



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:01 AM UTC

PDB ID : 4M5D / pdb_00004m5d
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

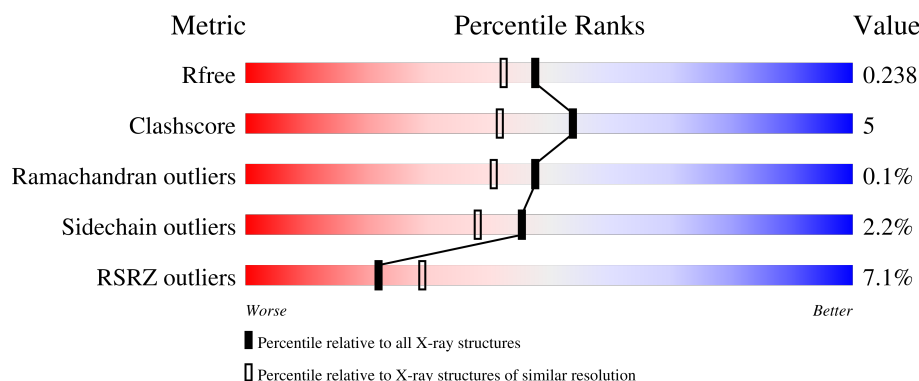
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

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}	180053	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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 $\leq 5\%$. 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	

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.

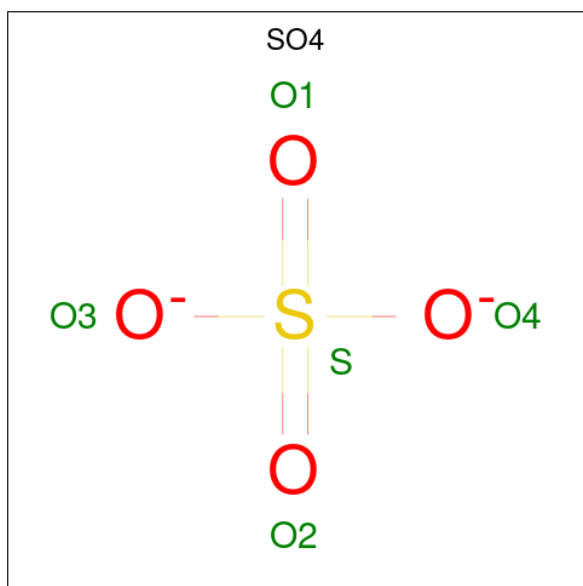
- Molecule 1 is a protein called U3 small nucleolar RNA-associated protein 22.

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

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

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

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



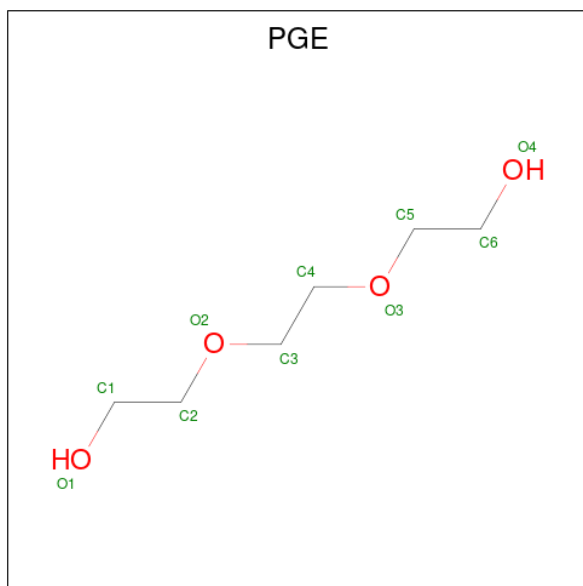
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	A	1	5	4	1	0	0
3	A	1	5	4	1	0	0

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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 (CCD ID: 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		

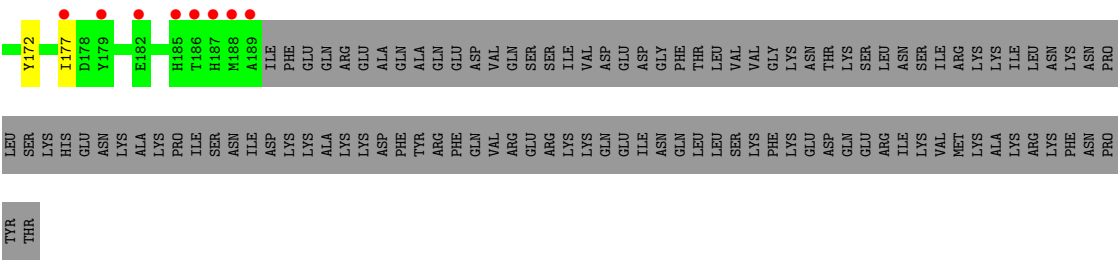
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	4	2		

- 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		



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) 99.8 (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 (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	25.7	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.009 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	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, 0.333 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: 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	0.58	0/9081	0.76	0/12283
2	B	0.51	0/1405	0.75	0/1903
All	All	0.57	0/10486	0.76	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 [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	8870	0	8975	91	0
2	B	1368	0	1330	13	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	101	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 (101) 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
2:B:9:MET:HE3	2:B:15:VAL:HG21	1.48	0.93
1:A:168:ILE:H	1:A:168:ILE:HD12	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
2:B:9:MET:HE3	2:B:15:VAL:CG2	2.11	0.81
1:A:638:MET:HE1	1:A:646:LYS:HD2	1.63	0.80
1:A:117:LYS:HB3	4:A:1313:PGE:H4	1.63	0.79
1:A:209:MET:HE1	1:A:298:PHE:HE1	1.46	0.78
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
1:A:209:MET:HE1	1:A:298:PHE:CE1	2.24	0.73
2:B:6:ILE:HG21	2:B:9:MET:HE1	1.71	0.72
1:A:352:THR:O	1:A:356:THR:HG23	1.91	0.69
2:B:6:ILE:CG2	2:B:9:MET:HE1	2.27	0.64
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:HD1	1.65	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:209:MET:HE2	1:A:296:ILE:HG22	1.83	0.60
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
1:A:781:ASP:OD2	5:A:2089:HOH:O	2.17	0.58
1:A:209:MET:CE	1:A:298:PHE:CE1	2.87	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:209:MET:HE3	1:A:298:PHE:CD1	2.40	0.56
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
1:A:494:GLU:CD	1:A:497:ARG:HH12	2.14	0.55
1:A:299:PRO:HB2	1:A:302:VAL:HG13	1.89	0.54
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
1:A:445:ASN:C	5:A:2006:HOH:O	2.52	0.52
1:A:268:LEU:HD23	1:A:294:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:558:LEU:O	1:A:558:LEU:HG	2.08	0.51
1:A:495:THR:HA	1:A:498:MET:HE3	1.94	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: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
1:A:185:LEU:O	1:A:346:LEU:HD22	2.13	0.49
2:B:6:ILE:HG22	2:B:9:MET:CE	2.43	0.49
1:A:894:ARG:HD2	1:A:1045:ASN:OD1	2.14	0.48
2:B:6:ILE:CG2	2:B:9:MET:CE	2.91	0.47
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:116:LEU:HD11	1:A:290:PHE:HZ	1.80	0.46
1:A:565:LYS:HE2	5:A:1632:HOH:O	2.16	0.46
1:A:168:ILE:HD12	1:A:168:ILE:N	2.12	0.46
1:A:515:ILE:CG2	1:A:947:PRO:HG2	2.46	0.46
1:A:866:ALA:C	1:A:878:LEU:HD23	2.41	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:193:ALA:O	1:A:367:ARG:NH2	2.50	0.45
1:A:1034:GLY:O	1:A:1038:GLN:HG3	2.16	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
1:A:1131:ASN:HB2	5:A:2061:HOH:O	2.17	0.43
2:B:19:LYS:HE2	2:B:155:LEU: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

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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: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
1:A:130:LYS:HD2	1:A:283:TYR:CZ	2.55	0.42
1:A:140:ASP:N	1:A:140:ASP:OD1	2.52	0.42
1:A:940:LYS:HD2	1:A:944:ASP:HB3	2.01	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:178:TYR:C	1:A:178:TYR:CD1	2.98	0.41
1:A:1022:MET:HE2	1:A:1022:MET:HB3	1.91	0.41
2:B:84:VAL:HG11	2:B:126:LEU:HD11	2.02	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%)	48	41
2	B	163/297 (55%)	158 (97%)	5 (3%)	0	100	100
All	All	1249/1534 (81%)	1228 (98%)	20 (2%)	1 (0%)	48	41

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%)	977 (98%)	23 (2%)	44	37
2	B	154/274 (56%)	152 (99%)	2 (1%)	61	57
All	All	1154/1399 (82%)	1129 (98%)	25 (2%)	45	38

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	LEU
1	A	155	ASN
1	A	156	LYS
1	A	168	ILE
1	A	175	LYS
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	585	MET
1	A	606	ASN
1	A	625	ASP
1	A	664	THR
1	A	781	ASP
1	A	827	ARG
1	A	967	GLN
1	A	1022	MET
1	A	1143	MET

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Mol	Chain	Res	Type
2	B	161	THR
2	B	177	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	HIS
1	A	173	ASN
1	A	197	GLN
1	A	237	HIS
1	A	253	GLN
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	530	GLN
1	A	606	ASN
1	A	683	ASN
1	A	687	GLN
1	A	841	ASN
1	A	967	GLN
1	A	1083	GLN
1	A	1154	ASN
2	B	83	HIS
2	B	151	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry

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	1310	-	4,4,4	0.25	0	6,6,6	0.18	0
4	PGE	A	1313	-	6,6,9	0.43	0	5,5,8	0.35	0
4	PGE	B	301	-	5,5,9	0.51	0	4,4,8	0.23	0
3	SO4	A	1301	-	4,4,4	0.25	0	6,6,6	0.12	0
3	SO4	A	1302	-	4,4,4	0.25	0	6,6,6	0.21	0
3	SO4	A	1306	-	4,4,4	0.25	0	6,6,6	0.10	0
4	PGE	A	1312	-	9,9,9	0.43	0	8,8,8	0.50	0
3	SO4	A	1303	-	4,4,4	0.27	0	6,6,6	0.21	0
3	SO4	A	1307	-	4,4,4	0.26	0	6,6,6	0.17	0
3	SO4	A	1311	-	4,4,4	0.32	0	6,6,6	0.11	0
3	SO4	A	1304	-	4,4,4	0.28	0	6,6,6	0.18	0
3	SO4	A	1308	-	4,4,4	0.26	0	6,6,6	0.08	0
3	SO4	A	1309	-	4,4,4	0.26	0	6,6,6	0.16	0
3	SO4	A	1305	-	4,4,4	0.23	0	6,6,6	0.21	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
4	PGE	A	1312	-	-	2/7/7/7	-
4	PGE	A	1313	-	-	3/4/4/7	-
4	PGE	B	301	-	-	1/3/3/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1313	PGE	O2-C3-C4-O3
4	A	1312	PGE	O2-C3-C4-O3
4	A	1313	PGE	C4-C3-O2-C2
4	B	301	PGE	O1-C1-C2-O2
4	A	1312	PGE	O3-C5-C6-O4
4	A	1313	PGE	C1-C2-O2-C3

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 [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

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%)	0.29	69 (6%) 26 34	13, 26, 51, 63	0
2	B	169/297 (56%)	0.81	21 (12%) 8 11	24, 35, 54, 60	0
All	All	1267/1534 (82%)	0.36	90 (7%) 22 29	13, 28, 51, 63	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	141	TRP	5.0
1	A	133	ASP	4.7
1	A	453	PRO	4.6
1	A	168	ILE	4.2
1	A	171	ASN	4.1
2	B	188	MET	4.1
2	B	32	ALA	4.0
1	A	317	ILE	3.8
1	A	286	TYR	3.6
1	A	149	VAL	3.6
1	A	1116	SER	3.5
1	A	196	TYR	3.5
2	B	179	TYR	3.4
1	A	234	TYR	3.4
2	B	3	ILE	3.4
1	A	1128	ALA	3.3
1	A	213	LEU	3.3
2	B	120	PRO	3.3
2	B	47	SER	3.3
1	A	176	PHE	3.2
2	B	189	ALA	3.2
1	A	274	LYS	3.2
2	B	186	THR	3.1
1	A	155	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	130	LYS	3.0
1	A	152	PHE	3.0
2	B	187	HIS	2.9
1	A	536	TYR	2.9
1	A	217	LYS	2.9
1	A	290	PHE	2.9
1	A	302	VAL	2.8
1	A	136	GLN	2.8
1	A	406	ILE	2.7
1	A	283	TYR	2.7
1	A	127	PHE	2.6
1	A	460	GLU	2.6
1	A	146	LEU	2.6
1	A	436	HIS	2.6
1	A	172	THR	2.6
1	A	1217	GLU	2.5
1	A	407	ASN	2.5
1	A	170	GLN	2.5
1	A	230	VAL	2.5
1	A	139	PRO	2.5
2	B	177	ILE	2.5
2	B	33	SER	2.4
1	A	144	LYS	2.4
1	A	134	ILE	2.4
1	A	248	LEU	2.4
1	A	657	ARG	2.4
1	A	169	PRO	2.4
2	B	27	PRO	2.4
1	A	326	LEU	2.3
1	A	1237	ASP	2.3
1	A	1189	LEU	2.3
2	B	161	THR	2.3
1	A	153	PHE	2.3
1	A	1073	ASN	2.3
1	A	637	THR	2.3
1	A	174	TYR	2.3
1	A	142	GLU	2.3
2	B	48	ASN	2.3
1	A	550	MET	2.3
1	A	177	ASN	2.2
1	A	261	ASN	2.2
2	B	45	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	124	VAL	2.2
1	A	1175	GLU	2.2
1	A	138	ILE	2.2
1	A	289	ARG	2.2
1	A	540	GLU	2.2
2	B	185	HIS	2.1
2	B	89	TYR	2.1
1	A	157	ILE	2.1
1	A	409	ASN	2.1
1	A	145	SER	2.1
2	B	182	GLU	2.1
1	A	198	PRO	2.1
2	B	8	ALA	2.1
2	B	105	SER	2.1
1	A	131	LEU	2.1
1	A	331	LEU	2.1
1	A	175	LYS	2.0
1	A	178	TYR	2.0
2	B	46	ASN	2.0
1	A	242	LEU	2.0
1	A	212	GLU	2.0
1	A	241	ILE	2.0
1	A	1076	GLN	2.0
1	A	210	PRO	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
4	PGE	A	1313	7/10	0.74	0.15	47,49,50,51	0
4	PGE	B	301	6/10	0.79	0.15	37,38,39,41	0
3	SO4	A	1304	5/5	0.82	0.18	55,55,57,57	0
3	SO4	A	1308	5/5	0.82	0.11	82,82,82,82	0
3	SO4	A	1306	5/5	0.83	0.11	88,88,88,88	0
3	SO4	A	1305	5/5	0.84	0.13	66,67,67,68	0
4	PGE	A	1312	10/10	0.85	0.12	38,41,44,46	0
3	SO4	A	1303	5/5	0.86	0.12	64,64,65,65	0
3	SO4	A	1301	5/5	0.87	0.08	80,80,80,80	0
3	SO4	A	1311	5/5	0.88	0.23	54,55,56,56	0
3	SO4	A	1309	5/5	0.90	0.11	54,54,55,55	0
3	SO4	A	1302	5/5	0.92	0.16	46,48,48,48	0
3	SO4	A	1307	5/5	0.94	0.11	44,44,45,45	0
3	SO4	A	1310	5/5	0.95	0.11	44,45,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.