



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2023 – 11:08 PM EDT

PDB ID : 2E7Y
Title : High resolution structure of *T. maritima* tRNase Z
Authors : Ishii, R.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2007-01-15
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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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

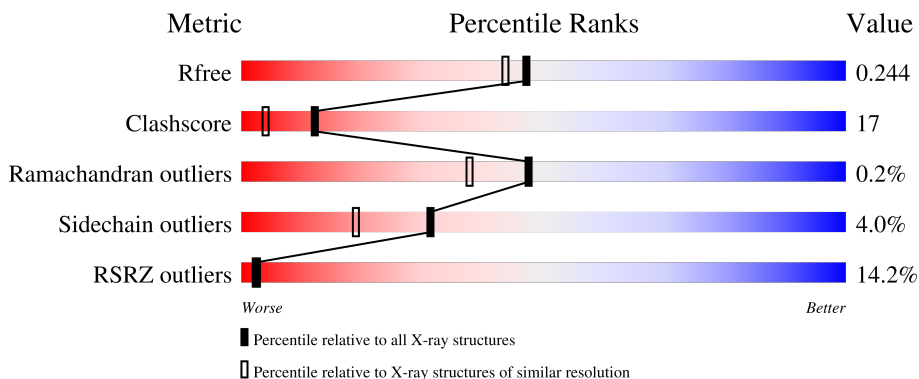
1 Overall quality at a glance

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}	130704	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (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 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	280	
1	B	280	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4820 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.

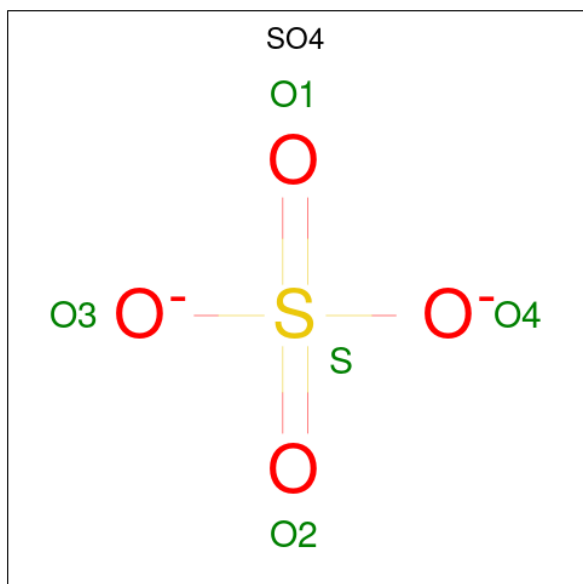
- Molecule 1 is a protein called tRNase Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	272	Total 2234	C 1440	N 386	O 401	S 7	0	0	0
1	B	269	Total 2227	C 1437	N 387	O 397	S 6	0	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

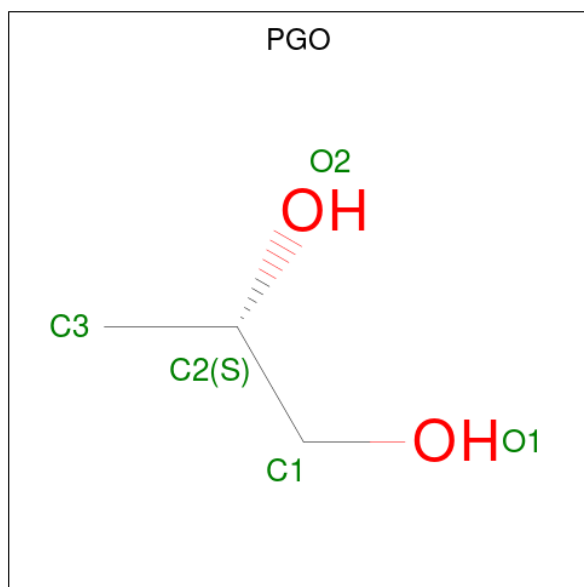
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total 2	Zn 2	0	0
2	B	2	Total 2	Zn 2	0	0

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



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

- Molecule 4 is S-1,2-PROPANEDIOL (three-letter code: PGO) (formula: C₃H₈O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 5 3 2	0	0
4	A	1	Total C O 5 3 2	0	0
4	B	1	Total C O 5 3 2	0	0
4	B	1	Total C O 5 3 2	0	0

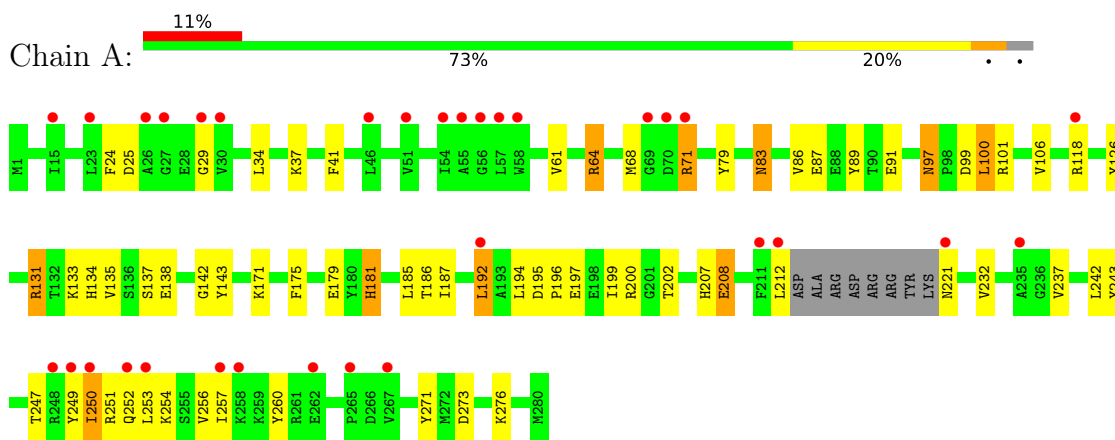
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	195	Total O 195 195	0	0
5	B	130	Total O 130 130	0	0

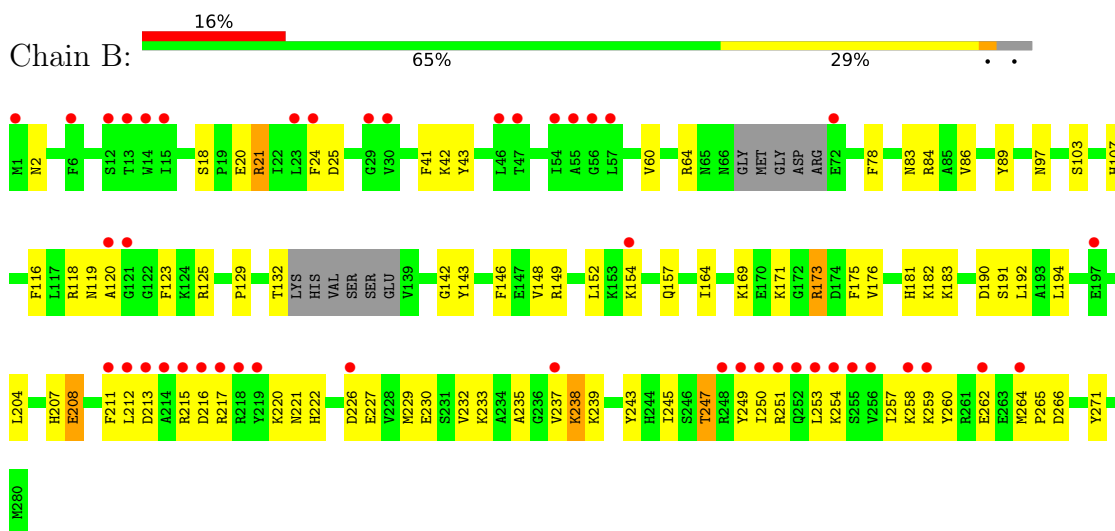
3 Residue-property plots [i](#)

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 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: tRNase Z



- Molecule 1: tRNase Z



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	150.30Å 172.69Å 64.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.44 – 1.97 37.44 – 1.97	Depositor EDS
% Data completeness (in resolution range)	97.4 (37.44-1.97) 97.5 (37.44-1.97)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 1.97Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.204 , 0.249 0.202 , 0.244	Depositor DCC
R_{free} test set	2950 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtrriage
Anisotropy	0.218	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 68.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4820	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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: SO4, PGO, ZN

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	0/2286	0.74	2/3072 (0.1%)
1	B	0.45	0/2278	0.73	2/3060 (0.1%)
All	All	0.47	0/4564	0.73	4/6132 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	142	GLY	N-CA-C	-6.33	97.28	113.10
1	B	142	GLY	N-CA-C	-6.07	97.93	113.10
1	B	216	ASP	CB-CG-OD2	5.70	123.43	118.30
1	A	64	ARG	NE-CZ-NH2	-5.02	117.79	120.30

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	2234	0	2239	65	0
1	B	2227	0	2235	87	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	10	0	16	5	0
4	B	10	0	16	2	0
5	A	195	0	0	4	1
5	B	130	0	0	7	0
All	All	4820	0	4506	154	1

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 17.

All (154) 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:135:VAL:HG13	1:A:137:SER:H	1.36	0.90
1:B:103:SER:HB2	5:B:2357:HOH:O	1.71	0.88
1:B:217:ARG:HH11	1:B:220:LYS:HG2	1.37	0.88
1:B:217:ARG:HD3	1:B:220:LYS:HA	1.55	0.86
1:B:42:LYS:HE3	1:B:118:ARG:HD3	1.58	0.85
1:B:266:ASP:HB2	5:B:2388:HOH:O	1.78	0.84
1:B:212:LEU:HD12	1:B:249:TYR:HB3	1.60	0.82
1:A:194:LEU:H	1:A:207:HIS:HE1	1.28	0.82
1:B:116:PHE:O	5:B:2375:HOH:O	1.99	0.80
1:B:118:ARG:HG3	1:B:119:ASN:H	1.47	0.79
1:B:84:ARG:NH1	1:B:84:ARG:HB3	1.98	0.78
1:A:253:LEU:O	1:A:257:ILE:HG12	1.84	0.78
1:B:232:VAL:HG13	1:B:237:VAL:HB	1.65	0.78
1:B:245:ILE:HG21	1:B:253:LEU:HD21	1.67	0.76
1:B:169:LYS:HB2	5:B:2343:HOH:O	1.86	0.75
1:A:185:LEU:HD21	1:A:187:ILE:HG23	1.67	0.75
1:B:173:ARG:CB	1:B:173:ARG:HH11	1.99	0.74
1:A:247:THR:O	1:A:250:ILE:HG13	1.89	0.73
1:A:250:ILE:CD1	1:A:251:ARG:H	2.02	0.72
1:B:41:PHE:O	1:B:64:ARG:NH2	2.23	0.72
1:B:119:ASN:CG	1:B:120:ALA:H	1.94	0.71
1:A:131:ARG:HG3	1:A:131:ARG:HH11	1.55	0.70
1:B:247:THR:O	1:B:250:ILE:HB	1.92	0.70
1:A:194:LEU:H	1:A:207:HIS:CE1	2.10	0.69
1:B:217:ARG:NH1	1:B:220:LYS:HG2	2.08	0.69
1:A:232:VAL:HG13	1:A:237:VAL:HB	1.74	0.69
1:A:254:LYS:HE2	1:A:271:TYR:OH	1.93	0.68
1:A:249:TYR:HB3	1:A:253:LEU:HD23	1.75	0.68
1:A:71:ARG:HD2	1:A:71:ARG:H	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:VAL:HG12	1:A:100:LEU:HG	1.77	0.67
1:A:29:GLY:HA3	4:A:601:PGO:H11	1.78	0.66
1:B:194:LEU:H	1:B:207:HIS:HE1	1.42	0.66
1:A:41:PHE:O	1:A:64:ARG:NH2	2.29	0.66
1:B:173:ARG:HH11	1:B:173:ARG:HB2	1.59	0.66
1:B:212:LEU:HB2	1:B:249:TYR:CD2	2.31	0.65
1:B:132:THR:HB	1:B:191:SER:HB3	1.78	0.65
1:A:126:TYR:OH	1:A:181:HIS:HD2	1.80	0.64
1:A:29:GLY:HA3	4:A:601:PGO:C1	2.29	0.62
1:A:171:LYS:HD3	1:A:175:PHE:CE2	2.35	0.62
1:B:83:ASN:HD22	1:B:86:VAL:H	1.47	0.62
4:A:604:PGO:H12	5:A:1354:HOH:O	2.00	0.61
1:B:118:ARG:HG3	1:B:119:ASN:N	2.15	0.61
1:A:250:ILE:HD12	1:A:251:ARG:H	1.64	0.61
1:A:143:TYR:HD1	1:A:187:ILE:HD11	1.66	0.61
1:A:135:VAL:HG13	1:A:137:SER:N	2.13	0.60
1:A:179:GLU:H	4:A:604:PGO:H31	1.64	0.60
1:A:212:LEU:HD23	1:A:253:LEU:HD22	1.81	0.60
1:A:252:GLN:O	1:A:256:VAL:HG23	2.00	0.60
1:A:79:TYR:CE2	1:A:106:VAL:HG12	2.37	0.60
1:B:118:ARG:O	1:B:119:ASN:HB3	2.01	0.60
1:A:118:ARG:HG3	5:A:1432:HOH:O	2.01	0.60
1:B:42:LYS:CE	1:B:118:ARG:HD3	2.29	0.60
1:B:119:ASN:ND2	1:B:120:ALA:H	2.00	0.59
1:A:197:GLU:OE2	1:A:200:ARG:NH1	2.34	0.59
1:B:84:ARG:HB3	1:B:84:ARG:HH11	1.67	0.59
1:A:185:LEU:HD23	1:A:186:THR:N	2.18	0.58
1:B:149:ARG:NH1	1:B:182:LYS:HG2	2.18	0.58
1:A:87:GLU:O	1:A:91:GLU:HG3	2.03	0.58
1:A:131:ARG:HG3	1:A:131:ARG:NH1	2.18	0.58
1:A:249:TYR:O	1:A:253:LEU:HD23	2.03	0.58
1:A:250:ILE:HD13	1:A:251:ARG:HG3	1.84	0.58
1:B:207:HIS:HD2	1:B:208:GLU:O	1.87	0.57
1:A:135:VAL:C	1:A:137:SER:H	2.07	0.56
1:A:79:TYR:HE2	1:A:106:VAL:HG12	1.69	0.56
1:A:187:ILE:HG13	1:A:187:ILE:O	2.06	0.56
1:B:254:LYS:O	1:B:258:LYS:HG2	2.06	0.56
1:A:249:TYR:HB3	1:A:253:LEU:CD2	2.36	0.55
1:B:116:PHE:HB3	1:B:123:PHE:HD2	1.72	0.55
1:A:194:LEU:HG	1:A:207:HIS:CE1	2.42	0.55
1:A:68:MET:O	1:A:71:ARG:HG2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:254:LYS:HG3	1:B:258:LYS:HE2	1.88	0.54
1:B:238:LYS:HG2	1:B:239:LYS:N	2.23	0.54
1:B:20:GLU:OE1	1:B:125:ARG:HD3	2.08	0.54
1:B:43:TYR:OH	1:B:118:ARG:HG2	2.08	0.53
1:B:249:TYR:O	1:B:253:LEU:HG	2.09	0.53
1:B:259:LYS:O	1:B:262:GLU:HB3	2.09	0.53
1:B:148:VAL:HG22	1:B:181:HIS:CD2	2.44	0.52
1:B:211:PHE:HE1	1:B:222:HIS:HB2	1.73	0.52
1:A:212:LEU:HB2	1:A:253:LEU:HD21	1.91	0.52
1:B:212:LEU:CD1	1:B:249:TYR:HB3	2.38	0.52
1:A:99:ASP:HB2	5:A:1325:HOH:O	2.10	0.52
1:A:83:ASN:HD22	1:A:86:VAL:H	1.58	0.52
1:A:71:ARG:HD2	1:A:71:ARG:N	2.25	0.51
1:B:119:ASN:ND2	1:B:120:ALA:N	2.58	0.51
1:B:119:ASN:CG	1:B:120:ALA:N	2.64	0.51
1:B:125:ARG:HA	1:B:146:PHE:O	2.10	0.51
1:B:217:ARG:NH2	1:B:227:GLU:OE1	2.44	0.51
1:A:185:LEU:CD2	1:A:187:ILE:HG23	2.37	0.50
1:A:133:LYS:O	1:A:192:LEU:HD13	2.10	0.50
1:A:135:VAL:C	1:A:137:SER:N	2.64	0.50
4:A:601:PGO:H33	4:B:602:PGO:H2	1.94	0.50
1:B:171:LYS:HG2	1:B:175:PHE:CD2	2.47	0.50
1:B:250:ILE:HG23	1:B:251:ARG:N	2.27	0.49
1:A:194:LEU:N	1:A:207:HIS:HE1	2.05	0.49
1:B:154:LYS:O	1:B:157:GLN:HG3	2.12	0.49
1:B:173:ARG:CB	1:B:173:ARG:NH1	2.72	0.49
1:B:190:ASP:O	1:B:191:SER:HB3	2.14	0.48
1:A:207:HIS:HD2	1:A:208:GLU:O	1.96	0.48
1:A:195:ASP:OD2	1:A:196:PRO:HD2	2.14	0.47
1:A:185:LEU:HD23	1:A:185:LEU:C	2.35	0.47
1:B:2:ASN:HA	1:B:18:SER:OG	2.13	0.47
1:B:84:ARG:HB3	1:B:84:ARG:CZ	2.44	0.47
1:B:217:ARG:HH22	1:B:227:GLU:CD	2.17	0.47
1:B:192:LEU:HD21	1:B:220:LYS:C	2.35	0.47
1:A:89:TYR:OH	5:A:1363:HOH:O	2.09	0.46
1:B:132:THR:HB	1:B:191:SER:CB	2.44	0.46
1:B:250:ILE:CG2	1:B:251:ARG:N	2.78	0.45
1:B:129:PRO:HB3	1:B:143:TYR:CE2	2.51	0.45
1:A:143:TYR:CD1	1:A:187:ILE:HD11	2.48	0.45
1:A:256:VAL:HG12	1:A:260:TYR:CD1	2.52	0.45
1:B:78:PHE:CD2	1:B:107:HIS:HB2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:TYR:OH	5:B:2306:HOH:O	2.06	0.45
1:B:194:LEU:H	1:B:207:HIS:CE1	2.29	0.45
1:B:213:ASP:OD1	1:B:215:ARG:HB2	2.16	0.44
1:B:230:GLU:O	1:B:233:LYS:HB3	2.17	0.44
1:A:71:ARG:HH11	1:A:71:ARG:HG3	1.82	0.44
1:A:134:HIS:O	1:A:221:ASN:N	2.51	0.44
1:B:146:PHE:CE2	1:B:183:LYS:HG3	2.52	0.44
1:B:154:LYS:HA	1:B:157:GLN:OE1	2.16	0.44
1:A:250:ILE:HD13	1:A:251:ARG:H	1.77	0.44
1:B:262:GLU:O	1:B:265:PRO:HG3	2.17	0.44
1:B:60:VAL:O	1:B:64:ARG:HG3	2.18	0.44
1:A:199:ILE:O	1:A:202:THR:HG22	2.18	0.44
1:A:273:ASP:HB3	1:A:276:LYS:HG2	1.99	0.43
1:B:229:MET:HG3	1:B:260:TYR:CD2	2.53	0.43
1:B:24:PHE:O	1:B:25:ASP:HB2	2.17	0.43
1:B:97:ASN:ND2	5:B:2328:HOH:O	2.51	0.43
1:B:152:LEU:HD23	1:B:157:GLN:HA	1.99	0.43
1:B:217:ARG:NH2	1:B:227:GLU:OE2	2.47	0.43
1:A:212:LEU:C	1:A:212:LEU:HD13	2.38	0.43
1:B:226:ASP:OD2	1:B:227:GLU:N	2.51	0.43
1:B:254:LYS:NZ	4:B:603:PGO:H31	2.32	0.43
1:B:257:ILE:HD13	1:B:271:TYR:CD2	2.54	0.43
1:B:212:LEU:HD23	1:B:212:LEU:HA	1.84	0.43
1:B:226:ASP:HB3	1:B:260:TYR:OH	2.19	0.43
1:B:233:LYS:O	1:B:235:ALA:O	2.37	0.43
1:B:21:ARG:HB2	1:B:42:LYS:HD3	2.00	0.43
1:B:251:ARG:C	1:B:253:LEU:N	2.71	0.42
1:B:262:GLU:O	1:B:265:PRO:HD3	2.19	0.42
1:B:227:GLU:O	1:B:230:GLU:HB3	2.19	0.42
1:A:135:VAL:O	1:A:135:VAL:HG22	2.20	0.42
1:A:24:PHE:O	1:A:25:ASP:HB2	2.20	0.42
1:B:191:SER:HB2	5:B:2415:HOH:O	2.19	0.41
1:A:135:VAL:CG1	1:A:138:GLU:H	2.34	0.41
1:A:192:LEU:N	1:A:192:LEU:CD1	2.83	0.41
1:B:164:ILE:HD11	1:B:176:VAL:HG11	2.02	0.41
1:A:37:LYS:HE3	1:A:37:LYS:HB2	1.84	0.41
1:B:173:ARG:NH1	1:B:173:ARG:HB3	2.36	0.41
1:B:264:MET:N	1:B:265:PRO:HD3	2.36	0.41
1:B:173:ARG:HH11	1:B:173:ARG:HB3	1.82	0.41
1:A:34:LEU:HD22	1:A:37:LYS:HD2	2.02	0.40
1:A:97:ASN:HB2	1:A:100:LEU:HD22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:233:LYS:HB2	1:B:233:LYS:HE3	1.88	0.40
1:B:84:ARG:CZ	1:B:84:ARG:CB	3.00	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:1484:HOH:O	5:A:1484:HOH:O[3_655]	2.19	0.01

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	268/280 (96%)	254 (95%)	14 (5%)	0	100	100
1	B	263/280 (94%)	244 (93%)	18 (7%)	1 (0%)	34	22
All	All	531/560 (95%)	498 (94%)	32 (6%)	1 (0%)	47	38

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	238	LYS

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	241/248 (97%)	229 (95%)	12 (5%)	24	12
1	B	239/248 (96%)	232 (97%)	7 (3%)	42	31
All	All	480/496 (97%)	461 (96%)	19 (4%)	31	19

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	ARG
1	A	83	ASN
1	A	97	ASN
1	A	100	LEU
1	A	101	ARG
1	A	131	ARG
1	A	181	HIS
1	A	192	LEU
1	A	208	GLU
1	A	242	LEU
1	A	243	TYR
1	A	250	ILE
1	B	21	ARG
1	B	173	ARG
1	B	204	LEU
1	B	208	GLU
1	B	221	ASN
1	B	243	TYR
1	B	247	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	ASN
1	A	83	ASN
1	A	119	ASN
1	A	134	HIS
1	A	181	HIS
1	A	207	HIS
1	B	83	ASN
1	B	97	ASN
1	B	119	ASN
1	B	207	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 for Mogul analysis.

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	$\# Z > 2$
4	PGO	B	603	-	3,4,4	0.35	0	1,4,4	0.02	0
4	PGO	A	604	-	3,4,4	0.35	0	1,4,4	0.13	0
3	SO4	A	501	-	4,4,4	0.21	0	6,6,6	0.19	0
3	SO4	A	502	-	4,4,4	0.25	0	6,6,6	0.11	0
4	PGO	A	601	-	3,4,4	0.22	0	1,4,4	0.22	0
4	PGO	B	602	-	3,4,4	0.27	0	1,4,4	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
4	PGO	B	603	-	-	0/2/2/2	-
4	PGO	A	604	-	-	0/2/2/2	-
4	PGO	A	601	-	-	0/2/2/2	-
4	PGO	B	602	-	-	0/2/2/2	-

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.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	603	PGO	1	0
4	A	604	PGO	2	0
4	A	601	PGO	3	0
4	B	602	PGO	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

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	272/280 (97%)	0.54	32 (11%) 4 5	22, 39, 84, 110	0
1	B	269/280 (96%)	0.94	45 (16%) 1 1	24, 50, 98, 125	0
All	All	541/560 (96%)	0.74	77 (14%) 2 2	22, 45, 91, 125	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	250	ILE	9.9
1	B	120	ALA	8.7
1	B	249	TYR	7.4
1	B	216	ASP	7.4
1	B	215	ARG	5.6
1	B	212	LEU	5.5
1	A	253	LEU	5.4
1	A	69	GLY	5.4
1	A	249	TYR	5.2
1	B	218	ARG	5.0
1	B	256	VAL	4.6
1	B	211	PHE	4.5
1	B	253	LEU	4.4
1	B	1	MET	4.2
1	B	252	GLN	4.2
1	B	214	ALA	4.1
1	B	213	ASP	3.9
1	A	55	ALA	3.9
1	A	248	ARG	3.7
1	B	197	GLU	3.5
1	A	250	ILE	3.4
1	A	211	PHE	3.4
1	A	70	ASP	3.4
1	A	57	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	252	GLN	3.3
1	B	15	ILE	3.2
1	B	251	ARG	3.1
1	B	54	ILE	3.1
1	B	219	TYR	3.1
1	B	259	LYS	3.0
1	A	71	ARG	3.0
1	A	30	VAL	3.0
1	A	212	LEU	2.9
1	B	57	LEU	2.9
1	B	255	SER	2.9
1	A	262	GLU	2.9
1	A	54	ILE	2.9
1	B	237	VAL	2.9
1	B	56	GLY	2.8
1	A	51	VAL	2.8
1	A	23	LEU	2.8
1	B	55	ALA	2.7
1	A	56	GLY	2.7
1	A	29	GLY	2.6
1	B	29	GLY	2.6
1	B	30	VAL	2.6
1	B	254	LYS	2.6
1	B	72	GLU	2.6
1	B	24	PHE	2.6
1	B	248	ARG	2.6
1	A	26	ALA	2.6
1	A	267	VAL	2.6
1	B	154	LYS	2.5
1	A	235	ALA	2.4
1	A	46	LEU	2.4
1	B	46	LEU	2.4
1	B	13	THR	2.4
1	B	14	TRP	2.4
1	A	192	LEU	2.4
1	A	258	LYS	2.4
1	A	265	PRO	2.4
1	B	258	LYS	2.4
1	B	12	SER	2.3
1	A	257	ILE	2.3
1	B	121	GLY	2.3
1	B	6	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	221	ASN	2.2
1	B	264	MET	2.2
1	B	23	LEU	2.2
1	B	217	ARG	2.2
1	A	118	ARG	2.1
1	B	226	ASP	2.1
1	A	27	GLY	2.1
1	A	58	TRP	2.1
1	B	262	GLU	2.1
1	A	15	ILE	2.1
1	B	47	THR	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
3	SO4	A	502	5/5	0.86	0.21	96,99,114,122	0
4	PGO	A	604	5/5	0.86	0.17	36,47,88,93	0
4	PGO	B	603	5/5	0.87	0.10	62,77,80,88	0
4	PGO	A	601	5/5	0.92	0.40	38,59,79,83	0
4	PGO	B	602	5/5	0.96	0.38	42,45,58,91	0
3	SO4	A	501	5/5	0.96	0.11	59,59,67,85	0
2	ZN	A	1301	1/1	0.99	0.07	43,43,43,43	0
2	ZN	A	1302	1/1	0.99	0.07	64,64,64,64	0
2	ZN	B	2302	1/1	0.99	0.03	72,72,72,72	0
2	ZN	B	2301	1/1	1.00	0.06	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.