



Full wwPDB X-ray Structure Validation Report ⓘ

May 7, 2026 – 08:40 AM EDT

PDB ID : 5LZR / pdb_00005lzh
Title : Crystal structure of Thermotoga maritima sodium pumping membrane integral pyrophosphatase in complex with tungstate and magnesium
Authors : Wilkinson, C.; Kellosalo, J.; Kajander, T.; Goldman, A.
Deposited on : 2016-10-01
Resolution : 4.00 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

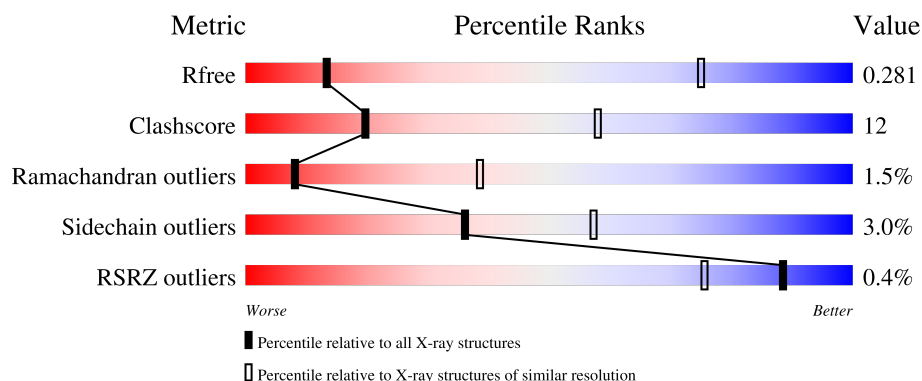
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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	1082 (4.20-3.80)
Clashscore	190562	1129 (4.20-3.80)
Ramachandran outliers	187476	1064 (4.20-3.80)
Sidechain outliers	187428	1055 (4.20-3.80)
RSRZ outliers	180081	1082 (4.20-3.80)

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	735	
1	B	735	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9796 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.

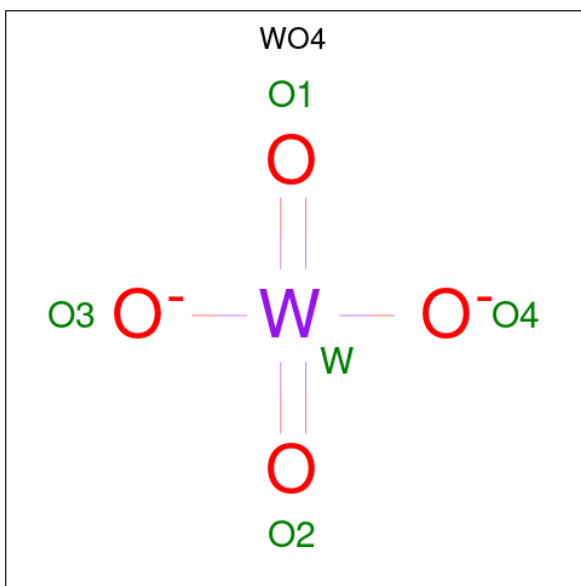
- Molecule 1 is a protein called K(+)-stimulated pyrophosphate-energized sodium pump.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	690	Total	C	N	O	S	0	0	0
			4859	3183	758	892	26			
1	B	697	Total	C	N	O	S	0	0	0
			4923	3219	771	907	26			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	initiating methionine	UNP Q9S5X0
A	-7	ARG	-	expression tag	UNP Q9S5X0
A	-6	GLY	-	expression tag	UNP Q9S5X0
A	-5	SER	-	expression tag	UNP Q9S5X0
A	-4	HIS	-	expression tag	UNP Q9S5X0
A	-3	HIS	-	expression tag	UNP Q9S5X0
A	-2	HIS	-	expression tag	UNP Q9S5X0
A	-1	HIS	-	expression tag	UNP Q9S5X0
A	0	HIS	-	expression tag	UNP Q9S5X0
A	1	HIS	-	expression tag	UNP Q9S5X0
A	353	LEU	VAL	engineered mutation	UNP Q9S5X0
A	395	GLY	SER	engineered mutation	UNP Q9S5X0
B	-8	MET	-	initiating methionine	UNP Q9S5X0
B	-7	ARG	-	expression tag	UNP Q9S5X0
B	-6	GLY	-	expression tag	UNP Q9S5X0
B	-5	SER	-	expression tag	UNP Q9S5X0
B	-4	HIS	-	expression tag	UNP Q9S5X0
B	-3	HIS	-	expression tag	UNP Q9S5X0
B	-2	HIS	-	expression tag	UNP Q9S5X0
B	-1	HIS	-	expression tag	UNP Q9S5X0
B	0	HIS	-	expression tag	UNP Q9S5X0
B	1	HIS	-	expression tag	UNP Q9S5X0
B	353	LEU	VAL	engineered mutation	UNP Q9S5X0
B	395	GLY	SER	engineered mutation	UNP Q9S5X0

- Molecule 2 is TUNGSTATE(VI)ION (CCD ID: WO4) (formula: O_4W).



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

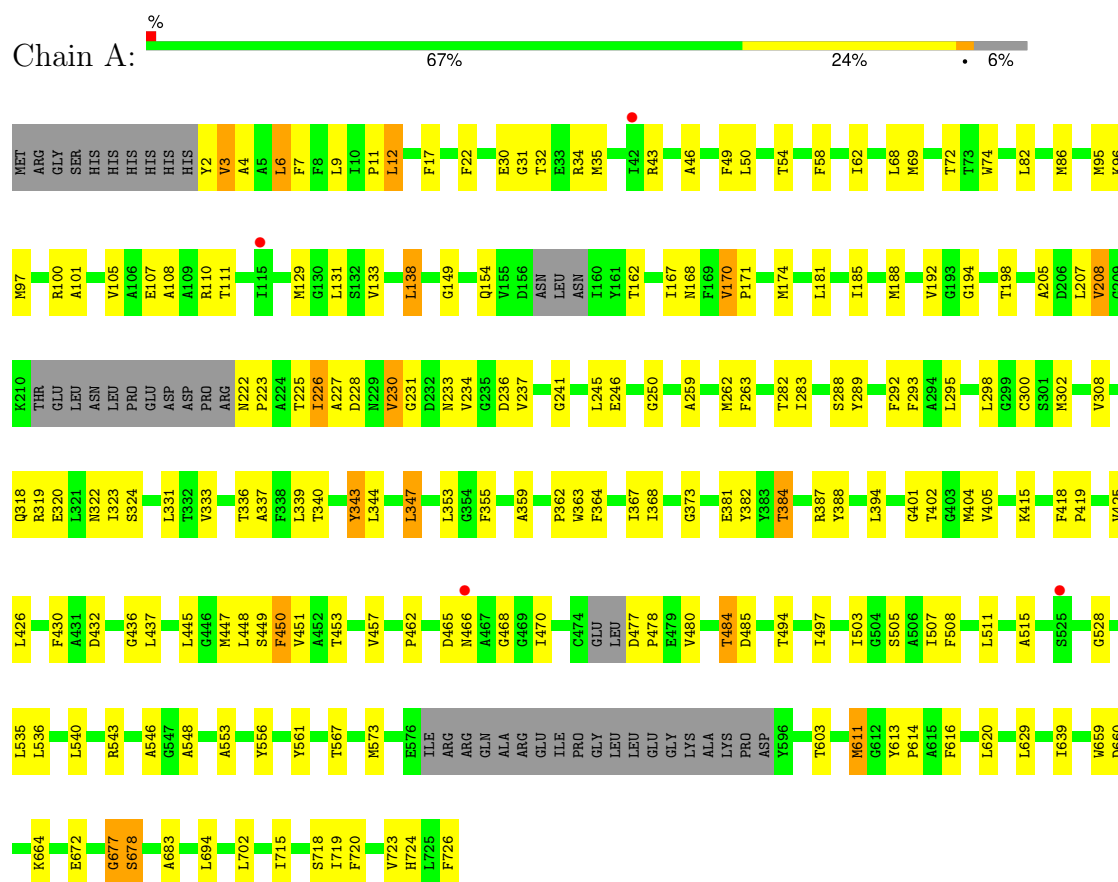
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		
3	B	2	Total	Mg	0	0
			2	2		

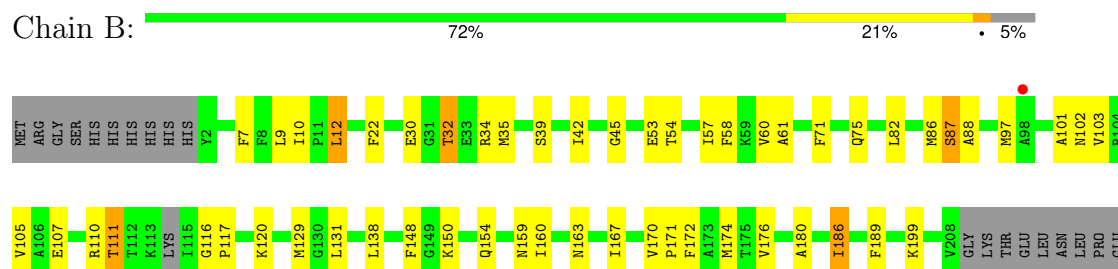
3 Residue-property plots

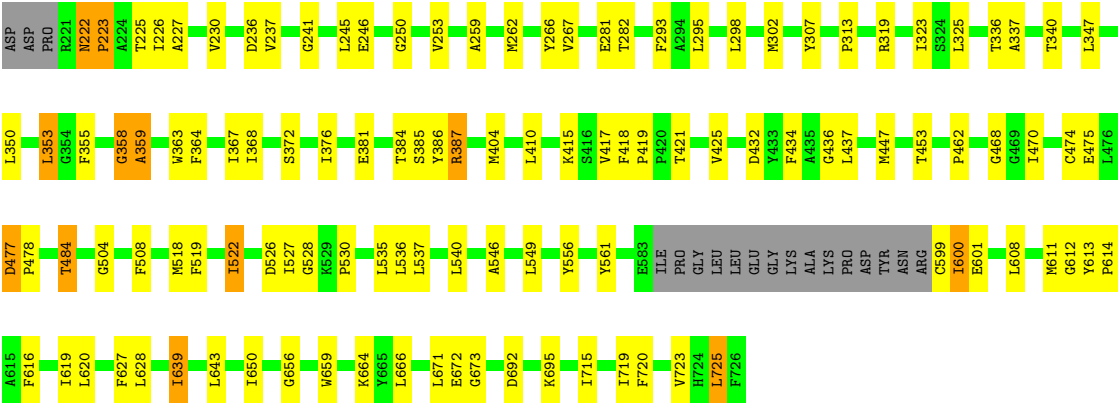
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: K(+)-stimulated pyrophosphate-energized sodium pump



- Molecule 1: K(+)-stimulated pyrophosphate-energized sodium pump





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.72Å 108.87Å 105.81Å 90.00° 108.79° 90.00°	Depositor
Resolution (Å)	28.46 – 4.00 28.46 – 4.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (28.46-4.00) 99.3 (28.46-4.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 3.98Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.232 , 0.279 0.237 , 0.281	Depositor DCC
R_{free} test set	1513 reflections (9.92%)	wwPDB-VP
Wilson B-factor (Å ²)	145.7	Xtriage
Anisotropy	0.569	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 81.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9796	wwPDB-VP
Average B, all atoms (Å ²)	134.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: WO4, MG

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	0.40	0/4960	1.04	11/6774 (0.2%)
1	B	0.40	0/5023	1.05	12/6858 (0.2%)
All	All	0.40	0/9983	1.04	23/13632 (0.2%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	611	MET	N-CA-C	-10.06	99.85	112.72
1	B	105	VAL	N-CA-C	-8.38	103.11	110.74
1	B	387	ARG	N-CA-C	-8.09	103.00	113.12
1	A	528	GLY	N-CA-C	-7.88	94.51	113.18
1	A	343	TYR	N-CA-C	-7.53	100.39	110.55
1	B	528	GLY	N-CA-C	-7.17	96.18	113.18
1	B	530	PRO	CA-C-N	6.83	126.34	119.24
1	B	530	PRO	C-N-CA	6.83	126.34	119.24
1	A	694	LEU	N-CA-C	6.67	118.34	111.14
1	A	677	GLY	N-CA-C	-6.28	101.77	111.12
1	A	230	VAL	N-CA-C	-6.11	104.55	110.72
1	B	222	ASN	CA-C-N	-6.02	112.32	119.84
1	B	222	ASN	C-N-CA	-6.02	112.32	119.84
1	B	526	ASP	N-CA-C	-5.99	106.02	113.38
1	A	170	VAL	CA-C-N	5.72	126.99	119.84
1	A	170	VAL	C-N-CA	5.72	126.99	119.84
1	A	222	ASN	CA-C-N	5.57	126.04	120.52
1	A	222	ASN	C-N-CA	5.57	126.04	120.52
1	B	170	VAL	CA-C-N	5.57	126.80	119.84
1	B	170	VAL	C-N-CA	5.57	126.80	119.84
1	B	101	ALA	N-CA-C	5.49	117.34	111.36
1	B	111	THR	N-CA-C	5.43	117.64	111.02

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	34	ARG	N-CA-C	5.06	116.80	111.28

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	4859	0	4699	123	0
1	B	4923	0	4783	115	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
All	All	9796	0	9482	222	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 12.

All (222) 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:75:GLN:HE21	1:B:148:PHE:HB3	1.35	0.89
1:A:536:LEU:HD11	1:B:536:LEU:HD11	1.53	0.88
1:A:540:LEU:HD23	1:B:535:LEU:HB2	1.70	0.72
1:A:223:PRO:HG2	1:A:225:THR:HG23	1.71	0.72
1:A:437:LEU:HD21	1:B:540:LEU:HG	1.71	0.72
1:A:535:LEU:HB3	1:B:540:LEU:HD23	1.72	0.71
1:A:613:TYR:HB3	1:A:614:PRO:HD3	1.72	0.69
1:A:318:GLN:O	1:A:322:ASN:ND2	2.26	0.68
1:B:237:VAL:HG23	1:B:462:PRO:HG2	1.77	0.66
1:B:107:GLU:OE2	1:B:111:THR:OG1	2.13	0.65
1:B:720:PHE:HA	1:B:723:VAL:HG12	1.78	0.65
1:B:180:ALA:HB2	1:B:253:VAL:HG21	1.78	0.64
1:A:337:ALA:HB2	1:A:363:TRP:CE2	2.32	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:MET:HE1	1:A:715:ILE:HG23	1.78	0.64
1:A:288:SER:HG	1:A:343:TYR:HH	1.41	0.64
1:B:45:GLY:HA2	1:B:600:ILE:HD13	1.80	0.64
1:B:75:GLN:OE1	1:B:154:GLN:NE2	2.32	0.63
1:B:223:PRO:HD2	1:B:225:THR:HG23	1.80	0.63
1:A:556:TYR:HH	1:B:556:TYR:HH	1.37	0.63
1:A:69:MET:HG2	1:A:74:TRP:HA	1.80	0.63
1:A:107:GLU:O	1:A:111:THR:N	2.28	0.62
1:A:720:PHE:HA	1:A:723:VAL:HG12	1.82	0.61
1:A:415:LYS:HE2	1:B:561:TYR:HA	1.83	0.61
1:B:337:ALA:HB2	1:B:363:TRP:CE2	2.35	0.61
1:B:176:VAL:HG12	1:B:253:VAL:HG22	1.82	0.61
1:B:612:GLY:O	1:B:616:PHE:N	2.33	0.60
1:A:336:THR:HA	1:A:339:LEU:HB3	1.83	0.60
1:A:616:PHE:HD1	1:A:620:LEU:HD12	1.65	0.60
1:B:262:MET:HE1	1:B:353:LEU:HG	1.83	0.60
1:B:656:GLY:HA3	1:B:695:LYS:HB3	1.84	0.60
1:B:417:VAL:HG22	1:B:650:ILE:HB	1.83	0.59
1:A:425:VAL:HG13	1:B:546:ALA:HB1	1.84	0.58
1:A:363:TRP:CZ2	1:A:367:ILE:HD11	2.38	0.58
1:B:87:SER:HB3	1:B:245:LEU:HD22	1.85	0.58
1:B:613:TYR:HB2	1:B:614:PRO:HD3	1.86	0.57
1:B:599:CYS:O	1:B:601:GLU:N	2.33	0.57
1:B:32:THR:HG22	1:B:34:ARG:H	1.69	0.57
1:B:39:SER:HB2	1:B:103:VAL:HG21	1.87	0.57
1:B:88:ALA:HA	1:B:186:ILE:HD13	1.87	0.56
1:B:363:TRP:CZ2	1:B:367:ILE:HD11	2.41	0.56
1:B:129:MET:HE3	1:B:241:GLY:HA3	1.87	0.56
1:A:336:THR:O	1:A:340:THR:N	2.33	0.56
1:A:289:TYR:OH	1:A:340:THR:OG1	2.20	0.56
1:B:474:CYS:O	1:B:475:GLU:HG2	2.06	0.56
1:A:540:LEU:HG	1:B:437:LEU:HD21	1.87	0.55
1:A:394:LEU:HD21	1:A:659:TRP:CD1	2.40	0.55
1:B:75:GLN:HE21	1:B:148:PHE:CB	2.14	0.55
1:A:31:GLY:O	1:A:35:MET:HB2	2.06	0.55
1:A:561:TYR:HA	1:B:415:LYS:HE2	1.88	0.55
1:A:225:THR:O	1:A:228:ASP:N	2.40	0.55
1:B:82:LEU:O	1:B:86:MET:HG2	2.07	0.55
1:A:68:LEU:O	1:A:72:THR:OG1	2.17	0.54
1:A:108:ALA:C	1:A:110:ARG:H	2.16	0.54
1:A:373:GLY:HA2	1:A:447:MET:HE3	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:336:THR:O	1:B:340:THR:N	2.37	0.54
1:B:174:MET:HE1	1:B:715:ILE:HG23	1.90	0.54
1:A:237:VAL:HG23	1:A:462:PRO:HG2	1.89	0.54
1:B:107:GLU:OE2	1:B:110:ARG:NH2	2.42	0.53
1:A:181:LEU:O	1:A:185:ILE:HG12	2.09	0.52
1:A:167:ILE:HD13	1:A:719:ILE:HG12	1.91	0.52
1:B:163:ASN:OD1	1:B:167:ILE:N	2.41	0.52
1:B:372:SER:HB2	1:B:447:MET:HE2	1.91	0.52
1:A:3:VAL:O	1:A:6:LEU:HG	2.10	0.52
1:B:432:ASP:OD1	1:B:436:GLY:HA2	2.10	0.51
1:B:150:LYS:HA	1:B:150:LYS:HE2	1.92	0.51
1:A:17:PHE:HB3	1:A:131:LEU:HD13	1.93	0.51
1:A:432:ASP:OD1	1:A:436:GLY:HA2	2.10	0.51
1:A:677:GLY:O	1:A:678:SER:OG	2.23	0.51
1:B:518:MET:SD	1:B:537:LEU:HG	2.51	0.51
1:B:71:PHE:O	1:B:163:ASN:ND2	2.44	0.51
1:B:418:PHE:HB3	1:B:419:PRO:HD3	1.94	0.50
1:A:333:VAL:O	1:A:363:TRP:NE1	2.42	0.50
1:A:263:PHE:HB2	1:A:283:ILE:HG13	1.94	0.50
1:B:22:PHE:HA	1:B:97:MET:HE1	1.93	0.50
1:B:692:ASP:OD1	1:B:695:LYS:NZ	2.41	0.50
1:A:515:ALA:HA	1:B:540:LEU:HD11	1.93	0.50
1:A:548:ALA:HB1	1:B:643:LEU:HD11	1.94	0.50
1:B:385:SER:C	1:B:387:ARG:H	2.20	0.50
1:A:226:ILE:O	1:A:230:VAL:HG13	2.13	0.49
1:A:450:PHE:O	1:A:453:THR:HG22	2.11	0.49
1:B:364:PHE:O	1:B:368:ILE:HG12	2.13	0.49
1:A:477:ASP:HB2	1:A:480:VAL:HB	1.94	0.49
1:A:511:LEU:HD11	1:B:549:LEU:HD11	1.95	0.49
1:A:300:CYS:SG	1:A:331:LEU:HB3	2.52	0.49
1:A:466:ASN:O	1:A:470:ILE:N	2.34	0.49
1:A:82:LEU:O	1:A:86:MET:HG2	2.12	0.49
1:B:293:PHE:CE2	1:B:336:THR:HG21	2.48	0.49
1:B:60:VAL:HG21	1:B:189:PHE:HZ	1.78	0.48
1:B:222:ASN:ND2	1:B:222:ASN:O	2.46	0.48
1:A:724:HIS:ND1	1:A:726:PHE:O	2.47	0.48
1:A:702:LEU:HD23	1:A:702:LEU:HA	1.76	0.47
1:A:418:PHE:HB3	1:A:419:PRO:HD3	1.97	0.47
1:B:57:ILE:HG13	1:B:58:PHE:N	2.28	0.47
1:B:319:ARG:O	1:B:323:ILE:HG13	2.15	0.47
1:A:611:MET:O	1:A:614:PRO:HD2	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:GLU:HG2	1:B:282:THR:N	2.30	0.47
1:A:7:PHE:HB3	1:A:295:LEU:HD13	1.97	0.47
1:A:567:THR:HB	1:B:404:MET:HE1	1.96	0.47
1:A:426:LEU:O	1:A:430:PHE:HD2	1.96	0.47
1:B:120:LYS:HE2	1:B:313:PRO:HG3	1.97	0.47
1:A:138:LEU:HD12	1:A:138:LEU:HA	1.76	0.46
1:A:573:MET:HB2	1:A:603:THR:HG21	1.97	0.46
1:B:7:PHE:HA	1:B:10:ILE:HD13	1.98	0.46
1:A:298:LEU:O	1:A:302:MET:HG3	2.16	0.46
1:A:95:MET:HE1	1:A:234:VAL:HG22	1.98	0.46
1:A:445:LEU:O	1:A:449:SER:N	2.48	0.46
1:B:87:SER:HB2	1:B:186:ILE:HG12	1.97	0.46
1:B:639:ILE:HD13	1:B:639:ILE:HA	1.84	0.46
1:A:46:ALA:HB1	1:A:95:MET:HE3	1.97	0.46
1:B:172:PHE:O	1:B:176:VAL:HG23	2.16	0.46
1:A:448:LEU:O	1:A:451:VAL:HB	2.16	0.46
1:B:9:LEU:HA	1:B:12:LEU:HD22	1.98	0.46
1:A:450:PHE:HB2	1:A:453:THR:HG22	1.98	0.45
1:B:664:LYS:HA	1:B:664:LYS:HD2	1.60	0.45
1:A:308:VAL:HG13	1:A:320:GLU:HG3	1.98	0.45
1:A:381:GLU:HA	1:A:384:THR:HG22	1.98	0.45
1:B:163:ASN:ND2	1:B:167:ILE:HB	2.31	0.45
1:B:719:ILE:HG22	1:B:723:VAL:HG11	1.98	0.45
1:A:58:PHE:CE2	1:A:62:ILE:HD11	2.51	0.45
1:A:129:MET:HE3	1:A:241:GLY:HA3	1.99	0.45
1:A:494:THR:HA	1:A:497:ILE:HG22	1.99	0.45
1:A:236:ASP:HB2	1:A:462:PRO:HG3	1.98	0.45
1:B:42:ILE:HD11	1:B:102:ASN:HD21	1.82	0.45
1:B:267:VAL:HG21	1:B:527:ILE:HG23	1.98	0.45
1:B:368:ILE:O	1:B:372:SER:OG	2.28	0.45
1:B:246:GLU:O	1:B:250:GLY:N	2.37	0.45
1:B:376:ILE:HG21	1:B:504:GLY:HA3	1.98	0.44
1:A:192:VAL:HG11	1:A:614:PRO:HB2	1.98	0.44
1:A:639:ILE:HD13	1:A:639:ILE:HA	1.88	0.44
1:A:660:ASP:O	1:A:664:LYS:HG2	2.17	0.44
1:B:174:MET:HE1	1:B:715:ILE:HG12	1.99	0.44
1:A:170:VAL:HA	1:A:171:PRO:HD2	1.80	0.44
1:A:308:VAL:HG21	1:A:324:SER:HB3	1.99	0.44
1:B:30:GLU:N	1:B:30:GLU:OE1	2.51	0.44
1:B:199:LYS:HD3	1:B:199:LYS:HA	1.55	0.44
1:A:30:GLU:OE1	1:A:30:GLU:N	2.48	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:259:ALA:O	1:B:262:MET:HB2	2.17	0.44
1:B:103:VAL:HG22	1:B:470:ILE:HD13	1.98	0.44
1:A:319:ARG:O	1:A:323:ILE:HG13	2.17	0.44
1:A:404:MET:HE2	1:A:404:MET:HB2	1.86	0.44
1:A:292:PHE:HA	1:A:295:LEU:HD12	2.00	0.43
1:B:358:GLY:O	1:B:359:ALA:HB3	2.17	0.43
1:A:227:ALA:O	1:A:230:VAL:HG22	2.18	0.43
1:A:401:GLY:O	1:A:405:VAL:HG23	2.17	0.43
1:B:364:PHE:HB3	1:B:434:PHE:CD2	2.54	0.43
1:B:627:PHE:O	1:B:725:LEU:N	2.50	0.43
1:A:2:TYR:CZ	1:A:4:ALA:HB2	2.54	0.43
1:A:347:LEU:HA	1:A:347:LEU:HD23	1.80	0.43
1:B:154:GLN:NE2	1:B:171:PRO:HB3	2.33	0.43
1:A:246:GLU:O	1:A:250:GLY:N	2.42	0.43
1:A:355:PHE:CE2	1:A:362:PRO:HD3	2.54	0.43
1:A:613:TYR:HB3	1:A:614:PRO:CD	2.46	0.43
1:A:262:MET:HE2	1:A:262:MET:HB3	1.88	0.43
1:A:382:TYR:HA	1:A:388:TYR:HD2	1.84	0.43
1:B:57:ILE:O	1:B:61:ALA:N	2.39	0.43
1:B:417:VAL:HA	1:B:650:ILE:HG21	2.01	0.43
1:A:9:LEU:O	1:A:12:LEU:HB2	2.19	0.43
1:A:11:PRO:HG3	1:A:138:LEU:HB3	2.00	0.43
1:B:226:ILE:O	1:B:230:VAL:HG13	2.19	0.42
1:B:325:LEU:HD23	1:B:453:THR:HG23	2.01	0.42
1:B:540:LEU:HD12	1:B:540:LEU:HA	1.70	0.42
1:A:108:ALA:C	1:A:110:ARG:N	2.76	0.42
1:A:402:THR:HA	1:A:683:ALA:HB1	2.01	0.42
1:A:546:ALA:HB1	1:B:425:VAL:HG13	2.00	0.42
1:A:198:THR:HG22	1:A:231:GLY:HA2	2.00	0.42
1:B:159:ASN:CG	1:B:160:ILE:H	2.26	0.42
1:B:611:MET:HE2	1:B:611:MET:HB3	1.86	0.42
1:B:628:LEU:HD23	1:B:628:LEU:HA	1.84	0.42
1:A:96:LYS:HD2	1:A:100:ARG:HH12	1.85	0.42
1:A:293:PHE:CD1	1:A:293:PHE:C	2.98	0.42
1:A:457:VAL:HG12	1:A:494:THR:HB	2.01	0.42
1:B:298:LEU:O	1:B:302:MET:HG3	2.19	0.42
1:B:75:GLN:HG3	1:B:148:PHE:CD1	2.54	0.42
1:B:116:GLY:N	1:B:117:PRO:HD2	2.35	0.42
1:B:138:LEU:HD13	1:B:295:LEU:HD23	2.01	0.42
1:B:468:GLY:HA2	1:B:484:THR:HG23	2.02	0.42
1:B:519:PHE:O	1:B:522:ILE:HG13	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:619:ILE:HG22	1:B:620:LEU:HD12	2.00	0.42
1:A:101:ALA:O	1:A:105:VAL:HG23	2.20	0.42
1:A:282:THR:HG23	1:A:347:LEU:HD13	2.00	0.42
1:A:503:ILE:O	1:A:507:ILE:HG12	2.19	0.42
1:A:536:LEU:CD1	1:B:536:LEU:HD11	2.38	0.42
1:A:553:ALA:HB2	1:B:421:THR:HG21	2.01	0.42
1:B:53:GLU:HG2	1:B:608:LEU:HD11	2.01	0.42
1:B:75:GLN:HE22	1:B:154:GLN:CD	2.27	0.42
1:A:22:PHE:HA	1:A:97:MET:HE1	2.02	0.41
1:A:337:ALA:HB2	1:A:363:TRP:CZ2	2.54	0.41
1:B:262:MET:HE3	1:B:266:TYR:CE2	2.55	0.41
1:A:162:THR:OG1	1:A:168:ASN:HB3	2.20	0.41
1:A:205:ALA:C	1:A:207:LEU:H	2.29	0.41
1:A:363:TRP:CE2	1:A:367:ILE:HD11	2.54	0.41
1:B:227:ALA:O	1:B:230:VAL:HG22	2.19	0.41
1:A:259:ALA:O	1:A:262:MET:HB2	2.19	0.41
1:B:262:MET:HE2	1:B:262:MET:HB3	1.64	0.41
1:B:611:MET:O	1:B:614:PRO:HD2	2.21	0.41
1:B:666:LEU:HD13	1:B:671:LEU:HG	2.01	0.41
1:A:149:GLY:HA2	1:A:154:GLN:HB2	2.02	0.41
1:A:364:PHE:O	1:A:368:ILE:HG12	2.20	0.41
1:A:511:LEU:HA	1:A:511:LEU:HD23	1.86	0.41
1:A:468:GLY:HA2	1:A:484:THR:HG23	2.03	0.41
1:B:350:LEU:O	1:B:355:PHE:HB2	2.21	0.41
1:A:43:ARG:HD3	1:A:100:ARG:CZ	2.51	0.41
1:A:69:MET:HE2	1:A:69:MET:HB3	1.83	0.41
1:A:108:ALA:HA	1:A:111:THR:HG22	2.02	0.41
1:A:262:MET:HE1	1:A:353:LEU:HA	2.02	0.41
1:A:543:ARG:NH1	1:A:629:LEU:O	2.54	0.41
1:B:32:THR:HB	1:B:35:MET:HG3	2.03	0.41
1:B:75:GLN:NE2	1:B:148:PHE:HB3	2.16	0.41
1:A:293:PHE:CE2	1:A:336:THR:HG21	2.56	0.41
1:A:133:VAL:HG13	1:A:245:LEU:HD12	2.02	0.40
1:A:167:ILE:CG2	1:A:718:SER:HB3	2.51	0.40
1:A:194:GLY:O	1:A:198:THR:HG23	2.20	0.40
1:A:46:ALA:O	1:A:50:LEU:N	2.50	0.40
1:A:484:THR:HG22	1:A:485:ASP:N	2.36	0.40
1:A:188:MET:O	1:A:192:VAL:N	2.43	0.40
1:B:57:ILE:HG13	1:B:58:PHE:H	1.86	0.40
1:B:307:TYR:HE2	1:B:323:ILE:HG21	1.86	0.40
1:B:131:LEU:HD21	1:B:302:MET:HG2	2.04	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:236:ASP:HB2	1:B:462:PRO:HG3	2.02	0.40
1:B:410:LEU:HA	1:B:410:LEU:HD23	1.83	0.40
1:A:448:LEU:HD11	1:A:505:SER:HB3	2.04	0.40
1:B:363:TRP:CE2	1:B:367:ILE:HD11	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	680/735 (92%)	630 (93%)	40 (6%)	10 (2%)	8	38
1	B	689/735 (94%)	640 (93%)	39 (6%)	10 (2%)	8	38
All	All	1369/1470 (93%)	1270 (93%)	79 (6%)	20 (2%)	8	38

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	359	ALA
1	B	386	TYR
1	B	672	GLU
1	A	32	THR
1	A	208	VAL
1	A	226	ILE
1	A	387	ARG
1	A	672	GLU
1	A	678	SER
1	B	32	THR
1	B	223	PRO
1	B	358	GLY
1	B	359	ALA
1	A	450	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	478	PRO
1	B	477	ASP
1	B	478	PRO
1	A	344	LEU
1	B	600	ILE
1	B	673	GLY

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	459/575 (80%)	446 (97%)	13 (3%)	38	60
1	B	469/575 (82%)	454 (97%)	15 (3%)	34	56
All	All	928/1150 (81%)	900 (97%)	28 (3%)	36	57

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

Mol	Chain	Res	Type
1	A	3	VAL
1	A	6	LEU
1	A	12	LEU
1	A	49	PHE
1	A	54	THR
1	A	138	LEU
1	A	208	VAL
1	A	233	ASN
1	A	347	LEU
1	A	384	THR
1	A	465	ASP
1	A	484	THR
1	A	508	PHE
1	B	12	LEU
1	B	54	THR
1	B	87	SER
1	B	186	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	347	LEU
1	B	353	LEU
1	B	381	GLU
1	B	384	THR
1	B	477	ASP
1	B	484	THR
1	B	508	PHE
1	B	522	ILE
1	B	639	ILE
1	B	659	TRP
1	B	725	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	233	ASN
1	A	268	GLN
1	A	466	ASN
1	B	21	ASN
1	B	75	GLN
1	B	154	GLN
1	B	492	ASN
1	B	661	ASN
1	B	681	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

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	$\# Z > 2$
2	WO4	B	801	3	2,4,4	12.59	2 (100%)	-		
2	WO4	A	801	3	2,4,4	12.56	2 (100%)	-		

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	WO4	W-O1	12.61	2.04	1.77
2	A	801	WO4	W-O1	12.60	2.04	1.77
2	B	801	WO4	W-O2	12.57	2.04	1.77
2	A	801	WO4	W-O2	12.53	2.04	1.77

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 [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	690/735 (93%)	-0.26	4 (0%)	85 71	101, 142, 170, 179	0
1	B	697/735 (94%)	-0.32	1 (0%)	92 87	98, 129, 171, 183	0
All	All	1387/1470 (94%)	-0.29	5 (0%)	88 75	98, 134, 171, 183	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	466	ASN	2.5
1	A	42	ILE	2.4
1	A	115	ILE	2.4
1	A	525	SER	2.1
1	B	98	ALA	2.1

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
3	MG	B	802	1/1	0.43	0.17	157,157,157,157	0
3	MG	A	803	1/1	0.63	0.21	161,161,161,161	0
3	MG	B	803	1/1	0.63	0.10	144,144,144,144	0
2	WO4	B	801	5/5	0.81	0.14	186,186,186,186	5
3	MG	A	802	1/1	0.88	0.13	142,142,142,142	0
2	WO4	A	801	5/5	0.94	0.11	210,210,210,210	5

6.5 Other polymers [i](#)

There are no such residues in this entry.