN
1	G	168	ASN
1	G	403	ASN
1	G	410	ASN
1	H	73	ASN
1	H	84	ASN
1	H	221	ASN
1	H	325	ASN
1	H	355	GLN
1	H	388	GLN
2	I	4	ASN
2	I	146	GLN
1	J	209	ASN
1	J	234	GLN
1	J	325	ASN
1	J	410	ASN
1	J	460	GLN
1	K	73	ASN
1	K	325	ASN
1	K	355	GLN
1	K	403	ASN

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Mol	Chain	Res	Type
1	K	449	GLN
2	L	4	ASN
1	M	230	ASN
1	M	403	ASN
1	N	73	ASN
1	N	221	ASN
1	N	355	GLN
1	N	360	ASN
1	N	388	GLN
1	N	410	ASN
1	P	73	ASN
1	P	234	GLN
1	P	325	ASN
1	P	410	ASN
1	Q	73	ASN
1	Q	84	ASN
1	Q	252	GLN
1	Q	325	ASN
1	Q	388	GLN
2	R	51	GLN
2	R	138	ASN
3	S	35	ASN
3	S	97	GLN
3	S	142	ASN
3	S	185	ASN
3	S	207	HIS
3	T	35	ASN
3	T	185	ASN
3	T	207	HIS
3	U	142	ASN
3	U	185	ASN
3	U	207	HIS
3	V	33	HIS
3	V	35	ASN
3	V	142	ASN
3	V	185	ASN
3	V	207	HIS
3	V	298	ASN
3	W	35	ASN
3	W	142	ASN
3	W	185	ASN
3	W	207	HIS

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Mol	Chain	Res	Type
3	X	142	ASN
3	X	185	ASN
3	X	207	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

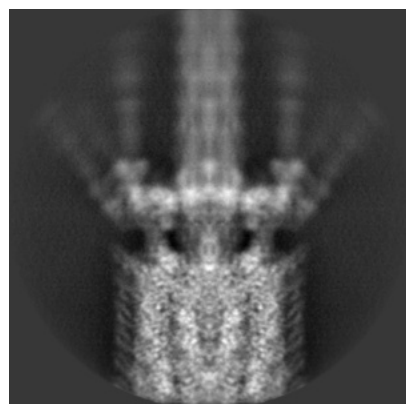
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74065. These allow visual inspection of the internal detail of the map and identification of artifacts.

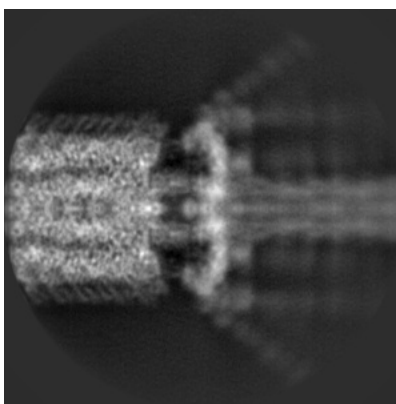
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

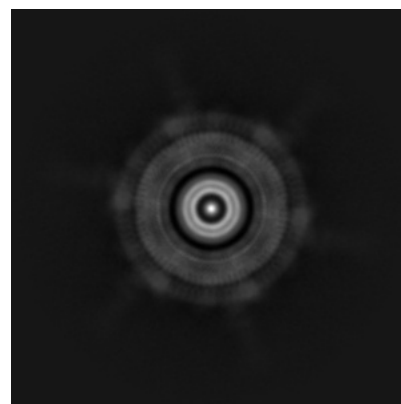
6.1.1 Primary map



X

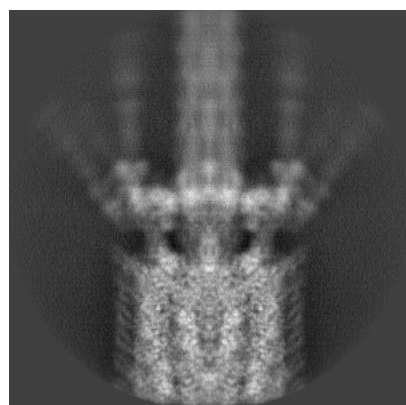


Y

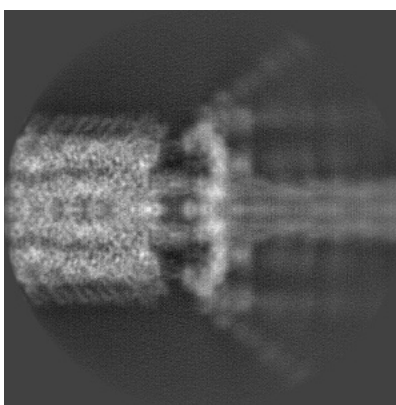


Z

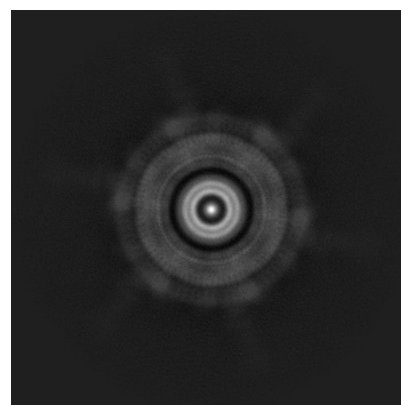
6.1.2 Raw map



X



Y

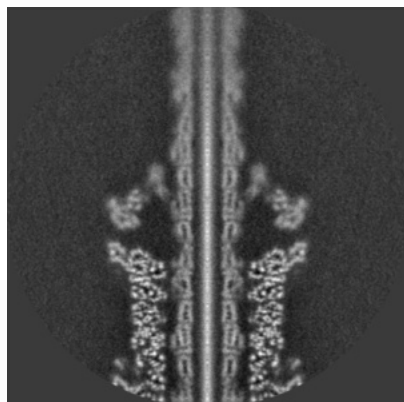


Z

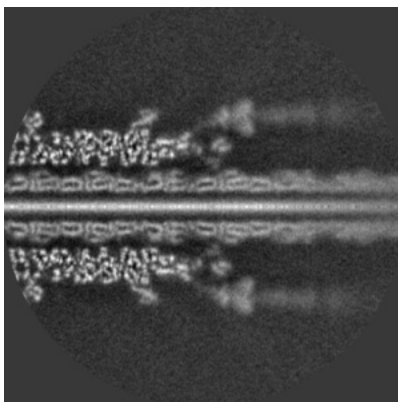
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

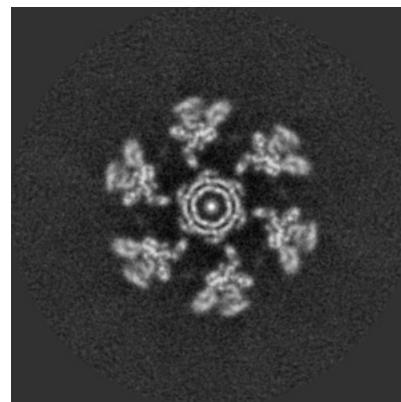
6.2.1 Primary map



X Index: 256

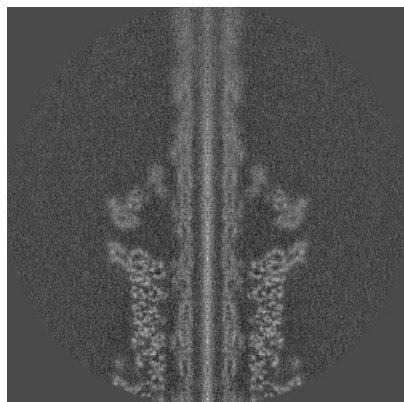


Y Index: 256

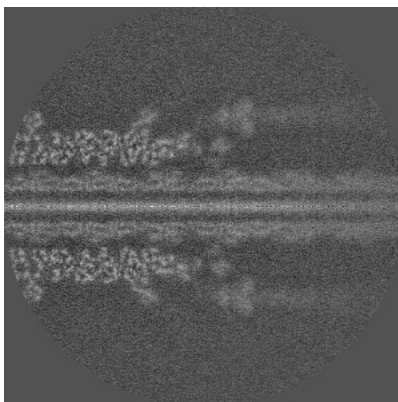


Z Index: 256

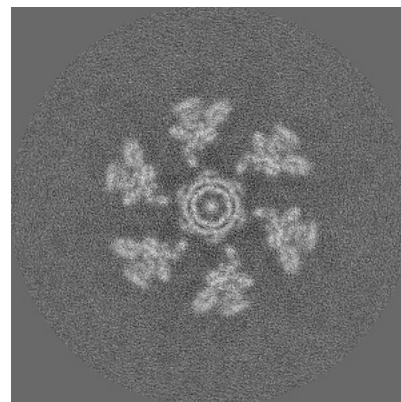
6.2.2 Raw map



X Index: 256



Y Index: 256

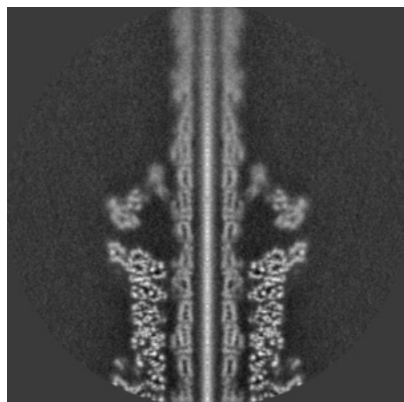


Z Index: 256

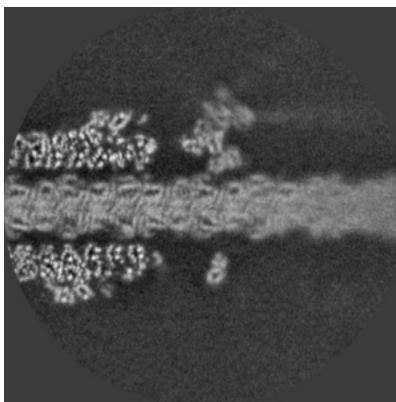
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

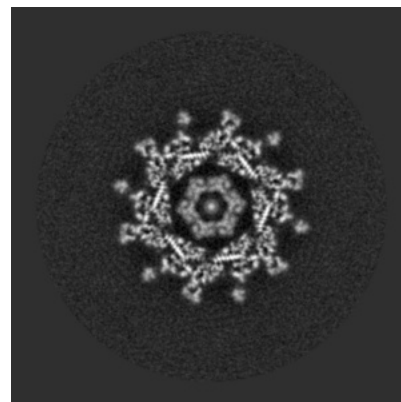
6.3.1 Primary map



X Index: 256

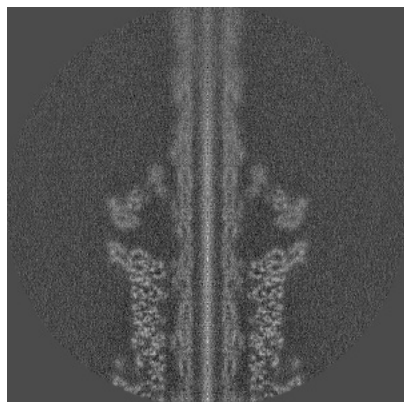


Y Index: 234

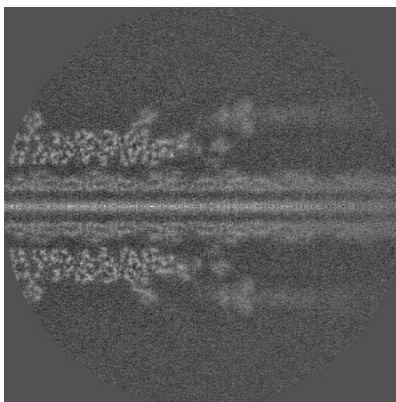


Z Index: 130

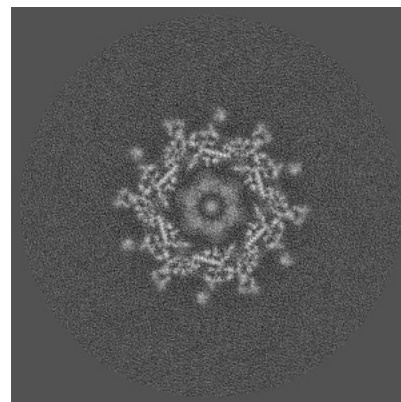
6.3.2 Raw map



X Index: 256



Y Index: 256

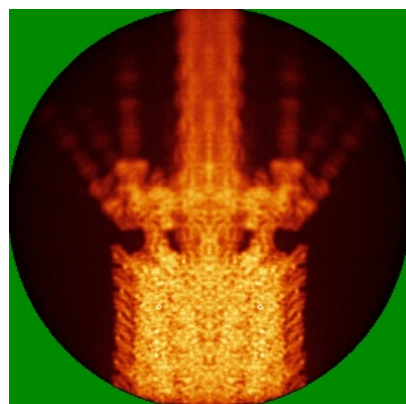


Z Index: 176

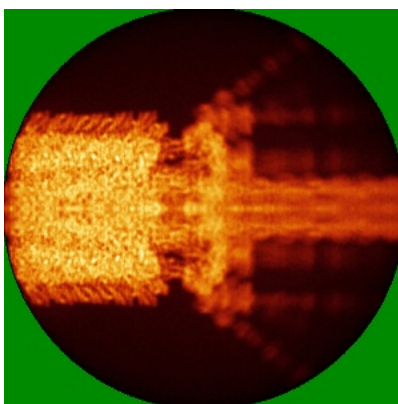
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

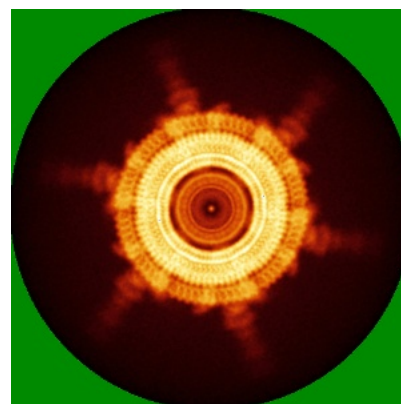
6.4.1 Primary map



X

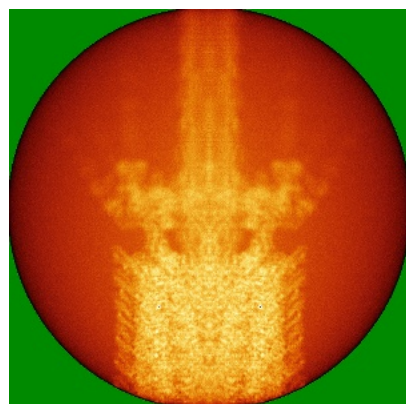


Y

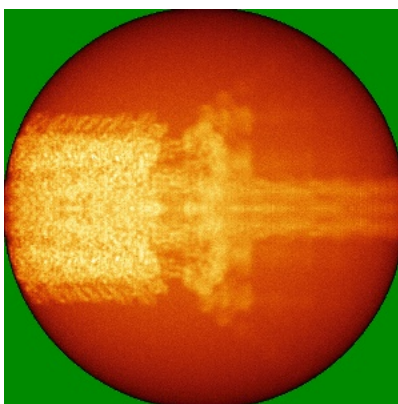


Z

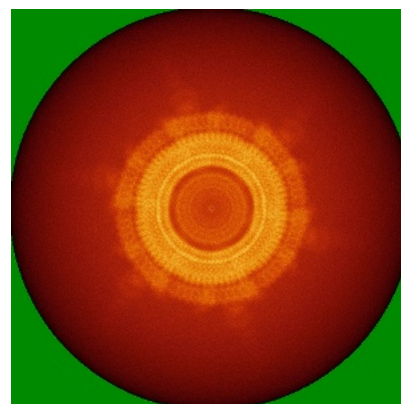
6.4.2 Raw map



X



Y



Z

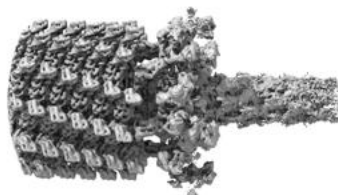
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

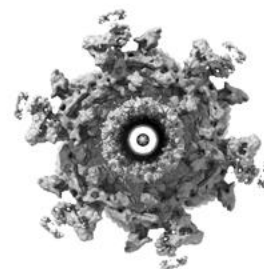
6.5.1 Primary map



X



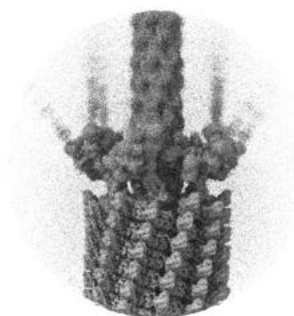
Y



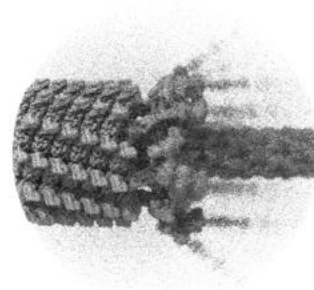
Z

The images above show the 3D surface view of the map at the recommended contour level 0.00709. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

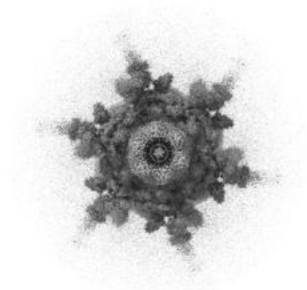
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

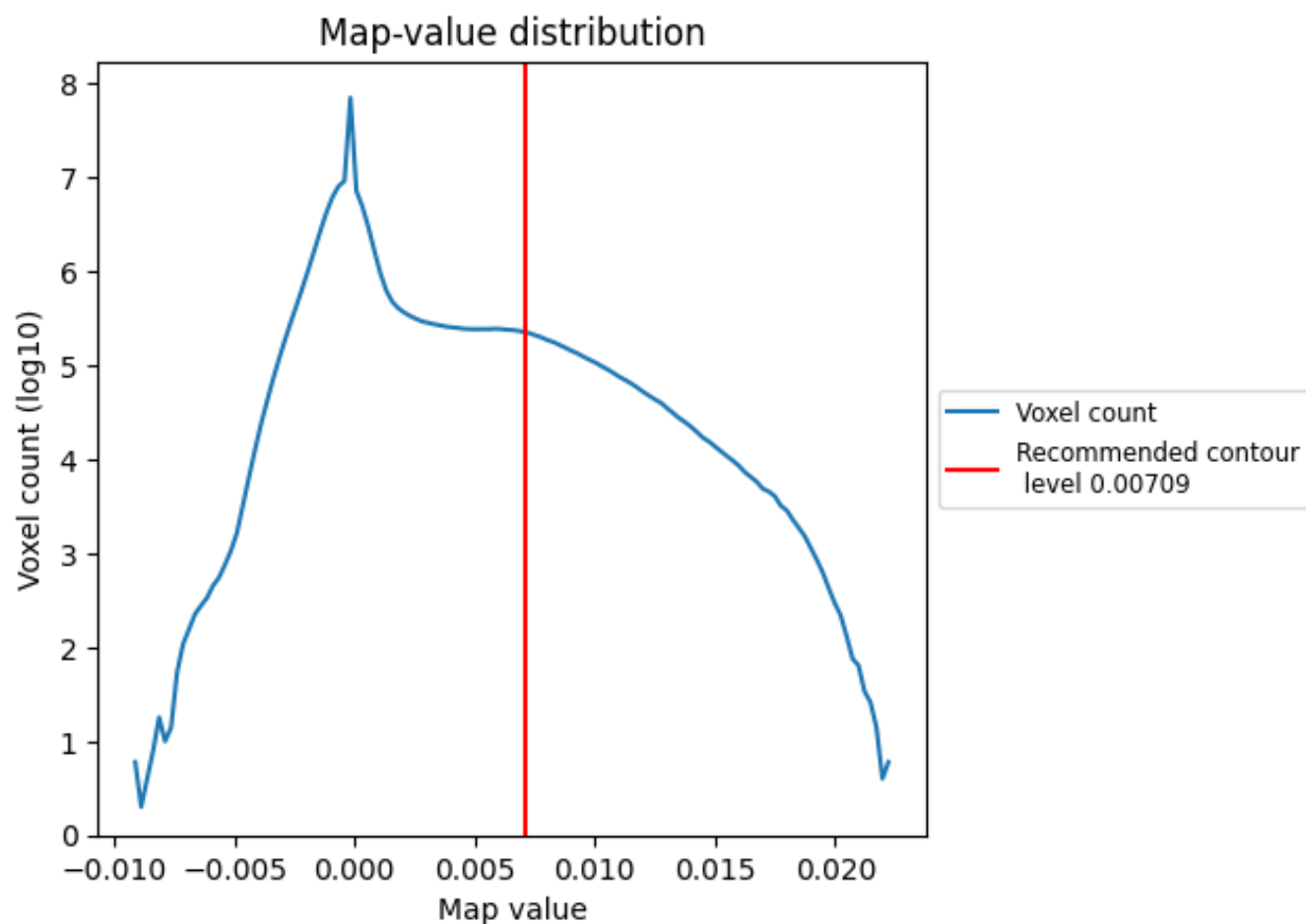
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

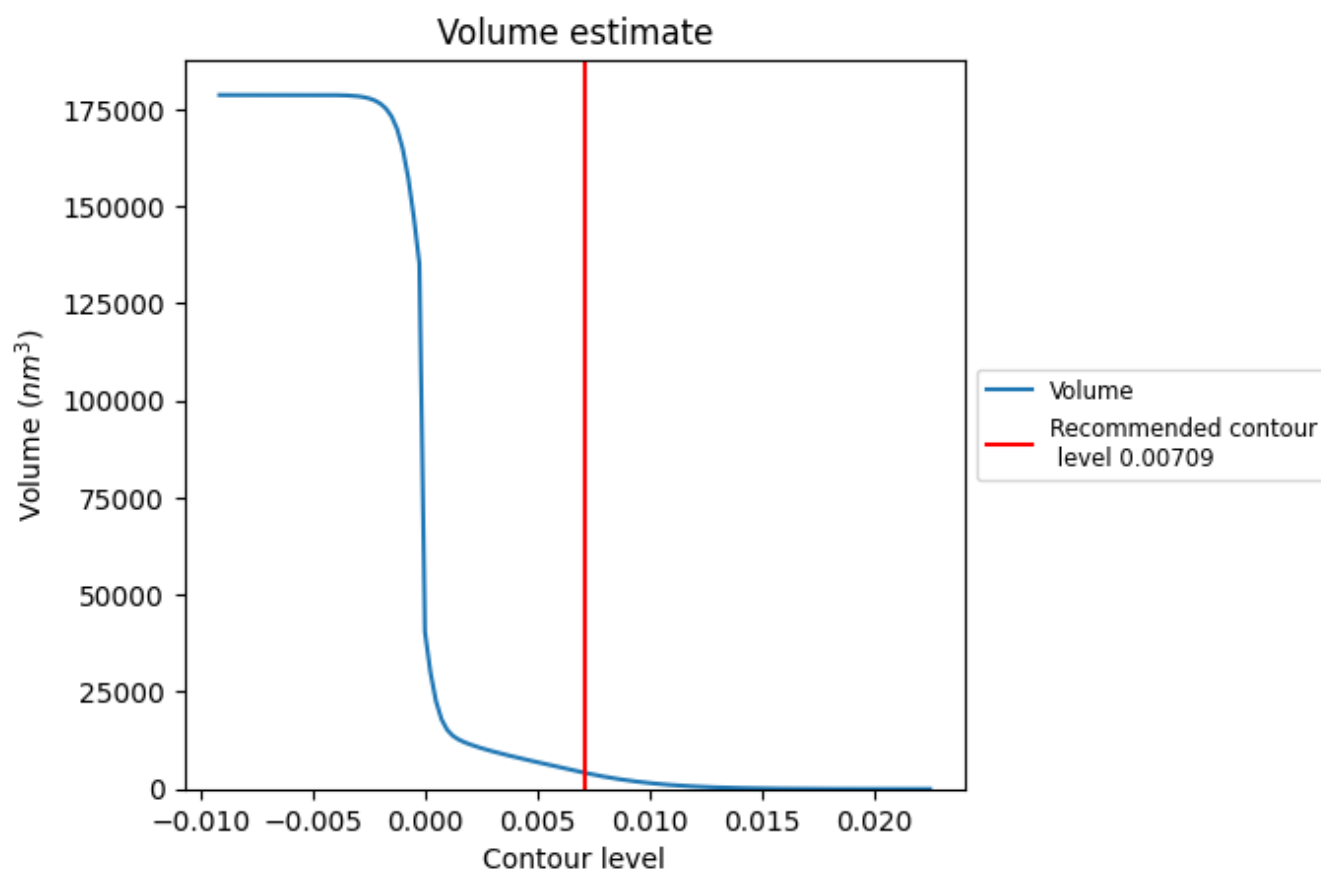
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

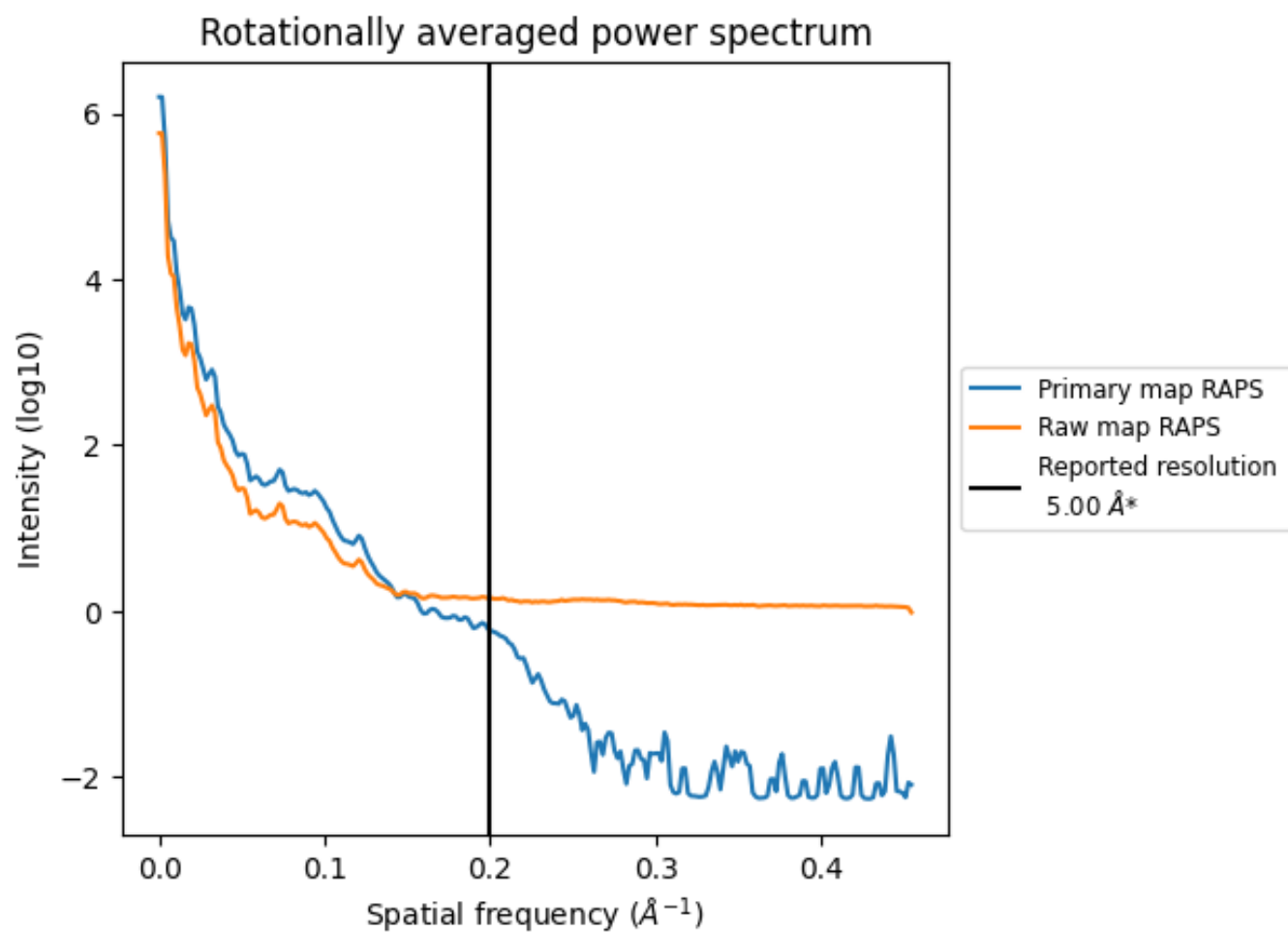
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4187 nm³; this corresponds to an approximate mass of 3782 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

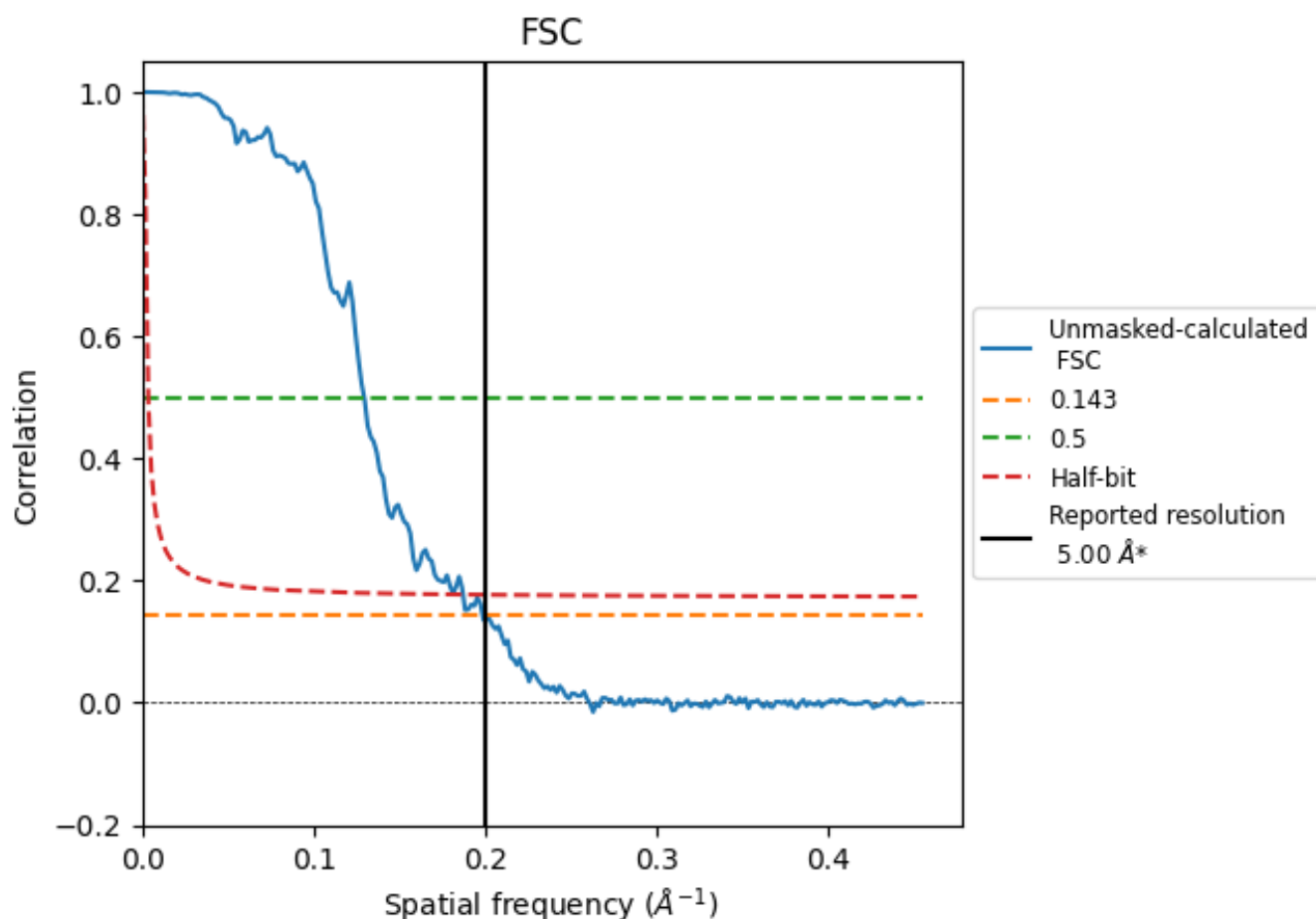


*Reported resolution corresponds to spatial frequency of 0.200 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.200 Å⁻¹

8.2 Resolution estimates [i](#)

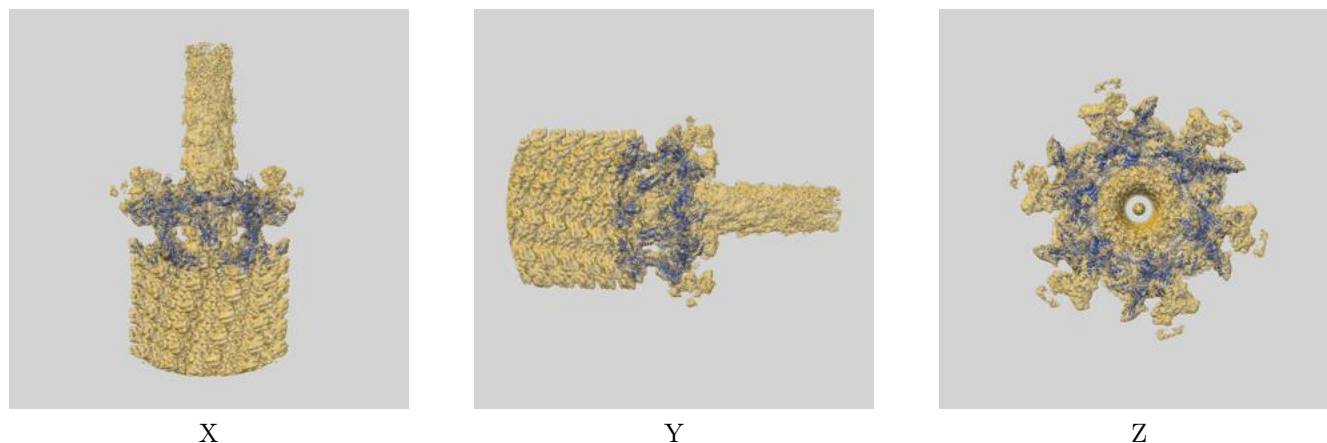
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.04	7.73	5.35

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

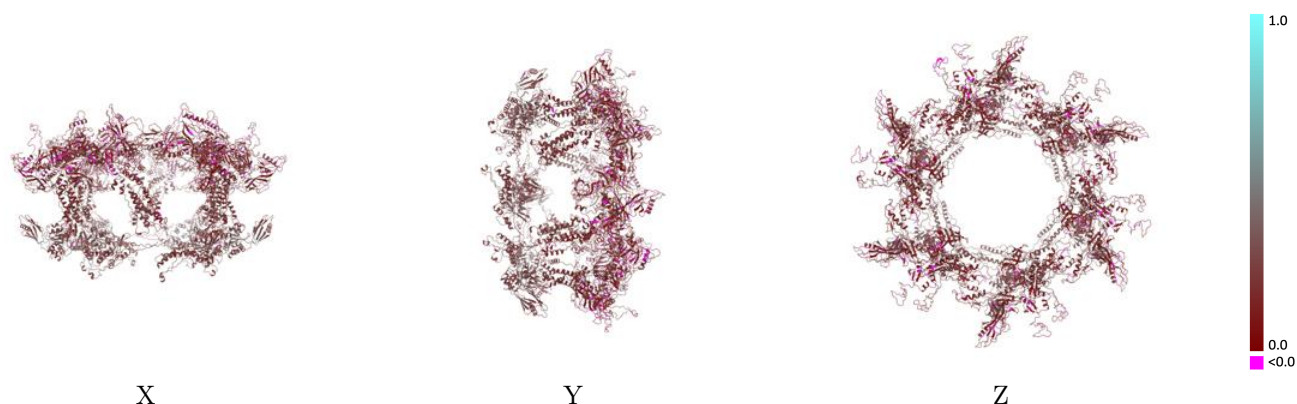
This section contains information regarding the fit between EMDB map EMD-74065 and PDB model 9ZDK. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



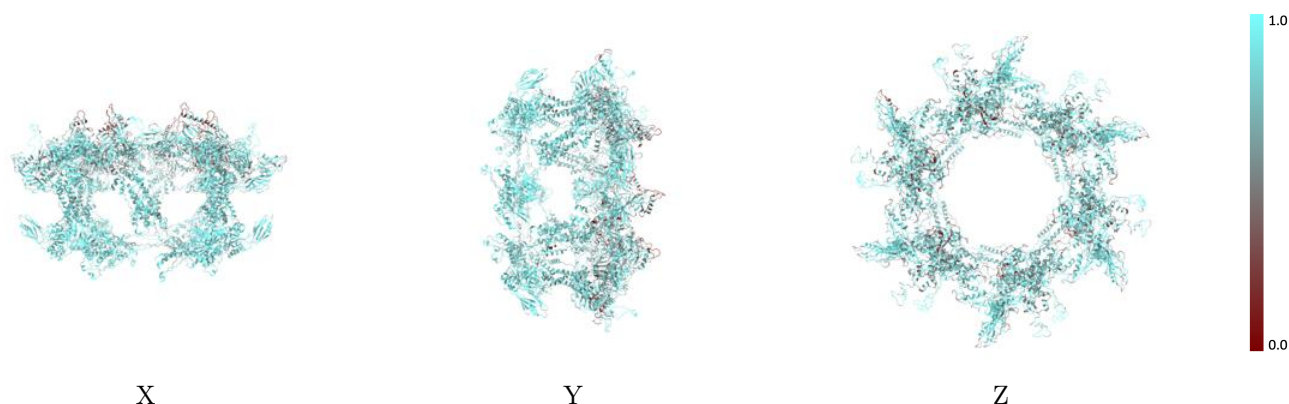
The images above show the 3D surface view of the map at the recommended contour level 0.00709 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



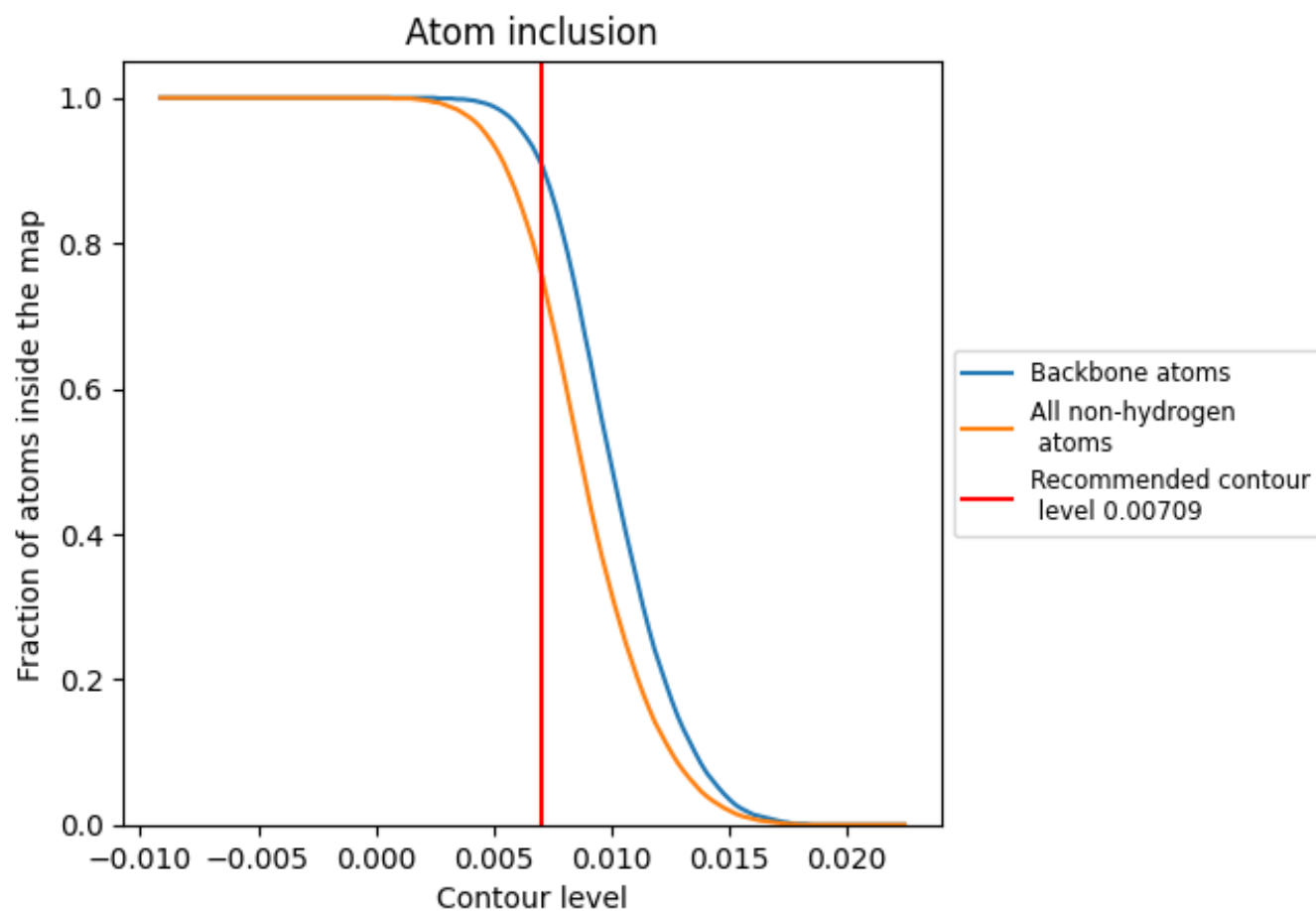
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00709).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.00709) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7530	 0.2190
A	 0.7890	 0.2050
B	 0.6650	 0.1850
C	 0.7510	 0.1880
D	 0.7510	 0.1900
E	 0.6650	 0.1840
F	 0.7850	 0.2110
G	 0.7900	 0.2070
H	 0.6480	 0.1730
I	 0.7210	 0.1610
J	 0.7690	 0.2000
K	 0.6720	 0.1890
L	 0.7510	 0.1880
M	 0.7440	 0.1890
N	 0.6500	 0.1770
O	 0.7500	 0.1880
P	 0.7750	 0.2000
Q	 0.6560	 0.1810
R	 0.7660	 0.2020
S	 0.8350	 0.2950
T	 0.8410	 0.3030
U	 0.8360	 0.3050
V	 0.8390	 0.3060
W	 0.8400	 0.3060
X	 0.8390	 0.3020

