



Full wwPDB X-ray Structure Validation Report i

Apr 28, 2024 – 11:28 am BST

PDB ID : 2IX3
Title : Structure of yeast Elongation Factor 3
Authors : Andersen, C.B.F.; Becker, T.; Blau, M.; Anand, M.; Halic, M.; Balar, B.; Mielke, T.; Boesen, T.; Pedersen, J.S.; Spahn, C.M.T.; Kinzy, T.G.; Andersen, G.R.; Beckmann, R.
Deposited on : 2006-07-06
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>
with specific help available everywhere you see the i 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](#) i) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

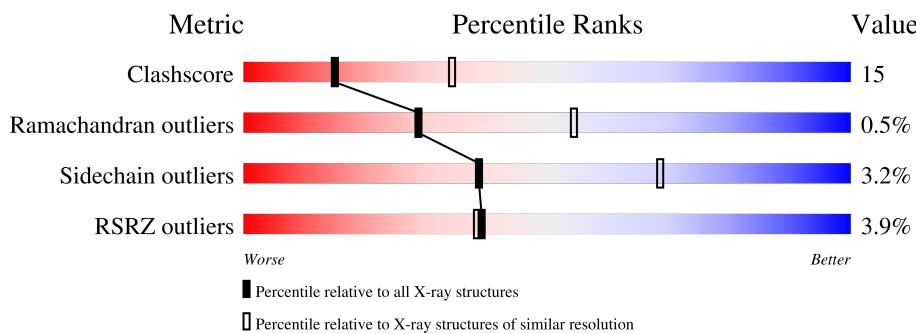
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

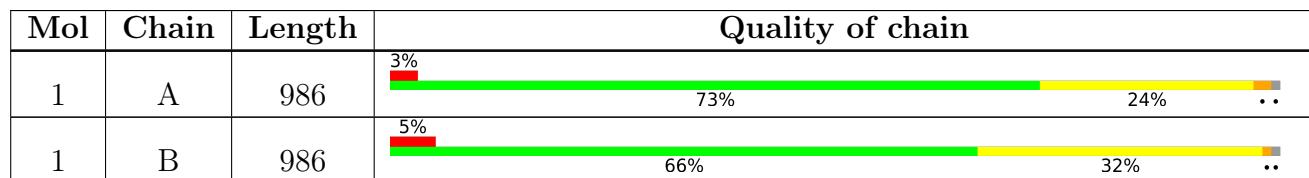
The reported resolution of this entry is 2.70 Å.

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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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%. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.



The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	2978	-	-	X	-
2	SO4	B	2974	-	X	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	2975	-	X	-	-

2 Entry composition [\(i\)](#)

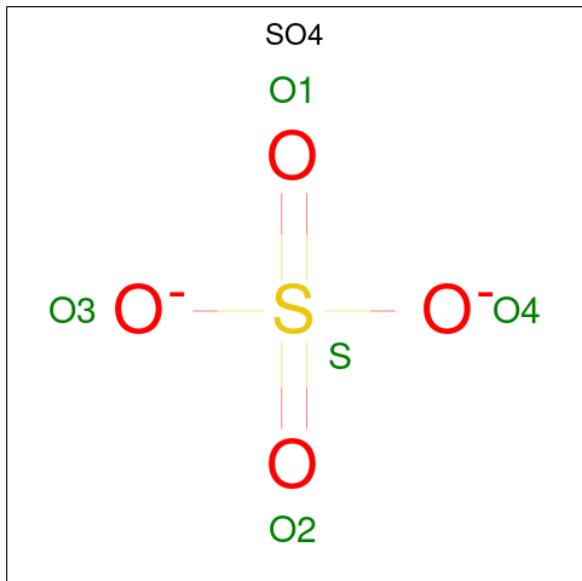
There are 2 unique types of molecules in this entry. The entry contains 15213 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 ELONGATION FACTOR 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	973	Total	C 7579	N 4790	O 1297	S 1455	37	0	0
1	B	973	Total	C 7579	N 4790	O 1297	S 1455	37	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O 5	S 4	1	0
2	A	1	Total	O 5	S 4	1	0
2	A	1	Total	O 5	S 4	1	0
2	A	1	Total	O 5	S 4	1	0

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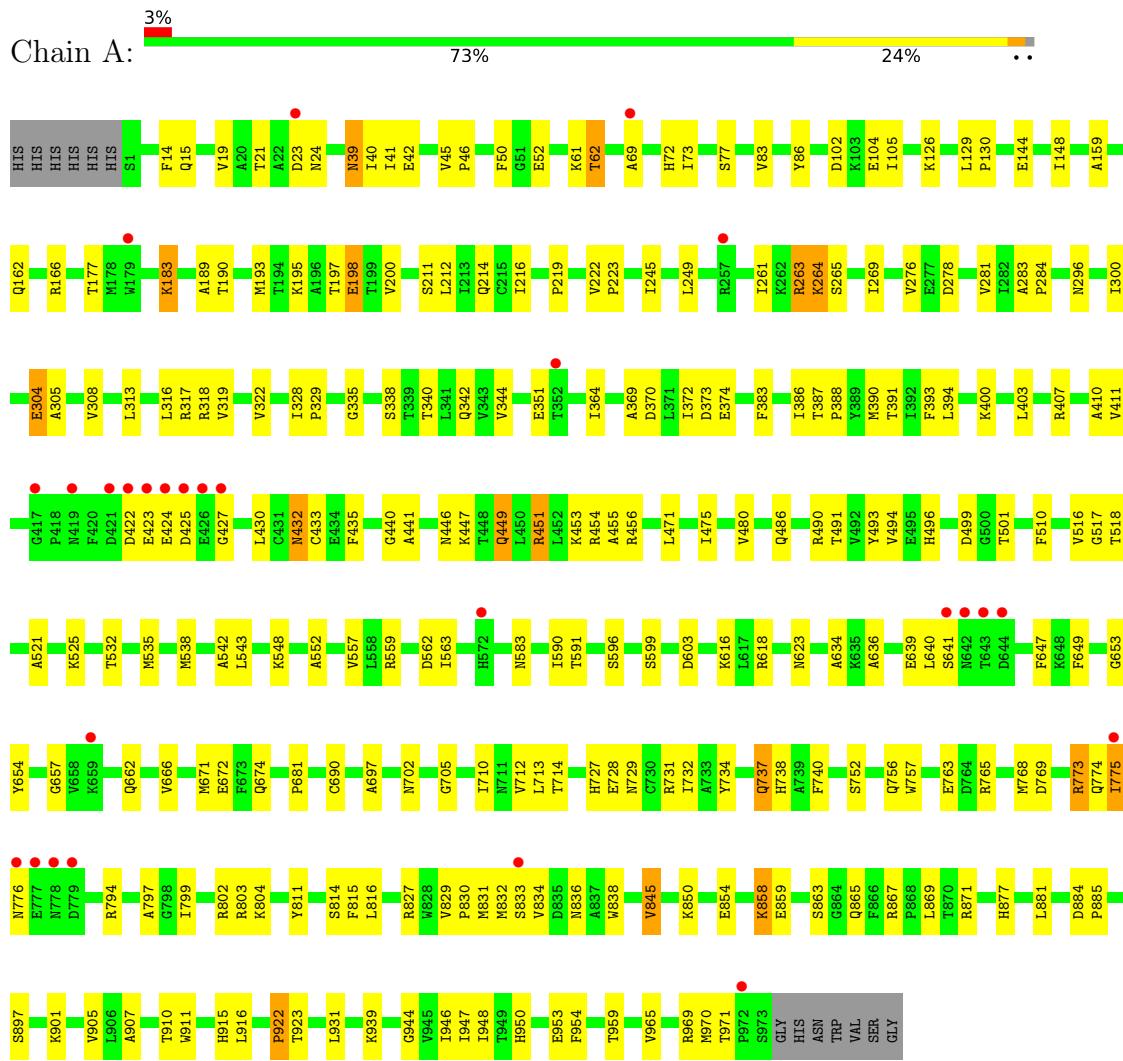
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

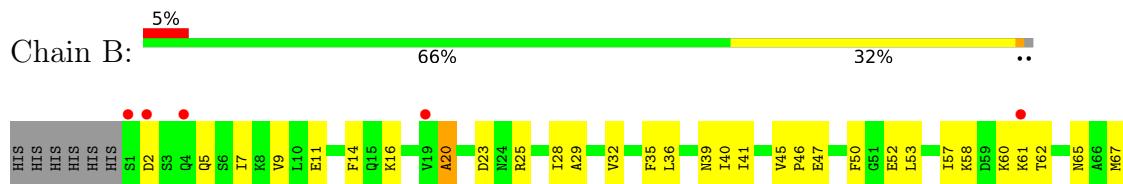
3 Residue-property plots

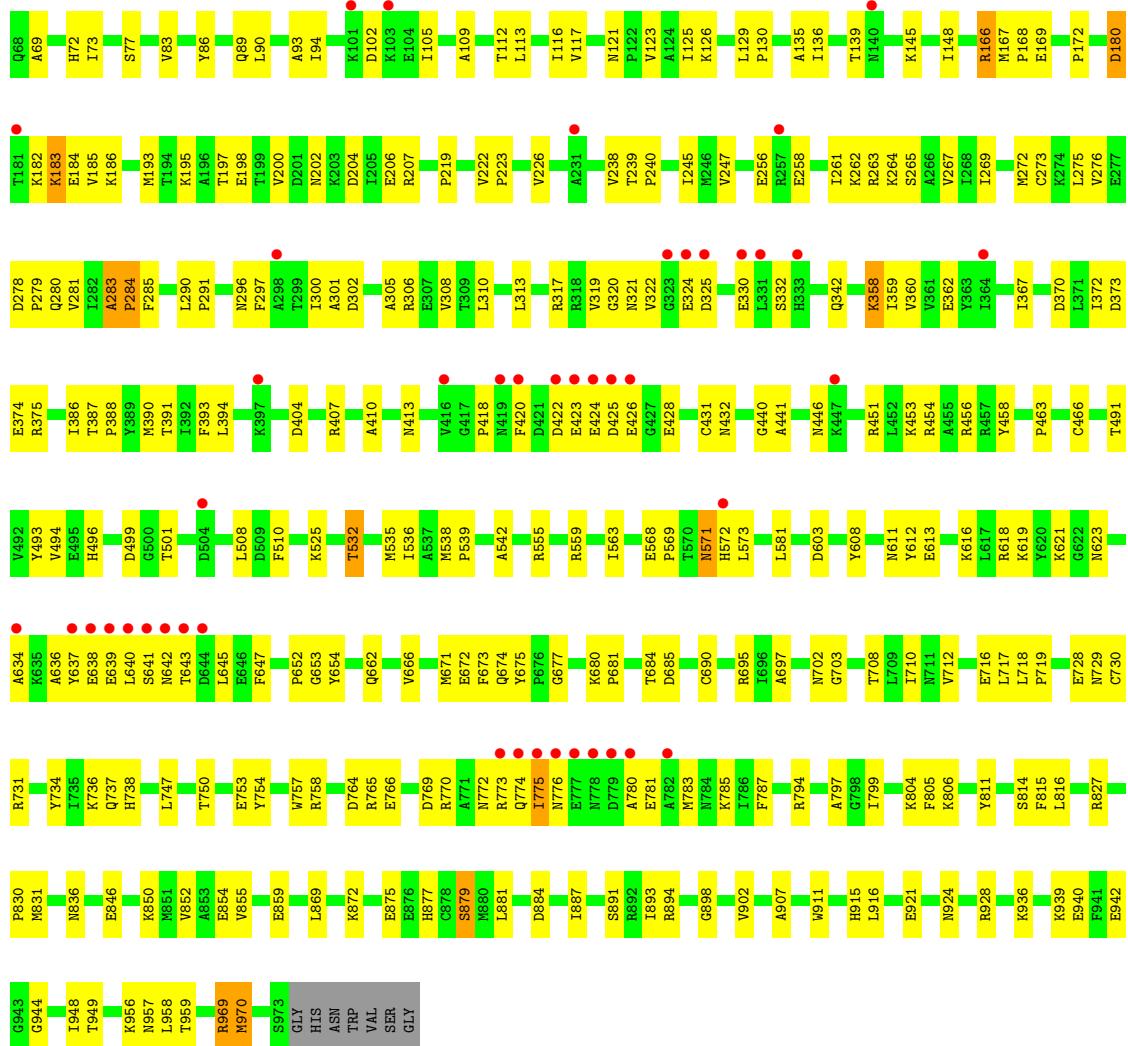
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: ELONGATION FACTOR 3



- Molecule 1: ELONGATION FACTOR 3





4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.61 Å 110.66 Å 212.65 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.63 – 2.70 20.16 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.63-2.70) 100.0 (20.16-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ ¹	5.09 (at 2.71 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R , R_{free}	0.216 , 0.269 0.215 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	48.9	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.6	EDS
L-test for twinning ²	$< L > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15213	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.36% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section:
SO4

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	0.41	0/7717	0.62	0/10456
1	B	0.39	0/7717	0.60	0/10456
All	All	0.40	0/15434	0.61	0/20912

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 i

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	7579	0	7627	215	0
1	B	7579	0	7627	249	0
2	A	30	0	0	3	0
2	B	25	0	0	3	0
All	All	15213	0	15254	460	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 15.

All (460) 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:B:769:ASP:HB2	1:B:774:GLN:NE2	1.55	1.22
1:A:731:ARG:H	1:A:915:HIS:HD2	1.13	0.96
1:B:774:GLN:O	1:B:776:ASN:N	1.98	0.96
1:B:262:LYS:HE3	1:B:296:ASN:ND2	1.83	0.92
1:B:372:ILE:HD11	1:B:410:ALA:HB1	1.51	0.91
1:A:183:LYS:HD3	1:A:183:LYS:H	1.36	0.90
1:A:318:ARG:CZ	1:A:423:GLU:HG3	2.01	0.89
1:A:773:ARG:O	1:A:774:GLN:HG2	1.74	0.87
1:B:731:ARG:H	1:B:915:HIS:HD2	1.22	0.85
1:B:50:PHE:HZ	1:B:83:VAL:HG13	1.40	0.85
1:B:67:MET:CE	1:B:94:ILE:HG23	2.07	0.84
1:A:794:ARG:HD3	1:A:831:MET:HE1	1.61	0.83
1:B:769:ASP:CB	1:B:774:GLN:NE2	2.39	0.83
1:A:881:LEU:HD13	1:A:907:ALA:HA	1.61	0.82
1:B:671:MET:SD	1:B:712:VAL:HG11	2.21	0.81
1:A:525:LYS:HE2	1:A:557:VAL:HG11	1.64	0.80
1:A:21:THR:HG23	1:A:23:ASP:H	1.46	0.80
1:A:45:VAL:HG11	1:A:86:TYR:CZ	2.19	0.78
1:A:671:MET:HG2	1:A:672:GLU:N	1.97	0.78
1:B:794:ARG:HD3	1:B:831:MET:HE3	1.65	0.78
1:B:769:ASP:HB2	1:B:774:GLN:HE21	1.44	0.77
1:A:532:THR:HG23	1:A:535:MET:H	1.50	0.77
1:B:263:ARG:NH2	1:B:264:LYS:HE3	2.00	0.77
1:B:14:PHE:CE2	1:B:52:GLU:HB3	2.21	0.76
1:B:67:MET:HE3	1:B:94:ILE:HG23	1.65	0.76
1:A:697:ALA:HB2	1:A:959:THR:HG21	1.68	0.75
1:A:729:ASN:HD22	1:A:865:GLN:HG3	1.51	0.75
1:B:769:ASP:CB	1:B:774:GLN:HE21	1.98	0.75
1:B:197:THR:HG22	1:B:245:ILE:HD13	1.67	0.74
1:B:731:ARG:H	1:B:915:HIS:CD2	2.04	0.73
1:A:647:PHE:HB2	1:A:881:LEU:HA	1.69	0.73
1:B:50:PHE:CZ	1:B:83:VAL:HG13	2.24	0.72
1:A:671:MET:SD	1:A:712:VAL:HG11	2.30	0.72
1:B:262:LYS:HE3	1:B:296:ASN:HD21	1.53	0.72
1:B:67:MET:CE	1:B:109:ALA:HA	2.20	0.72
1:B:265:SER:O	1:B:269:ILE:HG13	1.91	0.71
1:B:279:PRO:HG3	1:B:418:PRO:HG2	1.73	0.71
1:B:72:HIS:CE1	1:B:773:ARG:HD2	2.25	0.70
1:A:731:ARG:HH12	1:A:865:GLN:NE2	1.88	0.70
1:A:697:ALA:HB2	1:A:959:THR:CG2	2.22	0.70
1:B:183:LYS:H	1:B:183:LYS:HD3	1.57	0.70
1:B:772:ASN:HB3	1:B:846:GLU:HG3	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:67:MET:HE2	1:B:109:ALA:HA	1.74	0.69
1:B:718:LEU:HD12	1:B:719:PRO:HD2	1.75	0.68
1:B:815:PHE:HB2	1:B:831:MET:CE	2.24	0.68
1:A:969:ARG:HG3	1:A:969:ARG:HH11	1.57	0.68
1:B:718:LEU:HD11	1:B:806:LYS:HD2	1.77	0.67
1:B:532:THR:CG2	1:B:535:MET:HG3	2.24	0.67
1:B:263:ARG:HH22	1:B:264:LYS:HE3	1.59	0.67
1:A:881:LEU:HD13	1:A:907:ALA:CA	2.25	0.67
1:A:276:VAL:HB	1:A:319:VAL:HG11	1.78	0.66
1:B:757:TRP:CH2	1:B:765:ARG:HD2	2.29	0.66
1:B:799:ILE:HG22	1:B:855:VAL:HG21	1.78	0.66
1:B:850:LYS:O	1:B:854:GLU:HG3	1.95	0.66
1:A:532:THR:HG22	1:A:535:MET:HG3	1.78	0.66
1:A:41:ILE:HD12	1:A:46:PRO:HD3	1.75	0.66
1:A:518:THR:HG21	2:B:2977:SO4:O3	1.95	0.66
1:A:649:PHE:CD1	1:A:910:THR:HG21	2.31	0.66
1:A:144:GLU:O	1:A:148:ILE:HG13	1.96	0.66
1:B:634:ALA:HB1	1:B:637:TYR:CE2	2.31	0.66
1:B:647:PHE:HB2	1:B:881:LEU:HA	1.78	0.65
1:A:731:ARG:H	1:A:915:HIS:CD2	2.05	0.65
1:A:40:ILE:HG13	1:A:41:ILE:HG13	1.78	0.65
1:A:666:VAL:HB	1:A:690:CYS:HB2	1.77	0.65
1:A:731:ARG:N	1:A:915:HIS:HD2	1.92	0.65
1:A:501:THR:HG21	1:A:510:PHE:HD1	1.62	0.65
1:A:815:PHE:HB2	1:A:831:MET:CE	2.28	0.64
1:B:276:VAL:HB	1:B:319:VAL:CG1	2.27	0.64
1:B:276:VAL:HB	1:B:319:VAL:HG11	1.78	0.64
1:B:532:THR:HG23	1:B:535:MET:H	1.62	0.64
1:A:126:LYS:HE2	1:A:166:ARG:NH2	2.12	0.64
1:A:72:HIS:CE1	1:A:773:ARG:HD2	2.32	0.64
1:B:258:GLU:HB3	1:B:261:ILE:HD12	1.79	0.64
1:A:193:MET:O	1:A:197:THR:HG23	1.97	0.64
1:A:200:VAL:HG21	1:A:245:ILE:HD12	1.79	0.64
1:A:21:THR:HG22	1:A:24:ASN:CG	2.18	0.64
1:B:5:GLN:O	1:B:9:VAL:HG23	1.97	0.64
1:B:41:ILE:HD12	1:B:46:PRO:HD3	1.78	0.64
1:B:166:ARG:NH2	1:B:373:ASP:OD2	2.30	0.64
1:A:535:MET:O	1:A:538:MET:HG2	1.96	0.64
1:A:183:LYS:H	1:A:183:LYS:CD	2.08	0.63
1:A:264:LYS:HE3	1:A:264:LYS:HA	1.80	0.63
1:A:731:ARG:NH1	1:A:865:GLN:HE21	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:PRO:HB3	1:A:261:ILE:HD13	1.81	0.63
1:B:324:GLU:H	1:B:324:GLU:CD	2.02	0.63
1:A:126:LYS:HE2	1:A:166:ARG:HH21	1.62	0.63
1:A:50:PHE:HZ	1:A:83:VAL:HG13	1.62	0.63
1:A:456:ARG:O	1:A:591:THR:HG23	1.99	0.63
1:B:283:ALA:HB3	1:B:284:PRO:CD	2.29	0.63
1:A:757:TRP:CH2	1:A:765:ARG:HD2	2.34	0.62
1:A:491:THR:HG22	1:A:563:ILE:HB	1.80	0.62
1:B:219:PRO:O	1:B:222:VAL:HG23	2.00	0.62
1:A:922:PRO:O	1:A:931:LEU:HD21	2.00	0.62
1:B:313:LEU:O	1:B:317:ARG:HG3	2.00	0.62
1:B:794:ARG:HD3	1:B:831:MET:CE	2.30	0.61
1:B:45:VAL:HG11	1:B:86:TYR:CZ	2.35	0.61
1:B:815:PHE:HB2	1:B:831:MET:HE3	1.81	0.61
1:B:45:VAL:HG11	1:B:86:TYR:CE2	2.35	0.61
1:B:36:LEU:HD23	1:B:73:ILE:HD13	1.83	0.61
1:A:916:LEU:HD23	1:A:944:GLY:HA3	1.82	0.61
1:B:936:LYS:O	1:B:940:GLU:HG3	2.00	0.60
1:A:815:PHE:HB2	1:A:831:MET:HE1	1.82	0.60
1:B:555:ARG:NH2	1:B:559:ARG:HH21	1.99	0.60
1:B:710:ILE:HD13	1:B:948:ILE:HD13	1.81	0.60
1:B:202:ASN:OD1	1:B:204:ASP:HB2	2.02	0.60
1:B:222:VAL:HB	1:B:223:PRO:HD3	1.82	0.60
1:A:45:VAL:HG11	1:A:86:TYR:OH	2.02	0.60
1:B:774:GLN:C	1:B:776:ASN:N	2.54	0.60
1:B:877:HIS:HE1	1:B:907:ALA:O	1.85	0.59
1:A:69:ALA:O	1:A:73:ILE:HG13	2.03	0.59
1:A:832:MET:O	1:A:834:VAL:N	2.35	0.59
1:B:494:VAL:O	1:B:496:HIS:HD2	1.86	0.59
1:B:774:GLN:C	1:B:776:ASN:H	2.05	0.59
1:B:538:MET:CE	1:B:542:ALA:HB3	2.33	0.58
1:A:102:ASP:OD2	1:A:105:ILE:HG13	2.03	0.58
1:A:501:THR:HG21	1:A:510:PHE:CD1	2.38	0.58
1:B:538:MET:HE3	1:B:542:ALA:HB3	1.86	0.58
1:A:538:MET:HE2	1:A:542:ALA:HB3	1.85	0.58
1:B:183:LYS:HD3	1:B:183:LYS:N	2.18	0.58
1:B:673:PHE:CZ	1:B:717:LEU:HD13	2.39	0.58
1:B:634:ALA:HB1	1:B:637:TYR:CZ	2.39	0.58
1:A:45:VAL:HG11	1:A:86:TYR:CE2	2.38	0.57
1:A:425:ASP:HA	1:A:453:LYS:HE2	1.86	0.57
1:A:603:ASP:HA	1:A:623:ASN:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:794:ARG:CD	1:A:831:MET:HE1	2.34	0.57
1:B:40:ILE:HG13	1:B:41:ILE:HG13	1.86	0.57
1:A:19:VAL:HG12	1:A:19:VAL:O	2.02	0.57
1:B:102:ASP:OD2	1:B:105:ILE:HG13	2.04	0.57
1:B:145:LYS:HE2	1:B:180:ASP:OD1	2.03	0.57
1:B:222:VAL:O	1:B:226:VAL:HG23	2.04	0.57
1:B:283:ALA:HB3	1:B:284:PRO:HD3	1.86	0.57
1:A:525:LYS:HE2	1:A:557:VAL:CG1	2.33	0.57
1:B:898:GLY:O	1:B:902:VAL:HG23	2.04	0.57
1:A:757:TRP:CZ2	1:A:765:ARG:HD2	2.40	0.57
1:A:21:THR:HG22	1:A:24:ASN:OD1	2.05	0.57
1:B:262:LYS:HB3	1:B:296:ASN:ND2	2.20	0.57
1:A:265:SER:O	1:A:269:ILE:HG13	2.04	0.57
1:A:729:ASN:ND2	1:A:865:GLN:HG3	2.18	0.57
1:A:21:THR:HG23	1:A:23:ASP:N	2.17	0.56
1:A:372:ILE:HD11	1:A:410:ALA:HB1	1.87	0.56
1:A:731:ARG:NH1	1:A:865:GLN:NE2	2.54	0.56
1:B:671:MET:HG2	1:B:672:GLU:N	2.20	0.56
1:B:535:MET:O	1:B:538:MET:HG2	2.05	0.56
1:B:45:VAL:O	1:B:47:GLU:N	2.38	0.56
1:B:643:THR:C	1:B:645:LEU:H	2.08	0.56
1:A:850:LYS:O	1:A:854:GLU:HG3	2.06	0.56
1:B:639:GLU:O	1:B:641:SER:N	2.39	0.56
1:B:463:PRO:HG2	1:B:466:CYS:HB3	1.87	0.56
1:B:90:LEU:O	1:B:94:ILE:HG13	2.06	0.55
1:B:613:GLU:OE1	1:B:618:ARG:HG3	2.06	0.55
1:A:499:ASP:OD2	1:A:501:THR:HG23	2.06	0.55
1:A:794:ARG:HG2	1:A:831:MET:HE2	1.87	0.55
1:A:276:VAL:HB	1:A:319:VAL:CG1	2.36	0.55
1:B:135:ALA:O	1:B:139:THR:HG22	2.07	0.55
1:B:195:LYS:O	1:B:198:GLU:HB2	2.06	0.55
1:A:671:MET:CG	1:A:672:GLU:N	2.68	0.55
1:B:262:LYS:HB3	1:B:296:ASN:HD22	1.71	0.55
1:B:372:ILE:O	1:B:375:ARG:NH1	2.37	0.55
1:B:884:ASP:HB3	1:B:887:ILE:HD12	1.89	0.55
1:A:422:ASP:HA	1:A:424:GLU:OE1	2.06	0.54
1:A:858:LYS:HE2	1:B:428:GLU:OE2	2.07	0.54
1:B:53:LEU:O	1:B:57:ILE:HG13	2.07	0.54
1:B:320:GLY:O	1:B:321:ASN:HB3	2.06	0.54
1:A:200:VAL:CG2	1:A:245:ILE:HD12	2.37	0.54
1:A:455:ALA:N	1:A:591:THR:OG1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:LYS:HD3	1:B:185:VAL:HG11	1.89	0.54
1:A:969:ARG:HG3	1:A:969:ARG:NH1	2.19	0.54
1:B:223:PRO:HG3	1:B:256:GLU:HG2	1.88	0.54
1:A:532:THR:HG22	1:A:535:MET:CG	2.38	0.54
1:A:881:LEU:HD13	1:A:907:ALA:CB	2.36	0.54
1:B:67:MET:HE1	1:B:94:ILE:HG23	1.89	0.54
1:A:881:LEU:CD1	1:A:907:ALA:HA	2.37	0.54
1:A:916:LEU:CD2	1:A:944:GLY:HA3	2.37	0.54
1:B:747:LEU:HB3	1:B:894:ARG:HB2	1.90	0.54
1:B:129:LEU:HB3	1:B:130:PRO:HD3	1.90	0.54
1:B:538:MET:HB2	1:B:539:PRO:HD2	1.90	0.54
1:A:774:GLN:C	1:A:776:ASN:H	2.11	0.53
1:B:20:ALA:HB3	1:B:65:ASN:ND2	2.23	0.53
1:B:764:ASP:OD1	1:B:766:GLU:HB2	2.09	0.53
1:A:486:GLN:OE1	1:A:490:ARG:HD2	2.08	0.53
1:A:674:GLN:HB2	1:A:681:PRO:HB3	1.90	0.53
1:B:273:CYS:C	1:B:275:LEU:H	2.12	0.53
1:B:200:VAL:HG12	1:B:202:ASN:H	1.74	0.53
1:B:258:GLU:O	1:B:262:LYS:HG3	2.08	0.53
1:A:583:ASN:ND2	2:A:2976:SO4:O4	2.42	0.53
1:A:538:MET:CE	1:A:542:ALA:HB3	2.38	0.52
1:B:916:LEU:HD23	1:B:944:GLY:HA3	1.91	0.52
1:B:69:ALA:O	1:B:73:ILE:HG13	2.09	0.52
1:A:340:THR:O	1:A:344:VAL:HG22	2.10	0.52
1:B:386:ILE:HG22	1:B:390:MET:HG2	1.92	0.52
1:B:695:ARG:HB3	1:B:959:THR:HA	1.92	0.52
1:A:335:GLY:HA3	1:A:373:ASP:OD1	2.09	0.52
1:A:532:THR:CG2	1:A:535:MET:HG3	2.40	0.52
1:A:50:PHE:CZ	1:A:83:VAL:HG13	2.45	0.52
1:B:183:LYS:H	1:B:183:LYS:CD	2.22	0.52
1:A:166:ARG:NH2	1:A:373:ASP:OD2	2.32	0.52
1:B:815:PHE:HB2	1:B:831:MET:HE2	1.91	0.52
1:A:193:MET:HE2	1:A:216:ILE:HD12	1.91	0.51
1:B:719:PRO:HG2	1:B:806:LYS:HD3	1.92	0.51
1:B:734:TYR:CE2	1:B:736:LYS:HD2	2.46	0.51
1:B:169:GLU:O	1:B:172:PRO:HG2	2.10	0.51
1:A:773:ARG:HG2	1:A:773:ARG:HH11	1.75	0.51
1:B:123:VAL:HG13	1:B:370:ASP:OD2	2.10	0.51
1:A:317:ARG:HG2	1:A:322:VAL:HG21	1.92	0.51
1:A:318:ARG:NE	1:A:423:GLU:HG3	2.25	0.51
1:B:247:VAL:HG21	1:B:285:PHE:CD1	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:639:GLU:O	1:A:641:SER:N	2.44	0.51
1:B:773:ARG:HG2	1:B:846:GLU:CD	2.31	0.51
1:A:773:ARG:O	1:A:775:ILE:HG13	2.11	0.51
1:B:267:VAL:CG2	1:B:308:VAL:HG11	2.40	0.51
1:B:750:THR:OG1	1:B:753:GLU:HG3	2.10	0.51
1:A:802:ARG:HB3	1:A:859:GLU:HG3	1.93	0.51
1:B:532:THR:HG23	1:B:535:MET:HG3	1.93	0.51
1:B:653:GLY:O	1:B:915:HIS:HE1	1.94	0.50
1:A:212:LEU:CD2	1:A:249:LEU:HD22	2.42	0.50
1:A:494:VAL:O	1:A:496:HIS:HD2	1.95	0.50
1:A:435:PHE:CD1	1:A:480:VAL:HG13	2.46	0.50
1:A:543:LEU:O	1:A:548:LYS:HE3	2.12	0.50
1:A:177:THR:HG22	1:A:189:ALA:HB2	1.94	0.50
1:A:816:LEU:HD23	1:A:830:PRO:HA	1.92	0.50
1:A:494:VAL:HG13	1:A:552:ALA:HB1	1.94	0.50
1:A:763:GLU:OE1	1:A:768:MET:CE	2.60	0.50
1:B:666:VAL:HB	1:B:690:CYS:HB2	1.94	0.50
1:A:532:THR:CG2	1:A:535:MET:H	2.22	0.49
1:B:113:LEU:O	1:B:117:VAL:HG23	2.11	0.49
1:B:508:LEU:HB2	1:B:536:ILE:HG22	1.94	0.49
1:B:814:SER:HA	1:B:836:ASN:OD1	2.12	0.49
1:A:714:THR:HG21	1:A:734:TYR:CE1	2.48	0.49
1:A:77:SER:HA	1:A:738:HIS:CE1	2.47	0.49
1:A:197:THR:HG22	1:A:245:ILE:CD1	2.41	0.49
1:A:372:ILE:CD1	1:A:410:ALA:HB1	2.42	0.49
1:B:757:TRP:CZ2	1:B:765:ARG:HD2	2.47	0.49
1:B:731:ARG:N	1:B:915:HIS:HD2	2.01	0.49
1:B:223:PRO:HB3	1:B:261:ILE:CD1	2.43	0.49
1:B:420:PHE:HB3	1:B:619:LYS:HB3	1.94	0.49
1:B:603:ASP:HA	1:B:623:ASN:HB2	1.95	0.49
1:A:662:GLN:H	1:A:662:GLN:NE2	2.11	0.49
1:B:58:LYS:HE3	1:B:93:ALA:HB2	1.93	0.49
1:A:803:ARG:HG2	1:A:838:TRP:CZ3	2.48	0.49
1:B:805:PHE:O	1:B:806:LYS:HB2	2.13	0.49
1:B:869:LEU:HD23	1:B:911:TRP:CZ2	2.48	0.49
1:B:785:LYS:HD3	1:B:787:PHE:CZ	2.47	0.48
1:A:832:MET:C	1:A:834:VAL:H	2.17	0.48
1:B:324:GLU:O	1:B:325:ASP:HB2	2.12	0.48
1:B:440:GLY:O	1:B:441:ALA:HB3	2.13	0.48
1:A:129:LEU:HB3	1:A:130:PRO:HD3	1.95	0.48
1:A:393:PHE:CD1	1:A:394:LEU:HG	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:LYS:NZ	1:A:923:THR:O	2.45	0.48
1:B:532:THR:HG22	1:B:535:MET:SD	2.53	0.48
1:B:969:ARG:HG2	1:B:969:ARG:HH11	1.78	0.48
1:B:387:THR:HB	1:B:388:PRO:CD	2.44	0.48
1:A:212:LEU:HD13	1:A:245:ILE:HG22	1.96	0.48
1:A:195:LYS:O	1:A:198:GLU:HB2	2.14	0.48
1:A:752:SER:O	1:A:756:GLN:HG3	2.12	0.48
1:A:424:GLU:HG2	1:A:424:GLU:O	2.12	0.48
1:A:499:ASP:OD2	1:A:510:PHE:HE1	1.96	0.48
1:B:7:ILE:O	1:B:11:GLU:HG2	2.14	0.48
1:B:35:PHE:HB2	1:B:675:TYR:CZ	2.49	0.48
1:A:313:LEU:HD21	1:A:317:ARG:NH2	2.28	0.48
1:B:956:LYS:O	1:B:957:ASN:HB2	2.14	0.48
1:B:25:ARG:HD3	1:B:65:ASN:HA	1.96	0.48
1:B:634:ALA:O	1:B:637:TYR:CD2	2.66	0.48
1:A:393:PHE:O	1:A:394:LEU:HD23	2.13	0.48
1:B:728:GLU:O	1:B:729:ASN:HB2	2.14	0.48
1:A:737:GLN:HG3	1:A:738:HIS:N	2.28	0.47
1:A:159:ALA:HB1	1:A:162:GLN:HB2	1.97	0.47
1:A:773:ARG:C	1:A:775:ILE:H	2.17	0.47
1:B:136:ILE:HB	1:B:148:ILE:HG21	1.96	0.47
1:A:440:GLY:O	1:A:441:ALA:HB3	2.14	0.47
1:A:447:LYS:O	1:A:616:LYS:NZ	2.46	0.47
1:A:710:ILE:CD1	1:A:948:ILE:HD13	2.44	0.47
1:B:501:THR:HG21	1:B:510:PHE:CD1	2.49	0.47
1:B:754:TYR:HB2	1:B:893:ILE:HD11	1.97	0.47
1:B:89:GLN:NE2	1:B:359:ILE:HD13	2.30	0.47
1:B:928:ARG:NH1	1:B:928:ARG:HB2	2.30	0.47
1:A:283:ALA:HB3	1:A:284:PRO:CD	2.45	0.47
1:A:372:ILE:HD11	1:A:410:ALA:CB	2.44	0.47
1:B:262:LYS:HE3	1:B:296:ASN:CG	2.35	0.47
1:A:710:ILE:HG12	1:A:948:ILE:HD13	1.97	0.47
1:A:61:LYS:HD3	1:A:62:THR:HG23	1.96	0.47
1:B:267:VAL:HG22	1:B:308:VAL:HG11	1.95	0.47
1:B:684:THR:CG2	1:B:969:ARG:HE	2.27	0.47
1:A:916:LEU:HD23	1:A:944:GLY:CA	2.46	0.46
1:A:727:HIS:ND1	1:A:728:GLU:O	2.46	0.46
1:A:728:GLU:O	1:A:729:ASN:HB2	2.15	0.46
1:B:28:ILE:O	1:B:32:VAL:HG23	2.15	0.46
1:A:304:GLU:HG3	1:A:305:ALA:N	2.30	0.46
1:A:263:ARG:NH1	1:A:308:VAL:HG21	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:ILE:HG23	1:A:386:ILE:CG2	2.46	0.46
1:A:263:ARG:CZ	1:A:304:GLU:OE1	2.64	0.46
1:A:471:LEU:O	1:A:475:ILE:HG13	2.15	0.46
1:A:39:ASN:O	1:A:702:ASN:HB3	2.15	0.46
1:B:680:LYS:HB2	1:B:681:PRO:HD2	1.98	0.46
1:A:393:PHE:CE1	1:A:394:LEU:HG	2.50	0.46
1:B:193:MET:O	1:B:197:THR:HG23	2.15	0.46
1:B:881:LEU:HD22	1:B:907:ALA:N	2.30	0.46
1:B:939:LYS:HE2	1:B:957:ASN:O	2.16	0.46
1:B:39:ASN:O	1:B:702:ASN:HB3	2.15	0.46
1:B:674:GLN:HB2	1:B:681:PRO:HA	1.97	0.46
1:B:754:TYR:CZ	1:B:758:ARG:HD2	2.50	0.46
1:A:653:GLY:O	1:A:915:HIS:HE1	2.00	0.45
1:A:763:GLU:OE1	1:A:768:MET:HE1	2.16	0.45
1:A:802:ARG:HG2	1:A:803:ARG:N	2.31	0.45
1:B:391:THR:HG21	1:B:924:ASN:OD1	2.16	0.45
1:B:404:ASP:OD1	1:B:407:ARG:NH1	2.49	0.45
1:B:642:ASN:O	1:B:645:LEU:HB3	2.16	0.45
1:B:674:GLN:HB2	1:B:681:PRO:HB3	1.97	0.45
1:A:245:ILE:HG22	1:A:245:ILE:O	2.16	0.45
1:B:50:PHE:HZ	1:B:83:VAL:CG1	2.21	0.45
1:B:125:ILE:HG23	1:B:126:LYS:N	2.31	0.45
1:B:425:ASP:OD1	1:B:426:GLU:HG2	2.16	0.45
1:B:638:GLU:HG3	1:B:639:GLU:N	2.31	0.45
1:A:634:ALA:C	1:A:636:ALA:H	2.20	0.45
1:A:814:SER:HA	1:A:836:ASN:OD1	2.17	0.45
1:A:877:HIS:HE1	1:A:907:ALA:O	2.00	0.45
1:A:42:GLU:OE1	1:A:950:HIS:HE1	1.99	0.45
1:B:730:CYS:HA	1:B:915:HIS:CD2	2.52	0.45
1:A:197:THR:HG22	1:A:245:ILE:HD13	1.97	0.45
1:B:67:MET:HE1	1:B:109:ALA:HA	1.94	0.45
1:A:794:ARG:HB3	1:A:815:PHE:HB3	1.98	0.45
1:B:223:PRO:HB3	1:B:261:ILE:HD11	1.99	0.45
1:A:521:ALA:HB2	1:B:654:TYR:CE2	2.52	0.45
1:A:654:TYR:OH	2:A:2978:SO4:O2	2.33	0.45
1:B:301:ALA:HB3	2:B:2974:SO4:O3	2.17	0.45
1:A:815:PHE:HB2	1:A:831:MET:HE3	1.96	0.44
1:B:2:ASP:OD2	1:B:703:GLY:HA3	2.17	0.44
1:B:263:ARG:O	1:B:267:VAL:HG23	2.17	0.44
1:B:769:ASP:HB2	1:B:774:GLN:HE22	1.64	0.44
1:A:430:LEU:HD13	1:A:563:ILE:CG1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:729:ASN:HD21	1:A:863:SER:HB2	1.82	0.44
1:A:858:LYS:HG3	1:B:454:ARG:HD3	1.99	0.44
1:B:390:MET:HB3	1:B:390:MET:HE3	1.84	0.44
1:B:393:PHE:CD1	1:B:394:LEU:HG	2.52	0.44
1:B:652:PRO:HD2	1:B:942:GLU:HB2	1.99	0.44
1:A:432:ASN:HB2	1:A:451:ARG:HG3	1.99	0.44
1:B:301:ALA:N	2:B:2974:SO4:O1	2.38	0.44
1:B:816:LEU:HD23	1:B:830:PRO:HA	1.99	0.44
1:B:458:TYR:CD1	1:B:608:TYR:HB2	2.52	0.44
1:B:555:ARG:NH2	1:B:559:ARG:NH2	2.64	0.44
1:B:671:MET:CG	1:B:672:GLU:N	2.81	0.44
1:A:335:GLY:O	1:A:369:ALA:HB1	2.17	0.44
1:A:391:THR:HA	1:A:394:LEU:O	2.18	0.44
1:A:596:SER:O	1:A:639:GLU:OE1	2.35	0.44
1:A:871:ARG:HH11	1:A:871:ARG:CG	2.31	0.44
1:A:884:ASP:HA	1:A:885:PRO:HD3	1.91	0.44
1:A:732:ILE:HG12	1:A:916:LEU:HB2	1.99	0.44
1:A:799:ILE:HG23	1:A:811:TYR:HB3	2.00	0.44
1:B:112:THR:O	1:B:116:ILE:HG13	2.17	0.44
1:A:126:LYS:CE	1:A:166:ARG:NH2	2.80	0.44
1:B:167:MET:N	1:B:168:PRO:HD2	2.33	0.44
1:B:280:GLN:OE1	1:B:332:SER:HB3	2.18	0.43
1:B:297:PHE:CZ	1:B:310:LEU:HD13	2.53	0.43
1:B:921:GLU:CD	1:B:949:THR:HA	2.39	0.43
1:A:407:ARG:O	1:A:411:VAL:HG23	2.18	0.43
1:A:372:ILE:HD11	1:A:410:ALA:C	2.39	0.43
1:B:774:GLN:O	1:B:775:ILE:C	2.55	0.43
1:A:705:GLY:HA3	1:A:965:VAL:HG11	2.00	0.43
1:B:425:ASP:OD1	1:B:426:GLU:N	2.49	0.43
1:A:21:THR:CG2	1:A:24:ASN:H	2.31	0.43
1:A:662:GLN:NE2	1:A:662:GLN:N	2.67	0.43
1:B:453:LYS:HB3	1:B:456:ARG:CG	2.48	0.43
1:B:708:THR:O	1:B:712:VAL:HG23	2.17	0.43
1:A:562:ASP:O	1:A:590:ILE:HG23	2.19	0.43
1:B:83:VAL:CG1	1:B:83:VAL:O	2.66	0.43
1:B:571:ASN:O	1:B:572:HIS:HB2	2.18	0.43
1:B:970:MET:HE2	1:B:970:MET:HB3	1.74	0.43
1:A:737:GLN:HE21	1:A:737:GLN:HB2	1.54	0.43
1:B:207:ARG:HG2	1:B:207:ARG:HH11	1.82	0.43
1:B:451:ARG:HD3	1:B:453:LYS:NZ	2.33	0.43
1:B:123:VAL:HG12	1:B:367:ILE:HG23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:182:LYS:HE2	1:B:184:GLU:OE2	2.18	0.43
1:B:278:ASP:HB3	1:B:281:VAL:HG23	2.00	0.43
1:A:370:ASP:OD2	1:A:374:GLU:OE1	2.37	0.42
1:B:239:THR:HB	1:B:240:PRO:HD2	2.02	0.42
1:B:317:ARG:HA	1:B:322:VAL:HG22	2.01	0.42
1:B:634:ALA:C	1:B:636:ALA:H	2.21	0.42
1:A:713:LEU:HD21	1:A:946:ILE:HD13	2.01	0.42
1:B:166:ARG:HD3	1:B:166:ARG:HA	1.69	0.42
1:B:875:GLU:O	1:B:879:SER:HB2	2.19	0.42
1:A:869:LEU:HD23	1:A:911:TRP:CZ2	2.54	0.42
1:B:374:GLU:O	1:B:375:ARG:HB2	2.19	0.42
1:B:499:ASP:OD1	1:B:501:THR:HG23	2.20	0.42
1:B:508:LEU:HB2	1:B:536:ILE:CG2	2.50	0.42
1:A:383:PHE:HA	1:A:403:LEU:HD21	2.02	0.42
1:A:263:ARG:HH21	1:B:781:GLU:HA	1.84	0.42
1:A:768:MET:O	1:A:769:ASP:HB2	2.20	0.42
1:A:769:ASP:OD1	1:A:845:VAL:HG21	2.19	0.42
1:B:420:PHE:CB	1:B:619:LYS:HB3	2.49	0.42
1:A:516:VAL:HG12	1:A:559:ARG:HG2	2.01	0.42
1:B:804:LYS:HE3	1:B:806:LYS:O	2.19	0.42
1:A:740:PHE:HA	1:A:905:VAL:HG21	2.01	0.42
1:B:239:THR:HB	1:B:240:PRO:CD	2.50	0.42
1:B:359:ILE:HG23	1:B:360:VAL:N	2.35	0.42
1:B:611:ASN:ND2	1:B:612:TYR:H	2.17	0.42
1:A:799:ILE:CG2	1:A:811:TYR:HB3	2.49	0.42
1:B:16:LYS:HD2	1:B:677:GLY:HA3	2.01	0.42
1:B:77:SER:HA	1:B:738:HIS:CE1	2.55	0.42
1:B:301:ALA:O	1:B:302:ASP:C	2.57	0.42
1:B:423:GLU:HG2	1:B:451:ARG:NH2	2.34	0.42
1:B:780:ALA:O	1:B:783:MET:SD	2.78	0.42
1:A:219:PRO:O	1:A:222:VAL:HG23	2.19	0.42
1:A:797:ALA:HB3	1:A:814:SER:O	2.20	0.42
1:B:186:LYS:HE3	1:B:186:LYS:HB2	1.87	0.42
1:B:446:ASN:O	1:B:616:LYS:NZ	2.44	0.42
1:A:516:VAL:HG23	1:A:517:GLY:N	2.35	0.41
1:B:121:ASN:OD1	1:B:123:VAL:HB	2.18	0.41
1:B:313:LEU:HD21	1:B:317:ARG:HH21	1.85	0.41
1:A:278:ASP:HB3	1:A:281:VAL:HG23	2.01	0.41
1:A:773:ARG:HG2	1:A:773:ARG:NH1	2.34	0.41
1:A:970:MET:HG2	1:A:971:THR:N	2.29	0.41
1:B:422:ASP:O	1:B:424:GLU:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:THR:N	1:A:388:PRO:HD2	2.35	0.41
1:A:657:GLY:N	2:A:2978:SO4:O1	2.50	0.41
1:A:897:SER:O	1:A:901:LYS:HG3	2.21	0.41
1:B:290:LEU:N	1:B:291:PRO:HD2	2.35	0.41
1:B:358:LYS:O	1:B:362:GLU:HG3	2.19	0.41
1:B:916:LEU:CD2	1:B:944:GLY:HA3	2.50	0.41
1:A:425:ASP:OD1	1:A:427:GLY:O	2.38	0.41
1:B:697:ALA:HB2	1:B:959:THR:OG1	2.21	0.41
1:A:14:PHE:CZ	1:A:52:GLU:HB3	2.56	0.41
1:B:29:ALA:HB1	1:B:69:ALA:HA	2.03	0.41
1:B:413:ASN:N	1:B:413:ASN:HD22	2.17	0.41
1:B:491:THR:HG22	1:B:563:ILE:HB	2.01	0.41
1:B:501:THR:HG21	1:B:510:PHE:CE1	2.55	0.41
1:B:797:ALA:HB3	1:B:814:SER:OG	2.20	0.41
1:A:364:ILE:HD13	1:A:390:MET:HG2	2.01	0.41
1:A:947:ILE:HD13	1:A:954:PHE:CE2	2.55	0.41
1:A:971:THR:O	1:A:971:THR:HG23	2.18	0.41
1:B:572:HIS:O	1:B:573:LEU:HD12	2.20	0.41
1:B:652:PRO:HB3	1:B:915:HIS:HA	2.03	0.41
1:B:773:ARG:HG3	1:B:773:ARG:O	2.21	0.41
1:A:454:ARG:O	1:A:455:ALA:HB3	2.21	0.41
1:B:238:VAL:HG21	1:B:272:MET:O	2.21	0.41
1:B:14:PHE:CZ	1:B:52:GLU:HB3	2.54	0.41
1:B:608:TYR:CD1	1:B:621:LYS:HA	2.56	0.41
1:B:716:GLU:HB2	1:B:770:ARG:NH2	2.36	0.41
1:A:214:GLN:HA	1:A:214:GLN:OE1	2.20	0.41
1:A:328:ILE:HG23	1:A:329:PRO:HD2	2.01	0.41
1:A:829:VAL:HG13	1:A:830:PRO:HD2	2.02	0.41
1:A:21:THR:N	1:A:24:ASN:OD1	2.43	0.41
1:A:190:THR:O	1:A:193:MET:HB3	2.21	0.41
1:A:446:ASN:O	1:A:616:LYS:NZ	2.48	0.41
1:A:449:GLN:N	1:A:449:GLN:CD	2.74	0.41
1:B:532:THR:CG2	1:B:535:MET:CG	2.97	0.41
1:B:569:PRO:HB2	1:B:581:LEU:HD21	2.03	0.41
1:B:643:THR:C	1:B:645:LEU:N	2.74	0.41
1:A:193:MET:CE	1:A:216:ILE:HD12	2.51	0.40
1:A:710:ILE:HD13	1:A:948:ILE:HD13	2.03	0.40
1:A:881:LEU:HD13	1:A:907:ALA:HB2	2.03	0.40
1:A:939:LYS:HB2	1:A:939:LYS:HE3	1.77	0.40
1:A:803:ARG:NH2	1:A:838:TRP:CD1	2.89	0.40
1:B:60:LYS:H	1:B:60:LYS:HG3	1.76	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:VAL:O	1:B:83:VAL:HG12	2.22	0.40
1:B:300:ILE:HG21	1:B:305:ALA:HB3	2.03	0.40
1:B:568:GLU:N	1:B:569:PRO:CD	2.85	0.40
1:A:296:ASN:O	1:A:300:ILE:HG13	2.21	0.40
1:B:811:TYR:CZ	1:B:852:VAL:HG13	2.56	0.40
1:B:61:LYS:HD2	1:B:62:THR:HG23	2.02	0.40
1:B:302:ASP:O	1:B:306:ARG:HG3	2.21	0.40
1:B:887:ILE:O	1:B:891:SER:HB2	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 X-ray entries followed by that with respect to entries of similar resolution.

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	971/986 (98%)	926 (95%)	41 (4%)	4 (0%)	34 60
1	B	971/986 (98%)	907 (93%)	59 (6%)	5 (0%)	29 54
All	All	1942/1972 (98%)	1833 (94%)	100 (5%)	9 (0%)	29 54

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	640	LEU
1	A	833	SER
1	B	640	LEU
1	B	775	ILE
1	A	775	ILE
1	B	20	ALA
1	B	284	PRO
1	A	845	VAL
1	B	283	ALA

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 X-ray entries followed by that with respect to entries of similar resolution.

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	831/843 (99%)	802 (96%)	29 (4%)	36 65
1	B	831/843 (99%)	807 (97%)	24 (3%)	42 71
All	All	1662/1686 (99%)	1609 (97%)	53 (3%)	39 68

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	39	ASN
1	A	62	THR
1	A	104	GLU
1	A	183	LYS
1	A	198	GLU
1	A	211	SER
1	A	263	ARG
1	A	264	LYS
1	A	304	GLU
1	A	316	LEU
1	A	338	SER
1	A	342	GLN
1	A	351	GLU
1	A	432	ASN
1	A	433	CYS
1	A	449	GLN
1	A	451	ARG
1	A	493	TYR
1	A	599	SER
1	A	618	ARG
1	A	737	GLN
1	A	773	ARG
1	A	804	LYS
1	A	827	ARG
1	A	858	LYS
1	A	867	ARG

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Mol	Chain	Res	Type
1	A	922	PRO
1	A	953	GLU
1	B	23	ASP
1	B	166	ARG
1	B	180	ASP
1	B	183	LYS
1	B	206	GLU
1	B	330	GLU
1	B	342	GLN
1	B	358	LYS
1	B	431	CYS
1	B	432	ASN
1	B	493	TYR
1	B	525	LYS
1	B	532	THR
1	B	571	ASN
1	B	662	GLN
1	B	685	ASP
1	B	737	GLN
1	B	827	ARG
1	B	859	GLU
1	B	872	LYS
1	B	879	SER
1	B	958	LEU
1	B	969	ARG
1	B	970	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
1	A	97	ASN
1	A	271	ASN
1	A	321	ASN
1	A	413	ASN
1	A	432	ASN
1	A	496	HIS
1	A	577	ASN
1	A	604	ASN
1	A	611	ASN
1	A	662	GLN
1	A	711	ASN

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Mol	Chain	Res	Type
1	A	729	ASN
1	A	737	GLN
1	A	756	GLN
1	A	848	HIS
1	A	865	GLN
1	A	877	HIS
1	A	915	HIS
1	B	24	ASN
1	B	76	GLN
1	B	89	GLN
1	B	97	ASN
1	B	296	ASN
1	B	321	ASN
1	B	342	GLN
1	B	413	ASN
1	B	432	ASN
1	B	449	GLN
1	B	496	HIS
1	B	604	ASN
1	B	611	ASN
1	B	642	ASN
1	B	662	GLN
1	B	674	GLN
1	B	711	ASN
1	B	774	GLN
1	B	784	ASN
1	B	848	HIS
1	B	877	HIS
1	B	915	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

11 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	2973	-	4,4,4	2.03	2 (50%)	6,6,6	0.90	0
2	SO4	B	2973	-	4,4,4	2.09	2 (50%)	6,6,6	0.85	0
2	SO4	A	2975	-	4,4,4	1.99	2 (50%)	6,6,6	0.88	0
2	SO4	B	2975	-	4,4,4	2.03	2 (50%)	6,6,6	3.80	4 (66%)
2	SO4	A	2978	-	4,4,4	1.96	2 (50%)	6,6,6	0.87	0
2	SO4	B	2976	-	4,4,4	2.02	2 (50%)	6,6,6	0.88	0
2	SO4	A	2977	-	4,4,4	1.99	2 (50%)	6,6,6	0.90	0
2	SO4	B	2974	-	4,4,4	1.98	2 (50%)	6,6,6	3.82	4 (66%)
2	SO4	B	2977	-	4,4,4	2.01	2 (50%)	6,6,6	0.88	0
2	SO4	A	2974	-	4,4,4	2.05	2 (50%)	6,6,6	0.86	0
2	SO4	A	2976	-	4,4,4	2.03	2 (50%)	6,6,6	0.86	0

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2974	SO4	O1-S	3.12	1.62	1.46
2	A	2975	SO4	O1-S	3.07	1.62	1.46
2	B	2976	SO4	O1-S	3.06	1.62	1.46
2	B	2973	SO4	O1-S	3.05	1.62	1.46
2	A	2976	SO4	O1-S	3.04	1.62	1.46
2	B	2977	SO4	O1-S	2.99	1.62	1.46
2	B	2974	SO4	O1-S	2.97	1.62	1.46
2	A	2978	SO4	O1-S	2.95	1.62	1.46
2	B	2975	SO4	O1-S	2.92	1.61	1.46
2	A	2973	SO4	O1-S	2.89	1.61	1.46
2	A	2977	SO4	O1-S	2.82	1.61	1.46
2	A	2973	SO4	O2-S	-2.80	1.30	1.46
2	B	2973	SO4	O2-S	-2.77	1.31	1.46
2	B	2975	SO4	O2-S	-2.76	1.31	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2977	SO4	O2-S	-2.76	1.31	1.46
2	B	2977	SO4	O2-S	-2.65	1.31	1.46
2	A	2976	SO4	O2-S	-2.63	1.31	1.46
2	A	2974	SO4	O2-S	-2.61	1.31	1.46
2	B	2976	SO4	O2-S	-2.59	1.32	1.46
2	B	2974	SO4	O2-S	-2.58	1.32	1.46
2	A	2978	SO4	O2-S	-2.55	1.32	1.46
2	A	2975	SO4	O2-S	-2.49	1.32	1.46

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	2974	SO4	O3-S-O1	-5.96	78.21	109.31
2	B	2975	SO4	O3-S-O1	-5.83	78.90	109.31
2	B	2974	SO4	O4-S-O3	-5.67	84.85	109.06
2	B	2975	SO4	O4-S-O3	-5.64	85.00	109.06
2	B	2975	SO4	O3-S-O2	-3.45	91.28	109.31
2	B	2974	SO4	O3-S-O2	-3.27	92.25	109.31
2	B	2975	SO4	O4-S-O2	2.08	120.16	109.31
2	B	2974	SO4	O4-S-O2	2.03	119.89	109.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2978	SO4	2	0
2	B	2974	SO4	2	0
2	B	2977	SO4	1	0
2	A	2976	SO4	1	0

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 Fit of model and data i

6.1 Protein, DNA and RNA chains i

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	973/986 (98%)	-0.10	27 (2%) 53 54	20, 41, 70, 120	0
1	B	973/986 (98%)	0.09	49 (5%) 28 27	24, 48, 79, 114	0
All	All	1946/1972 (98%)	-0.00	76 (3%) 39 38	20, 44, 77, 120	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	640	LEU	11.2
1	A	778	ASN	9.3
1	B	642	ASN	7.3
1	B	641	SER	7.2
1	A	776	ASN	7.1
1	B	637	TYR	6.6
1	B	643	THR	6.5
1	B	639	GLU	6.4
1	B	775	ILE	6.1
1	A	777	GLU	5.9
1	B	426	GLU	5.6
1	B	778	ASN	5.6
1	B	779	ASP	5.5
1	B	424	GLU	5.3
1	B	774	GLN	5.3
1	A	423	GLU	4.8
1	B	780	ALA	4.7
1	A	779	ASP	4.6
1	A	425	ASP	4.4
1	B	416	VAL	4.1
1	A	833	SER	4.0
1	B	330	GLU	3.9
1	A	426	GLU	3.8
1	B	423	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	776	ASN	3.6
1	A	775	ILE	3.6
1	B	777	GLU	3.6
1	B	325	ASP	3.5
1	B	425	ASP	3.4
1	A	421	ASP	3.3
1	B	19	VAL	3.2
1	B	298	ALA	3.2
1	A	424	GLU	3.2
1	A	417	GLY	3.1
1	B	420	PHE	3.1
1	A	644	ASP	3.0
1	A	572	HIS	2.9
1	A	643	THR	2.9
1	B	257	ARG	2.9
1	A	422	ASP	2.9
1	A	427	GLY	2.9
1	B	638	GLU	2.9
1	B	103	LYS	2.8
1	B	447	LYS	2.8
1	B	422	ASP	2.8
1	B	101	LYS	2.7
1	B	61	LYS	2.7
1	B	572	HIS	2.7
1	A	972	PRO	2.6
1	B	419	ASN	2.6
1	A	257	ARG	2.6
1	A	419	ASN	2.6
1	B	324	GLU	2.6
1	B	782	ALA	2.6
1	A	641	SER	2.6
1	B	140	ASN	2.5
1	B	4	GLN	2.5
1	A	352	THR	2.4
1	B	1	SER	2.4
1	B	644	ASP	2.4
1	B	773	ARG	2.4
1	B	181	THR	2.4
1	B	397	LYS	2.3
1	B	2	ASP	2.2
1	B	331	LEU	2.2
1	A	69	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	323	GLY	2.2
1	A	642	ASN	2.2
1	B	231	ALA	2.1
1	B	333	HIS	2.1
1	B	504	ASP	2.1
1	A	659	LYS	2.1
1	B	364	ILE	2.1
1	B	634	ALA	2.0
1	A	23	ASP	2.0
1	A	179	TRP	2.0

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

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

6.3 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

6.4 Ligands [\(i\)](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SO4	A	2978	5/5	0.83	0.34	94,94,95,96	0
2	SO4	A	2975	5/5	0.89	0.26	93,93,94,94	0
2	SO4	B	2974	5/5	0.89	0.39	80,82,82,83	0
2	SO4	A	2974	5/5	0.91	0.36	96,96,96,98	0
2	SO4	B	2975	5/5	0.93	0.29	85,85,85,86	0
2	SO4	B	2977	5/5	0.95	0.29	91,92,93,93	0
2	SO4	B	2973	5/5	0.96	0.19	74,75,76,76	0
2	SO4	A	2976	5/5	0.96	0.22	75,75,76,76	0
2	SO4	A	2973	5/5	0.97	0.19	48,50,50,53	0
2	SO4	B	2976	5/5	0.98	0.10	50,50,52,53	0
2	SO4	A	2977	5/5	0.98	0.11	53,53,54,55	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.