Full wwPDB EM Validation Report ⓘ

Feb 29, 2024 – 10:08 PM JST

PDB ID	:	8X82
EMDB ID	:	EMD-38133
Title	:	The cryo-EM structure of insect gustatory receptor Gr43a I418A from Drosophila melanogaster
Authors	:	Ma, D.; Guo, J.
Deposited on	:	2023-11-27
Resolution	:	2.80 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:

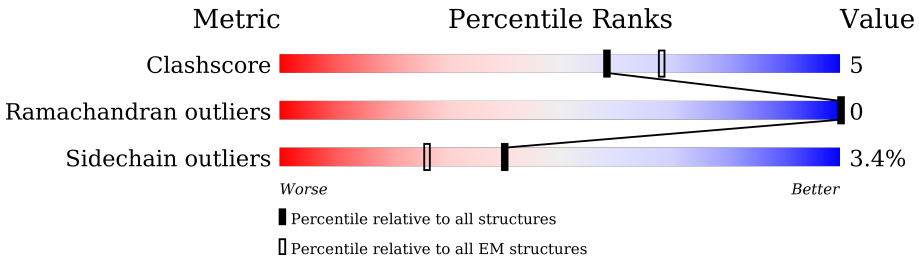
EMDB validation analysis	:	FAILED
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	443	73% 12% • 14%
1	B	443	72% 13% • 14%
1	C	443	73% 12% • 14%
1	D	443	72% 13% • 14%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 12004 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 Gustatory receptor for sugar taste 43a.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	380	Total	C	N	O	S	0	0
			3001	1949	512	522	18		
1	B	380	Total	C	N	O	S	0	0
			3001	1949	512	522	18		
1	C	380	Total	C	N	O	S	0	0
			3001	1949	512	522	18		
1	D	380	Total	C	N	O	S	0	0
			3001	1949	512	522	18		

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	418	ALA	ILE	engineered mutation	UNP Q9V4K2
A	428	LEU	-	expression tag	UNP Q9V4K2
A	429	GLU	-	expression tag	UNP Q9V4K2
A	430	GLY	-	expression tag	UNP Q9V4K2
A	431	GLY	-	expression tag	UNP Q9V4K2
A	432	SER	-	expression tag	UNP Q9V4K2
A	433	SER	-	expression tag	UNP Q9V4K2
A	434	GLY	-	expression tag	UNP Q9V4K2
A	435	GLY	-	expression tag	UNP Q9V4K2
A	436	TRP	-	expression tag	UNP Q9V4K2
A	437	SER	-	expression tag	UNP Q9V4K2
A	438	HIS	-	expression tag	UNP Q9V4K2
A	439	PRO	-	expression tag	UNP Q9V4K2
A	440	GLN	-	expression tag	UNP Q9V4K2
A	441	PHE	-	expression tag	UNP Q9V4K2
A	442	GLU	-	expression tag	UNP Q9V4K2
A	443	LYS	-	expression tag	UNP Q9V4K2
B	418	ALA	ILE	engineered mutation	UNP Q9V4K2
B	428	LEU	-	expression tag	UNP Q9V4K2
B	429	GLU	-	expression tag	UNP Q9V4K2
B	430	GLY	-	expression tag	UNP Q9V4K2
B	431	GLY	-	expression tag	UNP Q9V4K2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	432	SER	-	expression tag	UNP Q9V4K2
B	433	SER	-	expression tag	UNP Q9V4K2
B	434	GLY	-	expression tag	UNP Q9V4K2
B	435	GLY	-	expression tag	UNP Q9V4K2
B	436	TRP	-	expression tag	UNP Q9V4K2
B	437	SER	-	expression tag	UNP Q9V4K2
B	438	HIS	-	expression tag	UNP Q9V4K2
B	439	PRO	-	expression tag	UNP Q9V4K2
B	440	GLN	-	expression tag	UNP Q9V4K2
B	441	PHE	-	expression tag	UNP Q9V4K2
B	442	GLU	-	expression tag	UNP Q9V4K2
B	443	LYS	-	expression tag	UNP Q9V4K2
C	418	ALA	ILE	engineered mutation	UNP Q9V4K2
C	428	LEU	-	expression tag	UNP Q9V4K2
C	429	GLU	-	expression tag	UNP Q9V4K2
C	430	GLY	-	expression tag	UNP Q9V4K2
C	431	GLY	-	expression tag	UNP Q9V4K2
C	432	SER	-	expression tag	UNP Q9V4K2
C	433	SER	-	expression tag	UNP Q9V4K2
C	434	GLY	-	expression tag	UNP Q9V4K2
C	435	GLY	-	expression tag	UNP Q9V4K2
C	436	TRP	-	expression tag	UNP Q9V4K2
C	437	SER	-	expression tag	UNP Q9V4K2
C	438	HIS	-	expression tag	UNP Q9V4K2
C	439	PRO	-	expression tag	UNP Q9V4K2
C	440	GLN	-	expression tag	UNP Q9V4K2
C	441	PHE	-	expression tag	UNP Q9V4K2
C	442	GLU	-	expression tag	UNP Q9V4K2
C	443	LYS	-	expression tag	UNP Q9V4K2
D	418	ALA	ILE	engineered mutation	UNP Q9V4K2
D	428	LEU	-	expression tag	UNP Q9V4K2
D	429	GLU	-	expression tag	UNP Q9V4K2
D	430	GLY	-	expression tag	UNP Q9V4K2
D	431	GLY	-	expression tag	UNP Q9V4K2
D	432	SER	-	expression tag	UNP Q9V4K2
D	433	SER	-	expression tag	UNP Q9V4K2
D	434	GLY	-	expression tag	UNP Q9V4K2
D	435	GLY	-	expression tag	UNP Q9V4K2
D	436	TRP	-	expression tag	UNP Q9V4K2
D	437	SER	-	expression tag	UNP Q9V4K2
D	438	HIS	-	expression tag	UNP Q9V4K2
D	439	PRO	-	expression tag	UNP Q9V4K2

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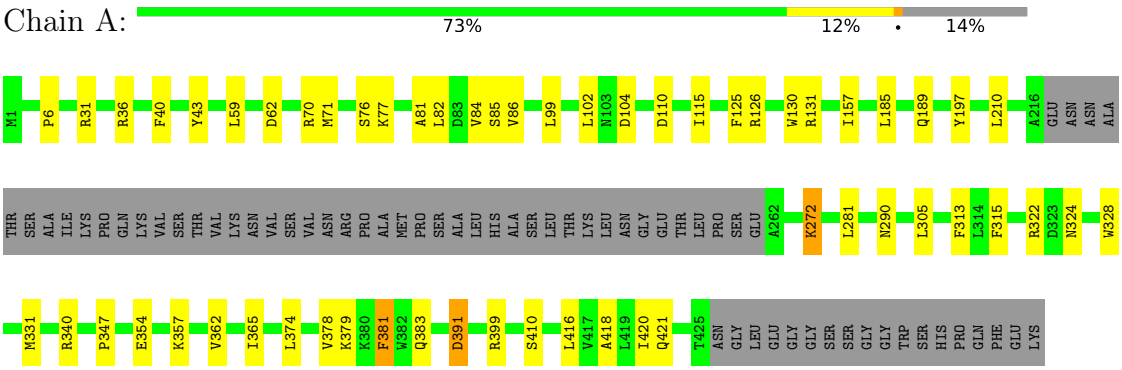
Chain	Residue	Modelled	Actual	Comment	Reference
D	440	GLN	-	expression tag	UNP Q9V4K2
D	441	PHE	-	expression tag	UNP Q9V4K2
D	442	GLU	-	expression tag	UNP Q9V4K2
D	443	LYS	-	expression tag	UNP Q9V4K2

3 Residue-property plots (i)

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. 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. 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.

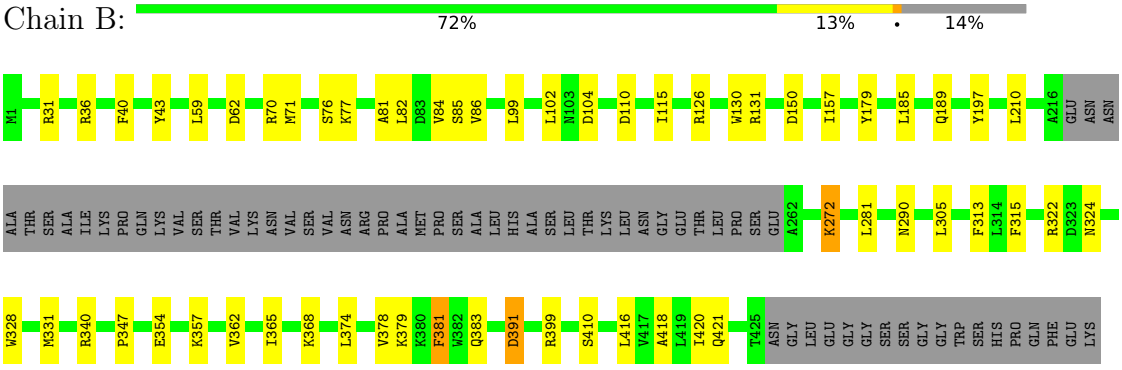
• Molecule 1: Gustatory receptor for sugar taste 43a

Chain A:



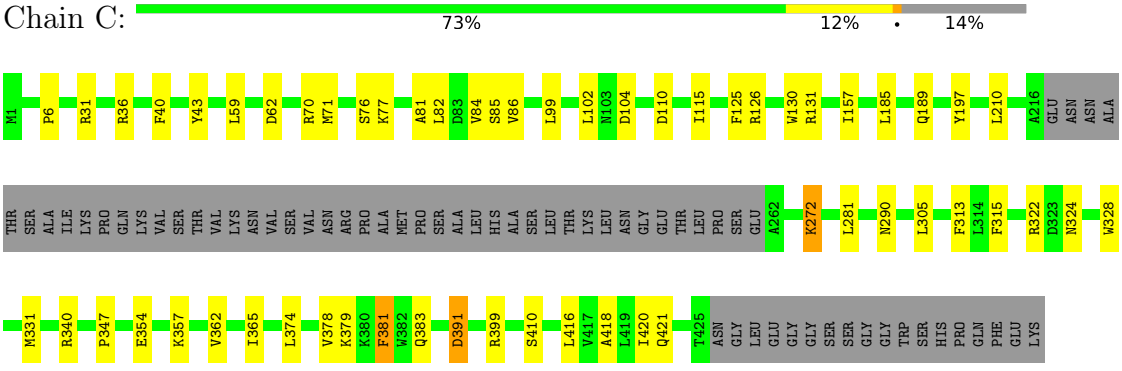
• Molecule 1: Gustatory receptor for sugar taste 43a

Chain B:



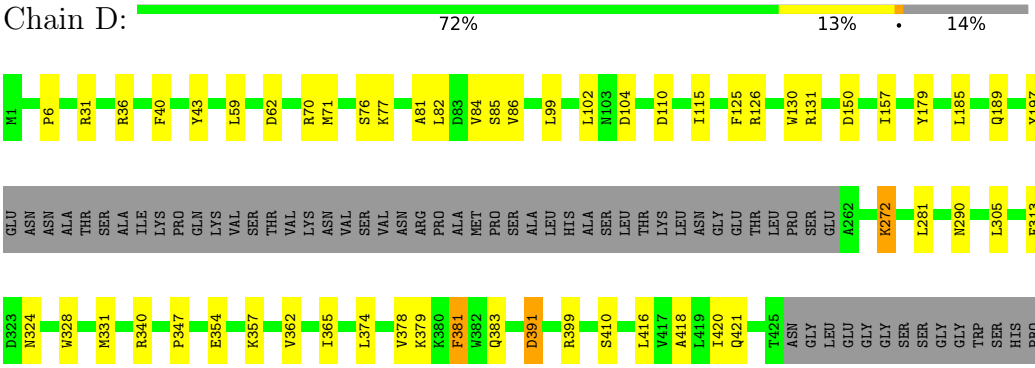
• Molecule 1: Gustatory receptor for sugar taste 43a

Chain C:



• Molecule 1: Gustatory receptor for sugar taste 43a

Chain D:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	200231	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	52	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	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	0.24	0/3059	0.43	0/4149
1	B	0.24	0/3059	0.43	0/4149
1	C	0.24	0/3059	0.43	0/4149
1	D	0.24	0/3059	0.43	0/4149
All	All	0.24	0/12236	0.43	0/16596

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	3001	0	3106	32	0
1	B	3001	0	3106	32	0
1	C	3001	0	3106	31	0
1	D	3001	0	3106	32	0
All	All	12004	0	12424	119	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 5.

All (119) 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:A:31:ARG:NH2	1:A:110:ASP:OD1	2.29	0.66
1:D:31:ARG:NH2	1:D:110:ASP:OD1	2.29	0.65
1:B:31:ARG:NH2	1:B:110:ASP:OD1	2.29	0.65
1:C:31:ARG:NH2	1:C:110:ASP:OD1	2.29	0.64
1:C:81:ALA:O	1:C:85:SER:OG	2.18	0.61
1:D:81:ALA:O	1:D:85:SER:OG	2.18	0.61
1:A:81:ALA:O	1:A:85:SER:OG	2.18	0.60
1:B:81:ALA:O	1:B:85:SER:OG	2.18	0.60
1:C:126:ARG:HH11	1:C:130:TRP:HE1	1.50	0.59
1:D:126:ARG:HH11	1:D:130:TRP:HE1	1.50	0.59
1:B:126:ARG:HH11	1:B:130:TRP:HE1	1.50	0.58
1:A:126:ARG:HH11	1:A:130:TRP:HE1	1.50	0.57
1:B:36:ARG:NH2	1:B:99:LEU:O	2.37	0.56
1:C:36:ARG:NH2	1:C:99:LEU:O	2.37	0.56
1:B:70:ARG:O	1:B:76:SER:OG	2.25	0.55
1:A:416:LEU:O	1:A:420:ILE:HG12	2.07	0.54
1:D:416:LEU:O	1:D:420:ILE:HG12	2.07	0.54
1:D:36:ARG:NH2	1:D:99:LEU:O	2.37	0.54
1:B:416:LEU:O	1:B:420:ILE:HG12	2.07	0.54
1:D:70:ARG:O	1:D:76:SER:OG	2.25	0.54
1:A:70:ARG:O	1:A:76:SER:OG	2.25	0.54
1:C:70:ARG:O	1:C:76:SER:OG	2.25	0.54
1:C:416:LEU:O	1:C:420:ILE:HG12	2.07	0.53
1:D:71:MET:HB3	1:D:77:LYS:HG2	1.92	0.52
1:A:391:ASP:HB3	1:A:399:ARG:HG2	1.92	0.52
1:D:82:LEU:HD13	1:D:305:LEU:HD11	1.92	0.52
1:D:391:ASP:HB3	1:D:399:ARG:HG2	1.92	0.52
1:A:115:ILE:HD13	1:A:281:LEU:HG	1.92	0.51
1:A:71:MET:HB3	1:A:77:LYS:HG2	1.92	0.51
1:A:82:LEU:HD13	1:A:305:LEU:HD11	1.92	0.51
1:B:391:ASP:HB3	1:B:399:ARG:HG2	1.92	0.51
1:B:115:ILE:HD13	1:B:281:LEU:HG	1.93	0.51
1:C:115:ILE:HD13	1:C:281:LEU:HG	1.93	0.51
1:C:391:ASP:HB3	1:C:399:ARG:HG2	1.92	0.51
1:B:71:MET:HB3	1:B:77:LYS:HG2	1.92	0.51
1:B:82:LEU:HD13	1:B:305:LEU:HD11	1.92	0.51
1:B:418:ALA:O	1:C:421:GLN:NE2	2.44	0.51
1:C:71:MET:HB3	1:C:77:LYS:HG2	1.92	0.51
1:C:418:ALA:O	1:D:421:GLN:NE2	2.44	0.51
1:A:421:GLN:NE2	1:D:418:ALA:O	2.44	0.50
1:D:115:ILE:HD13	1:D:281:LEU:HG	1.93	0.50
1:C:82:LEU:HD13	1:C:305:LEU:HD11	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:ARG:NH2	1:A:99:LEU:O	2.37	0.50
1:A:418:ALA:O	1:B:421:GLN:NE2	2.44	0.49
1:C:157:ILE:HG12	1:C:322:ARG:HH12	1.78	0.49
1:B:157:ILE:HG12	1:B:322:ARG:HH12	1.78	0.49
1:A:157:ILE:HG12	1:A:322:ARG:HH12	1.78	0.48
1:D:36:ARG:HB2	1:D:102:LEU:HD22	1.95	0.48
1:A:36:ARG:HB2	1:A:102:LEU:HD22	1.95	0.48
1:A:197:TYR:CE2	1:A:347:PRO:HG3	2.49	0.48
1:D:157:ILE:HG12	1:D:322:ARG:HH12	1.78	0.48
1:A:418:ALA:HB1	1:B:421:GLN:HE22	1.79	0.48
1:A:421:GLN:HE22	1:D:418:ALA:HB1	1.79	0.48
1:C:36:ARG:HB2	1:C:102:LEU:HD22	1.95	0.48
1:D:197:TYR:CE2	1:D:347:PRO:HG3	2.49	0.48
1:D:374:LEU:O	1:D:378:VAL:HG23	2.14	0.47
1:B:36:ARG:HB2	1:B:102:LEU:HD22	1.95	0.47
1:D:104:ASP:OD2	1:D:290:ASN:ND2	2.48	0.47
1:A:374:LEU:O	1:A:378:VAL:HG23	2.14	0.47
1:B:197:TYR:CE2	1:B:347:PRO:HG3	2.49	0.47
1:C:197:TYR:CE2	1:C:347:PRO:HG3	2.49	0.47
1:C:418:ALA:HB1	1:D:421:GLN:HE22	1.79	0.47
1:C:374:LEU:O	1:C:378:VAL:HG23	2.15	0.47
1:B:374:LEU:O	1:B:378:VAL:HG23	2.14	0.46
1:B:418:ALA:HB1	1:C:421:GLN:HE22	1.79	0.46
1:C:104:ASP:OD2	1:C:290:ASN:ND2	2.48	0.46
1:D:40:PHE:HA	1:D:43:TYR:HB3	1.98	0.46
1:B:40:PHE:HA	1:B:43:TYR:HB3	1.98	0.45
1:B:324:ASN:OD1	1:B:328:TRP:NE1	2.50	0.45
1:C:324:ASN:OD1	1:C:328:TRP:NE1	2.50	0.45
1:A:40:PHE:HA	1:A:43:TYR:HB3	1.98	0.44
1:A:59:LEU:HD13	1:A:84:VAL:HG21	2.00	0.44
1:C:40:PHE:HA	1:C:43:TYR:HB3	1.98	0.44
1:D:59:LEU:HD13	1:D:84:VAL:HG21	1.99	0.44
1:A:324:ASN:OD1	1:A:328:TRP:NE1	2.50	0.43
1:D:324:ASN:OD1	1:D:328:TRP:NE1	2.50	0.43
1:B:104:ASP:OD2	1:B:290:ASN:ND2	2.48	0.43
1:A:185:LEU:HD21	1:A:340:ARG:NH2	2.34	0.43
1:A:189:GLN:NE2	1:A:340:ARG:HE	2.17	0.43
1:B:59:LEU:HD13	1:B:84:VAL:HG21	1.99	0.43
1:C:272:LYS:HD3	1:C:272:LYS:HA	1.80	0.43
1:C:59:LEU:HD13	1:C:84:VAL:HG21	1.99	0.43
1:C:185:LEU:HD21	1:C:340:ARG:NH2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:185:LEU:HD21	1:D:340:ARG:NH2	2.34	0.42
1:C:189:GLN:NE2	1:C:340:ARG:HE	2.17	0.42
1:D:189:GLN:NE2	1:D:340:ARG:HE	2.17	0.42
1:A:104:ASP:OD2	1:A:290:ASN:ND2	2.48	0.42
1:B:185:LEU:HD21	1:B:340:ARG:NH2	2.34	0.42
1:B:354:GLU:OE1	1:B:357:LYS:HD2	2.19	0.42
1:C:59:LEU:HG	1:C:71:MET:SD	2.60	0.42
1:D:354:GLU:OE1	1:D:357:LYS:HD2	2.19	0.42
1:B:189:GLN:NE2	1:B:340:ARG:HE	2.17	0.42
1:D:59:LEU:HG	1:D:71:MET:SD	2.60	0.42
1:A:354:GLU:OE1	1:A:357:LYS:HD2	2.19	0.42
1:A:59:LEU:HG	1:A:71:MET:SD	2.60	0.42
1:B:362:VAL:HA	1:B:365:ILE:HD12	2.02	0.42
1:C:210:LEU:HD11	1:C:381:PHE:HE2	1.85	0.42
1:C:362:VAL:HA	1:C:365:ILE:HD12	2.02	0.41
1:B:272:LYS:HD3	1:B:272:LYS:HA	1.80	0.41
1:C:354:GLU:OE1	1:C:357:LYS:HD2	2.19	0.41
1:B:150:ASP:OD2	1:B:179:TYR:OH	2.28	0.41
1:D:150:ASP:OD2	1:D:179:TYR:OH	2.28	0.41
1:A:362:VAL:HA	1:A:365:ILE:HD12	2.02	0.41
1:D:210:LEU:HD11	1:D:381:PHE:HE2	1.85	0.41
1:D:272:LYS:HD3	1:D:272:LYS:HA	1.80	0.41
1:D:362:VAL:HA	1:D:365:ILE:HD12	2.02	0.41
1:B:59:LEU:HG	1:B:71:MET:SD	2.60	0.41
1:B:82:LEU:O	1:B:86:VAL:HG22	2.21	0.41
1:C:82:LEU:O	1:C:86:VAL:HG22	2.21	0.41
1:D:82:LEU:O	1:D:86:VAL:HG22	2.21	0.41
1:A:357:LYS:HE3	1:A:357:LYS:HB3	1.94	0.41
1:A:272:LYS:HA	1:A:272:LYS:HD3	1.80	0.40
1:B:210:LEU:HD11	1:B:381:PHE:HE2	1.85	0.40
1:D:6:PRO:HG3	1:D:125:PHE:CD2	2.56	0.40
1:A:82:LEU:O	1:A:86:VAL:HG22	2.21	0.40
1:C:6:PRO:HG3	1:C:125:PHE:CD2	2.56	0.40
1:A:210:LEU:HD11	1:A:381:PHE:HE2	1.85	0.40
1:A:6:PRO:HG3	1:A:125:PHE:CD2	2.56	0.40
1:B:368:LYS:HG2	1:B:368:LYS:O	2.22	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	376/443 (85%)	373 (99%)	3 (1%)	0	100	100
1	B	376/443 (85%)	373 (99%)	3 (1%)	0	100	100
1	C	376/443 (85%)	373 (99%)	3 (1%)	0	100	100
1	D	376/443 (85%)	373 (99%)	3 (1%)	0	100	100
All	All	1504/1772 (85%)	1492 (99%)	12 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	327/379 (86%)	316 (97%)	11 (3%)	37	71
1	B	327/379 (86%)	316 (97%)	11 (3%)	37	71
1	C	327/379 (86%)	316 (97%)	11 (3%)	37	71
1	D	327/379 (86%)	316 (97%)	11 (3%)	37	71
All	All	1308/1516 (86%)	1264 (97%)	44 (3%)	40	71

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	ASP
1	A	131	ARG

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Mol	Chain	Res	Type
1	A	272	LYS
1	A	313	PHE
1	A	315	PHE
1	A	331	MET
1	A	379	LYS
1	A	381	PHE
1	A	383	GLN
1	A	391	ASP
1	A	410	SER
1	B	62	ASP
1	B	131	ARG
1	B	272	LYS
1	B	313	PHE
1	B	315	PHE
1	B	331	MET
1	B	379	LYS
1	B	381	PHE
1	B	383	GLN
1	B	391	ASP
1	B	410	SER
1	C	62	ASP
1	C	131	ARG
1	C	272	LYS
1	C	313	PHE
1	C	315	PHE
1	C	331	MET
1	C	379	LYS
1	C	381	PHE
1	C	383	GLN
1	C	391	ASP
1	C	410	SER
1	D	62	ASP
1	D	131	ARG
1	D	272	LYS
1	D	313	PHE
1	D	315	PHE
1	D	331	MET
1	D	379	LYS
1	D	381	PHE
1	D	383	GLN
1	D	391	ASP
1	D	410	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	189	GLN
1	A	383	GLN
1	A	384	GLN
1	A	421	GLN
1	A	423	GLN
1	B	189	GLN
1	B	383	GLN
1	B	384	GLN
1	B	421	GLN
1	B	423	GLN
1	C	189	GLN
1	C	383	GLN
1	C	384	GLN
1	C	421	GLN
1	C	423	GLN
1	D	189	GLN
1	D	383	GLN
1	D	384	GLN
1	D	421	GLN
1	D	423	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

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.