



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:36 PM GMT

PDB ID : 4M5D
Title : Crystal structure of the Utp22 and Rrp7 complex from *Saccharomyces cerevisiae*
Authors : Lin, J.; Ye, K.
Deposited on : 2013-08-08
Resolution : 1.97 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

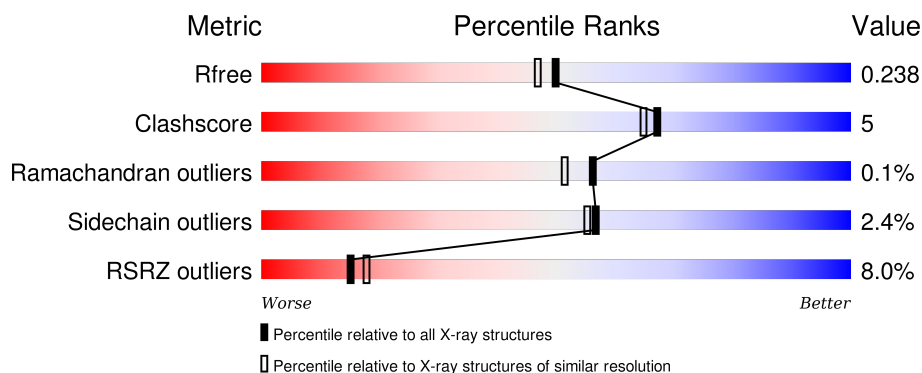
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.97 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))
R_{free}	91344	8664 (2.00-1.96)
Clashscore	102246	9905 (2.00-1.96)
Ramachandran outliers	100387	9792 (2.00-1.96)
Sidechain outliers	100360	9791 (2.00-1.96)
RSRZ outliers	91569	8679 (2.00-1.96)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1237	
2	B	297	

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
3	SO4	A	1302	-	-	-	X
3	SO4	A	1303	-	-	-	X
3	SO4	A	1304	-	-	-	X
3	SO4	A	1311	-	-	-	X
4	PGE	A	1312	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 11079 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.

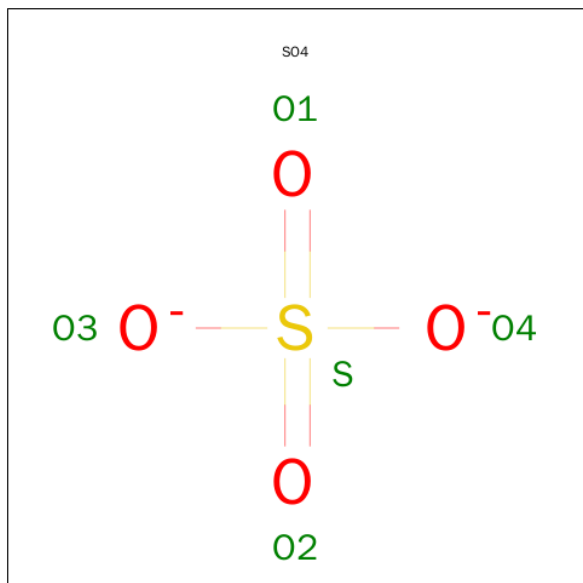
- Molecule 1 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1098	Total	C	N	O	S	0	0	0
			8870	5763	1462	1621	24			

- Molecule 2 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	169	Total	C	N	O	S	0	0	0
			1368	884	225	252	7			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



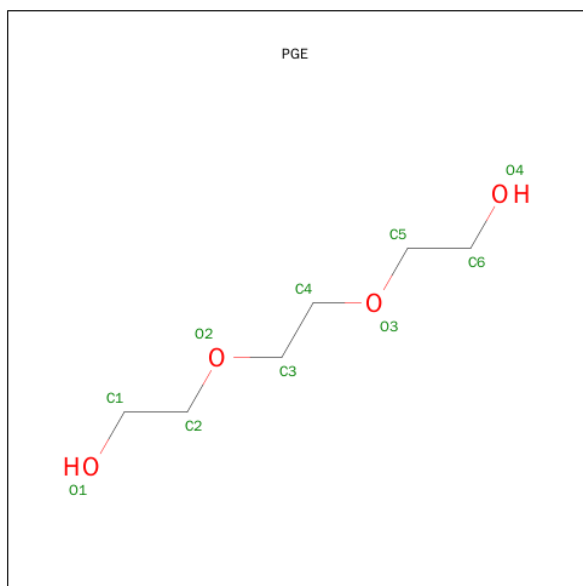
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			7	4	3		

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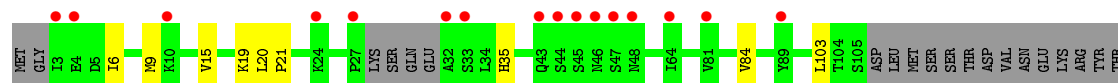
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	4	2		

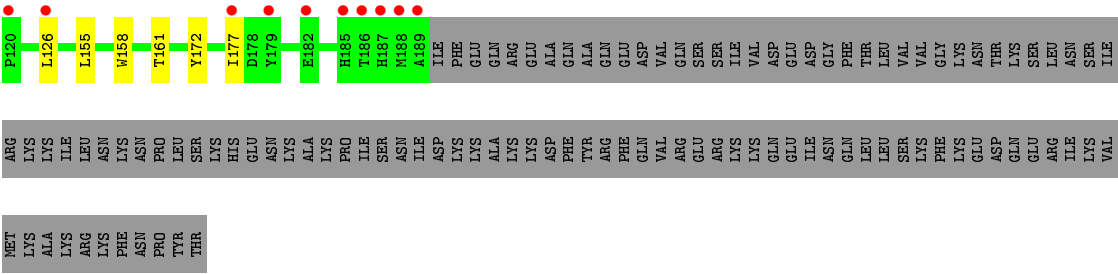
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	690	Total	O	0	0
			690	690		
5	B	73	Total	O	0	0
			73	73		

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

- Chain A:  6% 78% 9% 11%





4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	126.26Å 129.56Å 214.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.94 – 1.97 19.94 – 1.97	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.94-1.97) 100.0 (19.94-1.97)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.208 , 0.238 0.207 , 0.238	Depositor DCC
R_{free} test set	6183 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	25.7	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 56.3	EDS
Estimated twinning fraction	0.009 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 123148 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11079	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PGE, 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	0.49	0/9081	0.55	0/12283
2	B	0.45	0/1405	0.52	0/1903
All	All	0.48	0/10486	0.55	0/14186

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	8870	0	8975	88	0
2	B	1368	0	1330	15	0
3	A	55	0	0	0	0
4	A	17	0	23	2	0
4	B	6	0	7	0	0
5	A	690	0	0	13	0
5	B	73	0	0	0	0
All	All	11079	0	10335	100	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 (100) 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:168:ILE:HD13	1:A:171:ASN:HB2	1.46	0.97
1:A:168:ILE:HD12	1:A:168:ILE:H	1.31	0.92
1:A:606:ASN:HD22	1:A:608:PHE:H	1.21	0.89
1:A:878:LEU:HD21	2:B:103:LEU:HD13	1.55	0.88
1:A:168:ILE:CD1	1:A:171:ASN:HB2	2.09	0.83
1:A:117:LYS:HB3	4:A:1313:PGE:H4	1.63	0.79
1:A:142:GLU:O	1:A:144:LYS:HG2	1.87	0.75
1:A:356:THR:HG21	1:A:401:LEU:HD13	1.68	0.74
2:B:6:ILE:CG2	2:B:9:MET:HE1	2.20	0.71
1:A:352:THR:O	1:A:356:THR:HG23	1.91	0.69
1:A:209:MET:HE3	1:A:298:PHE:CD1	2.29	0.67
1:A:1063:ARG:HD3	5:A:1898:HOH:O	1.97	0.64
1:A:317:ILE:HG12	1:A:549:SER:HB3	1.80	0.62
1:A:232:LEU:HD13	1:A:296:ILE:HD11	1.81	0.62
1:A:209:MET:HE3	1:A:298:PHE:CE1	2.35	0.62
1:A:870:ALA:HB2	1:A:878:LEU:HD22	1.82	0.61
1:A:168:ILE:HD13	1:A:171:ASN:CB	2.27	0.61
1:A:518:PHE:CZ	1:A:1076:GLN:HG2	2.36	0.61
1:A:1143:MET:HB3	2:B:172:TYR:CE2	2.36	0.60
1:A:1149:LEU:HD12	1:A:1226:PHE:CD2	2.37	0.60
1:A:606:ASN:ND2	1:A:608:PHE:H	1.95	0.59
2:B:9:MET:HE2	2:B:15:VAL:CG2	2.31	0.59
2:B:6:ILE:HG22	2:B:9:MET:HE1	1.84	0.59
1:A:209:MET:CE	1:A:298:PHE:CE1	2.87	0.58
1:A:781:ASP:OD2	5:A:2089:HOH:O	2.17	0.58
1:A:918:ARG:O	1:A:922:THR:HG23	2.04	0.57
1:A:219:PHE:CE2	1:A:220:LEU:HD13	2.40	0.57
1:A:536:TYR:OH	1:A:552:ARG:HD3	2.06	0.56
1:A:406:ILE:H	1:A:406:ILE:HD12	1.71	0.56
2:B:9:MET:HE2	2:B:15:VAL:HG21	1.89	0.54
1:A:299:PRO:HB2	1:A:302:VAL:HG13	1.89	0.54
2:B:6:ILE:HG21	2:B:9:MET:HE1	1.90	0.53
1:A:827:ARG:NH2	5:A:1789:HOH:O	2.41	0.53
1:A:209:MET:CE	1:A:298:PHE:CD1	2.92	0.52
2:B:9:MET:CE	2:B:15:VAL:HG21	2.38	0.52
1:A:268:LEU:HD23	1:A:294:LEU:HD12	1.92	0.51
1:A:156:LYS:HG2	1:A:237:HIS:CE1	2.45	0.51
1:A:1191:LYS:HE2	5:A:1991:HOH:O	2.10	0.51
1:A:299:PRO:O	1:A:302:VAL:HG22	2.11	0.51
1:A:547:PHE:CZ	1:A:552:ARG:HG2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:558:LEU:HG	1:A:558:LEU:O	2.08	0.51
1:A:494:GLU:CD	1:A:497:ARG:HH12	2.14	0.50
1:A:143:GLU:HG2	1:A:175:LYS:HG3	1.92	0.50
1:A:639:SER:OG	1:A:641:GLU:HG3	2.12	0.49
1:A:240:LEU:O	1:A:244:LYS:HG2	2.13	0.49
1:A:209:MET:HE3	1:A:298:PHE:HD1	1.77	0.49
1:A:1063:ARG:CD	5:A:1898:HOH:O	2.59	0.49
1:A:133:ASP:O	1:A:137:GLU:HG3	2.12	0.49
2:B:6:ILE:HG22	2:B:9:MET:CE	2.43	0.49
1:A:185:LEU:O	1:A:346:LEU:HD22	2.13	0.49
2:B:6:ILE:CG2	2:B:9:MET:CE	2.91	0.48
1:A:894:ARG:HD2	1:A:1045:ASN:OD1	2.14	0.48
1:A:853:ARG:HD3	1:A:889:TYR:CZ	2.49	0.47
1:A:884:LYS:HE3	5:A:1913:HOH:O	2.15	0.47
1:A:209:MET:CE	1:A:298:PHE:HE1	2.27	0.47
1:A:445:ASN:C	5:A:2006:HOH:O	2.52	0.47
1:A:565:LYS:HE2	5:A:1632:HOH:O	2.16	0.46
1:A:116:LEU:HD11	1:A:290:PHE:HZ	1.80	0.46
1:A:168:ILE:N	1:A:168:ILE:HD12	2.12	0.46
1:A:515:ILE:CG2	1:A:947:PRO:HG2	2.46	0.46
1:A:352:THR:O	1:A:356:THR:CG2	2.63	0.46
2:B:20:LEU:HD21	2:B:35:HIS:HB2	1.98	0.46
1:A:1034:GLY:O	1:A:1038:GLN:HG3	2.16	0.45
1:A:193:ALA:O	1:A:367:ARG:NH2	2.50	0.45
1:A:924:LEU:HD21	1:A:1181:VAL:HG13	1.99	0.45
1:A:1143:MET:HB3	2:B:172:TYR:CD2	2.53	0.44
1:A:619:VAL:HG13	1:A:624:CYS:HB3	2.00	0.44
2:B:21:PRO:HD3	2:B:158:TRP:O	2.18	0.44
1:A:232:LEU:HD13	1:A:296:ILE:CD1	2.47	0.44
1:A:1058:LEU:O	1:A:1062:THR:HG23	2.17	0.44
1:A:343:GLU:HG2	1:A:347:LYS:HE3	1.99	0.43
2:B:19:LYS:HE2	2:B:155:LEU:O	2.17	0.43
1:A:1131:ASN:HB2	5:A:2061:HOH:O	2.17	0.43
1:A:527:TYR:CD2	1:A:698:ASN:HB2	2.54	0.43
1:A:124:VAL:HG11	1:A:290:PHE:CD2	2.54	0.43
1:A:445:ASN:HD22	1:A:471:SER:HB3	1.83	0.43
1:A:253:GLN:HB2	1:A:271:SER:OG	2.19	0.43
1:A:207:LEU:HD11	1:A:294:LEU:HD22	2.01	0.42
1:A:606:ASN:ND2	5:A:1769:HOH:O	2.53	0.42
1:A:118:GLN:H	4:A:1313:PGE:H2	1.83	0.42
1:A:219:PHE:HB3	1:A:303:PHE:CG	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:LYS:HB2	5:A:2055:HOH:O	2.19	0.42
1:A:209:MET:HE3	1:A:214:PHE:HZ	1.84	0.42
1:A:130:LYS:HD2	1:A:283:TYR:CZ	2.55	0.42
1:A:940:LYS:HD2	1:A:944:ASP:HB3	2.01	0.42
1:A:140:ASP:OD1	1:A:140:ASP:N	2.52	0.42
1:A:482:VAL:O	1:A:486:GLN:HG2	2.18	0.42
1:A:1206:PRO:HA	1:A:1212:VAL:HG12	2.01	0.42
1:A:116:LEU:HD11	1:A:290:PHE:CZ	2.55	0.42
1:A:217:LYS:HA	1:A:217:LYS:HD3	1.79	0.41
1:A:638:MET:CE	1:A:646:LYS:HD2	2.50	0.41
2:B:84:VAL:HG11	2:B:126:LEU:HD11	2.02	0.41
1:A:866:ALA:C	1:A:878:LEU:HD23	2.41	0.41
1:A:907:GLN:HG2	5:A:1885:HOH:O	2.20	0.41
1:A:1102:LEU:HA	1:A:1230:MET:O	2.21	0.41
1:A:699:GLU:N	5:A:1992:HOH:O	2.52	0.41
1:A:771:PHE:HB2	1:A:1129:PRO:HB2	2.02	0.41
1:A:734:PHE:HB2	1:A:850:PHE:CZ	2.56	0.40
1:A:841:ASN:HD22	1:A:841:ASN:N	2.19	0.40
1:A:174:TYR:CE1	1:A:223:ARG:HG2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1086/1237 (88%)	1070 (98%)	15 (1%)	1 (0%)	56	51
2	B	163/297 (55%)	158 (97%)	5 (3%)	0	100	100
All	All	1249/1534 (81%)	1228 (98%)	20 (2%)	1 (0%)	56	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1228	ASN

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 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	1000/1125 (89%)	974 (97%)	26 (3%)	54	51
2	B	154/274 (56%)	152 (99%)	2 (1%)	76	77
All	All	1154/1399 (82%)	1126 (98%)	28 (2%)	57	55

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	PHE
1	A	131	LEU
1	A	141	TRP
1	A	155	ASN
1	A	156	LYS
1	A	168	ILE
1	A	197	GLN
1	A	216	LYS
1	A	217	LYS
1	A	220	LEU
1	A	282	ASP
1	A	302	VAL
1	A	356	THR
1	A	407	ASN
1	A	409	ASN
1	A	571	ARG
1	A	585	MET
1	A	606	ASN
1	A	625	ASP
1	A	781	ASP
1	A	827	ARG
1	A	918	ARG
1	A	967	GLN

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Mol	Chain	Res	Type
1	A	1022	MET
1	A	1143	MET
1	A	1191	LYS
2	B	161	THR
2	B	177	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	261	ASN
1	A	344	ASN
1	A	407	ASN
1	A	409	ASN
1	A	436	HIS
1	A	445	ASN
1	A	606	ASN
1	A	683	ASN
1	A	841	ASN
1	A	967	GLN
1	A	1083	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

14 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	$\# Z > 2$
3	SO4	A	1301	-	4,4,4	0.23	0	6,6,6	0.12	0
3	SO4	A	1302	-	4,4,4	0.19	0	6,6,6	0.32	0
3	SO4	A	1303	-	4,4,4	0.20	0	6,6,6	0.17	0
3	SO4	A	1304	-	4,4,4	0.16	0	6,6,6	0.23	0
3	SO4	A	1305	-	4,4,4	0.29	0	6,6,6	0.19	0
3	SO4	A	1306	-	4,4,4	0.21	0	6,6,6	0.11	0
3	SO4	A	1307	-	4,4,4	0.22	0	6,6,6	0.15	0
3	SO4	A	1308	-	4,4,4	0.31	0	6,6,6	0.07	0
3	SO4	A	1309	-	4,4,4	0.22	0	6,6,6	0.13	0
3	SO4	A	1310	-	4,4,4	0.32	0	6,6,6	0.15	0
3	SO4	A	1311	-	4,4,4	0.09	0	6,6,6	0.16	0
4	PGE	A	1312	-	9,9,9	0.43	0	8,8,8	0.52	0
4	PGE	A	1313	-	6,6,9	0.42	0	5,5,8	0.37	0
4	PGE	B	301	-	5,5,9	0.50	0	4,4,8	0.25	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	A	1301	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1302	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1303	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1304	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1305	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1306	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1307	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1308	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1309	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1310	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1311	-	-	0/0/0/0	0/0/0/0
4	PGE	A	1312	-	-	0/7/7/7	0/0/0/0
4	PGE	A	1313	-	-	0/4/4/7	0/0/0/0
4	PGE	B	301	-	-	0/3/3/7	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1313	PGE	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	1098/1237 (88%)	0.48	75 (6%) 20 24	13, 26, 51, 63	0
2	B	169/297 (56%)	0.99	26 (15%) 3 3	24, 35, 54, 60	0
All	All	1267/1534 (82%)	0.55	101 (7%) 15 18	13, 28, 51, 63	0

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	171	ASN	6.6
2	B	47	SER	6.0
1	A	286	TYR	6.0
1	A	168	ILE	6.0
1	A	326	LEU	5.8
2	B	32	ALA	5.8
1	A	155	ASN	5.8
1	A	317	ILE	5.4
2	B	179	TYR	5.4
1	A	274	LYS	5.4
2	B	45	SER	5.3
1	A	133	ASP	5.3
2	B	3	ILE	5.2
2	B	43	GLN	5.0
1	A	198	PRO	5.0
1	A	1116	SER	4.9
1	A	170	GLN	4.9
1	A	453	PRO	4.8
1	A	196	TYR	4.8
1	A	199	ASN	4.6
1	A	637	THR	4.5
1	A	1237	ASP	4.5
2	B	187	HIS	4.4
1	A	136	GLN	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	407	ASN	4.1
2	B	189	ALA	4.1
2	B	24	LYS	4.0
2	B	27	PRO	4.0
2	B	48	ASN	4.0
2	B	126	LEU	4.0
1	A	154	LYS	3.9
2	B	188	MET	3.9
1	A	141	TRP	3.9
1	A	217	LYS	3.8
1	A	247	LYS	3.8
2	B	46	ASN	3.8
1	A	1189	LEU	3.7
2	B	44	SER	3.7
1	A	132	TYR	3.6
1	A	1128	ALA	3.4
1	A	241	ILE	3.1
1	A	289	ARG	3.1
1	A	142	GLU	3.1
2	B	33	SER	3.1
1	A	406	ILE	3.1
1	A	1094	LYS	3.1
2	B	185	HIS	3.0
1	A	232	LEU	2.9
1	A	1175	GLU	2.9
2	B	182	GLU	2.9
2	B	186	THR	2.8
1	A	287	LYS	2.8
1	A	659	LYS	2.8
1	A	212	GLU	2.7
1	A	182	ASP	2.7
1	A	282	ASP	2.7
1	A	536	TYR	2.7
1	A	244	LYS	2.7
1	A	1010	GLU	2.7
1	A	983	GLU	2.7
1	A	460	GLU	2.7
1	A	871	ARG	2.7
2	B	89	TYR	2.6
1	A	1083	GLN	2.6
1	A	636	GLU	2.6
1	A	180	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	124	VAL	2.6
1	A	1223	ILE	2.6
2	B	4	GLU	2.6
1	A	1095	ASP	2.6
1	A	440	LEU	2.6
2	B	81	VAL	2.6
1	A	152	PHE	2.5
1	A	173	ASN	2.5
1	A	436	HIS	2.5
1	A	873	GLU	2.5
1	A	251	PHE	2.5
1	A	550	MET	2.4
1	A	872	ASN	2.4
1	A	230	VAL	2.4
1	A	176	PHE	2.4
2	B	177	ILE	2.3
1	A	216	LYS	2.3
1	A	130	LYS	2.3
1	A	602	ASN	2.3
1	A	1182	ILE	2.3
1	A	1090	THR	2.3
1	A	270	ILE	2.2
1	A	537	ASN	2.2
1	A	1217	GLU	2.2
2	B	120	PRO	2.2
2	B	10	LYS	2.1
1	A	127	PHE	2.1
1	A	409	ASN	2.1
1	A	234	TYR	2.1
1	A	137	GLU	2.1
2	B	64	ILE	2.0
1	A	149	VAL	2.0
1	A	283	TYR	2.0
1	A	197	GLN	2.0
1	A	245	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	SO4	A	1303	5/5	0.93	0.28	7.62	64,64,65,65	0
3	SO4	A	1302	5/5	0.97	0.20	7.43	46,48,48,48	0
3	SO4	A	1311	5/5	0.93	0.35	4.96	54,55,56,56	0
4	PGE	A	1312	10/10	0.81	0.19	2.19	38,41,44,46	0
3	SO4	A	1304	5/5	0.86	0.21	2.12	55,55,57,57	0
4	PGE	B	301	6/10	0.91	0.13	1.77	37,38,39,41	0
3	SO4	A	1310	5/5	0.98	0.14	0.01	44,45,46,46	0
3	SO4	A	1307	5/5	0.97	0.11	-0.54	44,44,45,45	0
3	SO4	A	1309	5/5	0.94	0.10	-0.82	54,54,55,55	0
3	SO4	A	1305	5/5	0.93	0.21	-	66,67,67,68	0
4	PGE	A	1313	7/10	0.82	0.16	-	47,49,50,51	0
3	SO4	A	1301	5/5	0.94	0.27	-	80,80,80,80	0
3	SO4	A	1308	5/5	0.91	0.22	-	82,82,82,82	0
3	SO4	A	1306	5/5	0.86	0.30	-	88,88,88,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.