



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 04:04 PM UTC

PDB ID : 8B24 / pdb_00008b24
Title : Time-resolved structure of K⁺-dependent Na⁺-PPase from *Thermotoga maritima* 3600-seconds post reaction initiation with Na⁺
Authors : Strauss, J.; Vidilaseris, K.; Goldman, A.
Deposited on : 2022-09-12
Resolution : 4.53 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

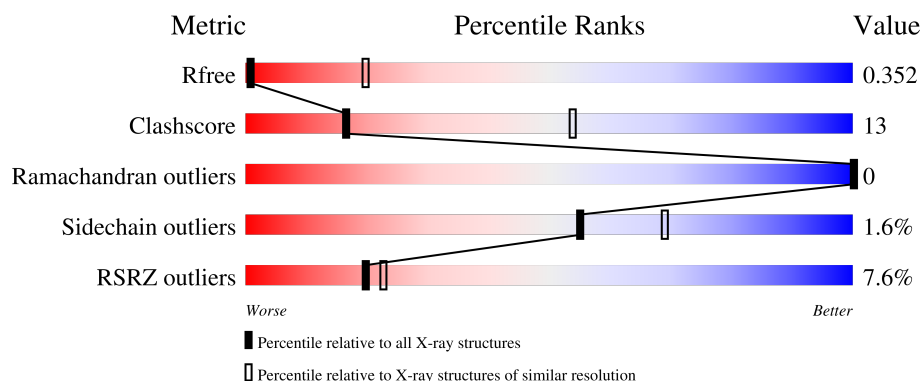
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.53 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	1131 (5.14-3.90)
Clashscore	190562	1009 (5.14-3.94)
Ramachandran outliers	187476	1061 (5.12-3.90)
Sidechain outliers	187428	1044 (5.12-3.90)
RSRZ outliers	180081	1126 (5.14-3.90)

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	9% 70% 27% .
1	B	735	6% 71% 24% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10276 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.

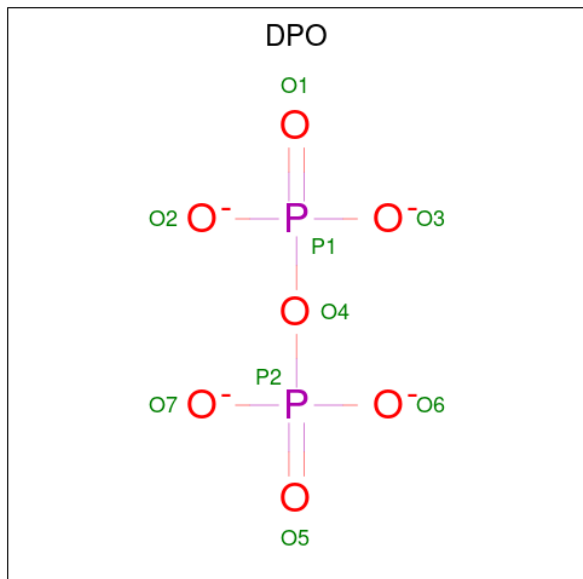
- Molecule 1 is a protein called K(+)-stimulated pyrophosphate-energized sodium pump.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	710	Total	C	N	O	S	0	0	0
			5076	3327	789	935	25			
1	B	705	Total	C	N	O	S	0	4	0
			5170	3389	811	943	27			

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 DIPHOSPHATE (CCD ID: DPO) (formula: O_7P_2) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			9	7	2		

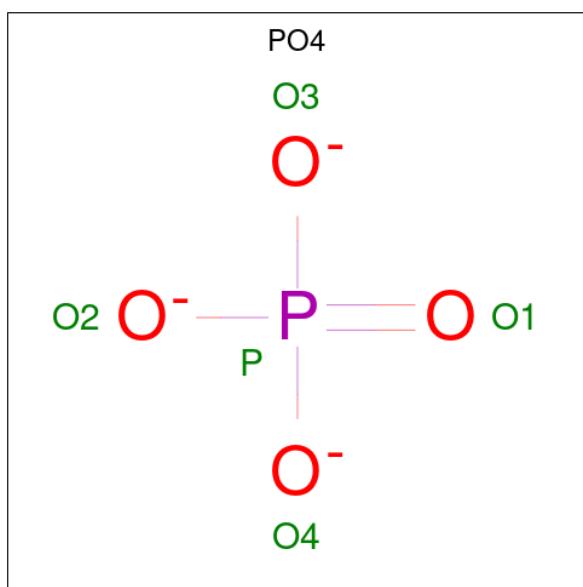
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	Mg	0	0
			5	5		
3	B	5	Total	Mg	0	0
			5	5		

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	K	0	0
			1	1		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).

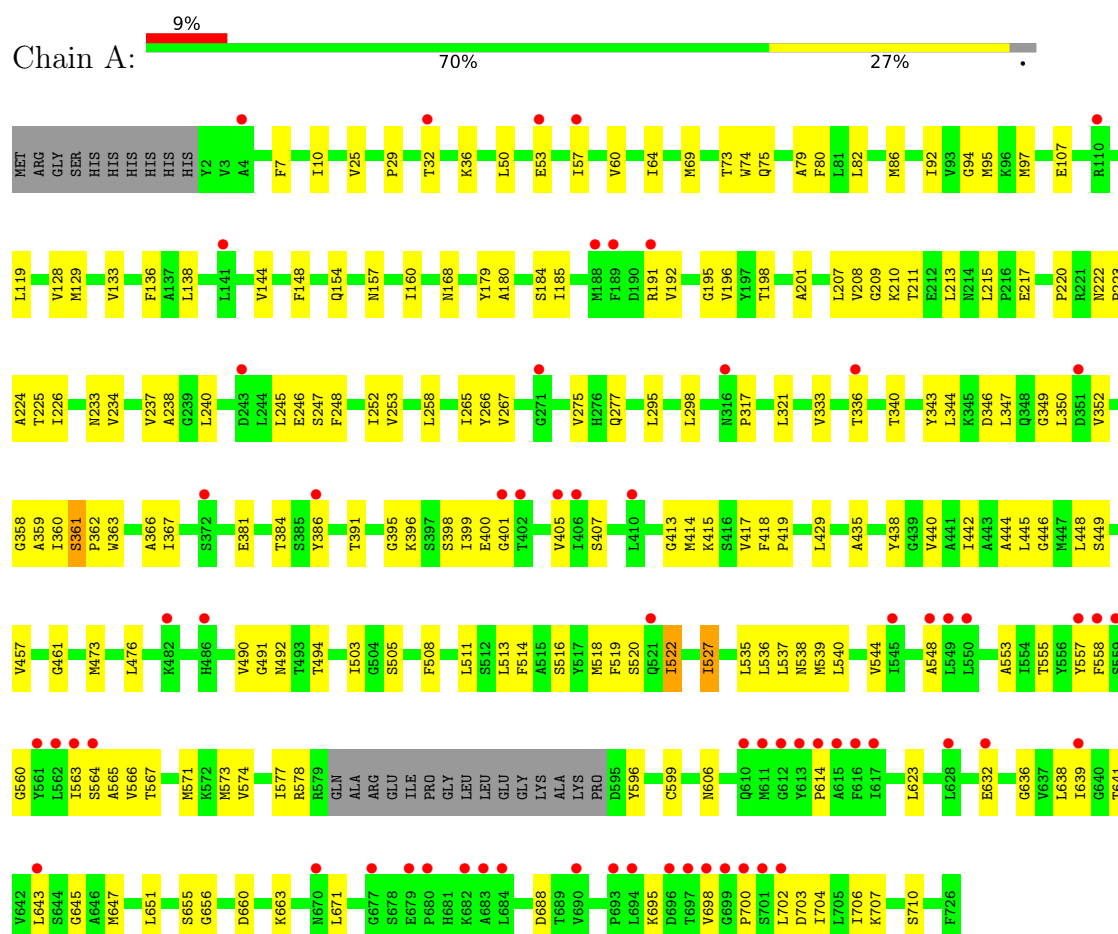


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		

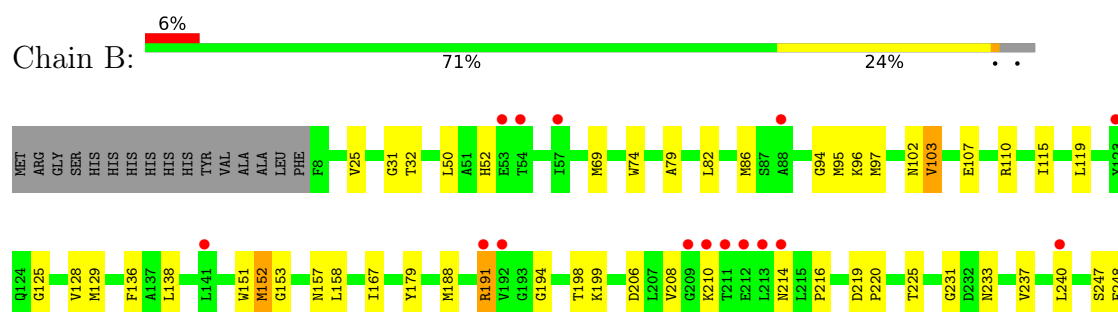
3 Residue-property plots [i](#)

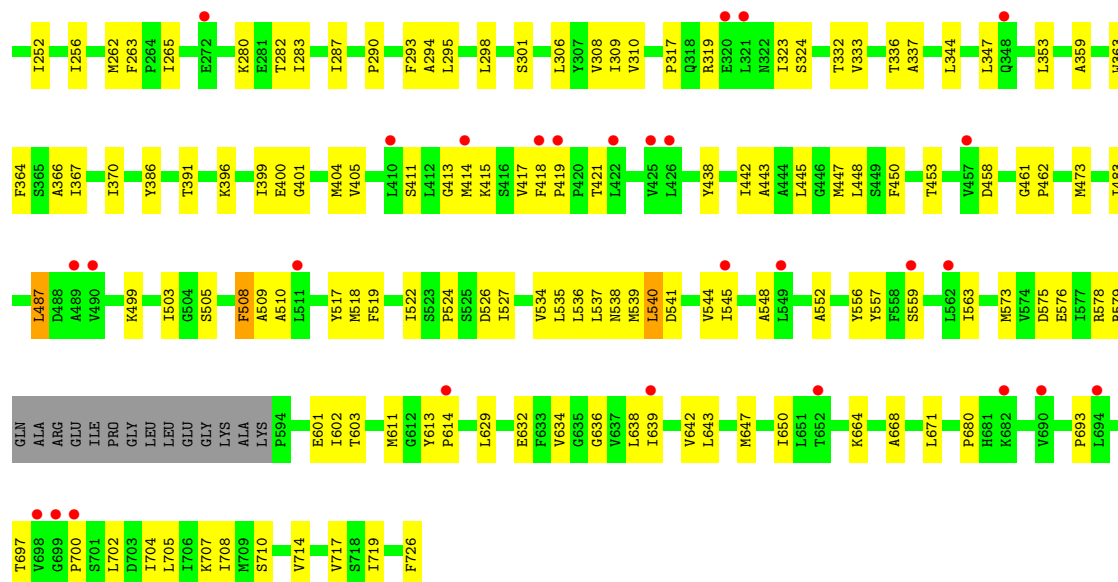
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: 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	83.11Å 111.07Å 105.42Å 90.00° 108.90° 90.00°	Depositor
Resolution (Å)	99.74 – 4.53 99.73 – 4.53	Depositor EDS
% Data completeness (in resolution range)	56.3 (99.74-4.53) 56.4 (99.73-4.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 4.47Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.326 , 0.361 0.322 , 0.352	Depositor DCC
R_{free} test set	330 reflections (2.99%)	wwPDB-VP
Wilson B-factor (Å ²)	287.4	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 480.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	10276	wwPDB-VP
Average B, all atoms (Å ²)	389.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.35% 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: DPO, K, MG, PO4

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	0.18	0/5184	0.37	0/7093
1	B	0.18	0/5280	0.37	0/7199
All	All	0.18	0/10464	0.37	0/14292

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	5076	0	4991	156	0
1	B	5170	0	5197	146	0
2	A	9	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	1	0	0	0	0
5	B	10	0	0	0	0
All	All	10276	0	10188	265	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 13.

All (265) 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:573:MET:HE3	1:A:599:CYS:HB3	1.62	0.82
1:A:94:GLY:HA3	1:A:129:MET:HE3	1.66	0.77
1:B:576:GLU:HG3	1:B:602:ILE:HG13	1.66	0.76
1:A:540:LEU:HD22	1:B:535:LEU:HB3	1.67	0.76
1:A:247:SER:HA	1:A:707:LYS:HE3	1.66	0.75
1:A:340:THR:HG22	1:A:360:ILE:HD12	1.69	0.74
1:B:386:TYR:HA	1:B:391:THR:HB	1.69	0.74
1:B:194:GLY:O	1:B:198:THR:HG23	1.87	0.74
1:A:636:GLY:HA2	1:A:639:ILE:HD12	1.74	0.70
1:B:399:ILE:HA	1:B:680:PRO:HG3	1.73	0.70
1:A:639:ILE:HG12	1:B:539:MET:HG2	1.76	0.68
1:A:184:SER:HA	1:A:246:GLU:HG3	1.76	0.68
1:A:565:ALA:O	1:A:606:ASN:ND2	2.26	0.67
1:A:641:THR:HG22	1:A:706:ILE:HG12	1.76	0.67
1:B:138:LEU:HD13	1:B:295:LEU:HD23	1.77	0.66
1:B:308:VAL:HG21	1:B:324:SER:HB2	1.76	0.66
1:A:386:TYR:HA	1:A:391:THR:HB	1.79	0.65
1:B:95:MET:SD	1:B:96:LYS:N	2.70	0.64
1:A:350:LEU:HD22	1:A:358:GLY:HA2	1.79	0.64
1:A:538:ASN:ND2	1:B:535:LEU:O	2.30	0.64
1:B:115:ILE:HG23	1:B:487:LEU:HD11	1.79	0.64
1:B:366:ALA:HA	1:B:443:ALA:HA	1.81	0.63
1:A:444:ALA:HB2	1:A:508:PHE:HB3	1.81	0.62
1:A:553:ALA:HB2	1:B:421:THR:HG21	1.81	0.62
1:A:210:LYS:HA	1:A:215:LEU:O	2.00	0.62
1:B:138:LEU:HD12	1:B:298:LEU:HD22	1.82	0.62
1:A:535:LEU:O	1:B:538:ASN:ND2	2.32	0.61
1:B:50:LEU:HD11	1:B:95:MET:SD	2.40	0.61
1:A:511:LEU:HG	1:B:545:ILE:HD12	1.82	0.61
1:A:440:VAL:HG11	1:A:511:LEU:HD22	1.82	0.61
1:A:395:GLY:O	1:A:398:SER:OG	2.13	0.61
1:B:366:ALA:HB2	1:B:442:ILE:HG22	1.82	0.61
1:A:133:VAL:HG13	1:A:245:LEU:HB2	1.83	0.60
1:A:223:PRO:HA	1:A:596:TYR:CD1	2.35	0.60
1:A:7:PHE:HB3	1:A:295:LEU:HD13	1.83	0.60
1:A:220:PRO:HD3	1:A:473:MET:HA	1.83	0.60
1:A:358:GLY:O	1:A:361:SER:OG	2.18	0.60
1:A:223:PRO:HA	1:A:596:TYR:HD1	1.66	0.60
1:B:102:ASN:OD1	1:B:103:VAL:N	2.36	0.59
1:B:505:SER:HA	1:B:508:PHE:CE2	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:220:PRO:HA	1:B:473:MET:HE3	1.85	0.59
1:B:364:PHE:O	1:B:367:ILE:HG13	2.03	0.58
1:A:347:LEU:HB3	1:A:350:LEU:HD21	1.83	0.58
1:B:240:LEU:HD23	1:B:458:ASP:HB3	1.84	0.58
1:A:574:VAL:HG11	1:B:400:GLU:O	2.04	0.57
1:B:333:VAL:HG22	1:B:367:ILE:HG22	1.87	0.57
1:A:224:ALA:HB2	1:A:577:ILE:HD11	1.86	0.56
1:A:321:LEU:HD13	1:A:457:VAL:HG13	1.87	0.56
1:A:191:ARG:HH21	1:A:240:LEU:HA	1.70	0.56
1:A:540:LEU:HD13	1:B:535:LEU:C	2.29	0.56
1:A:643:LEU:O	1:A:647:MET:HG2	2.06	0.56
1:B:629:LEU:HD23	1:B:726:PHE:HB2	1.87	0.56
1:A:651:LEU:HD12	1:B:556:TYR:HD2	1.71	0.56
1:B:97:MET:HG2	1:B:128:VAL:HB	1.87	0.56
1:A:267:VAL:HA	1:A:275:VAL:O	2.05	0.56
1:A:492:ASN:ND2	1:A:660:ASP:OD2	2.39	0.56
1:A:381:GLU:HA	1:A:384:THR:HG22	1.88	0.55
1:A:79:ALA:HB1	1:A:179:TYR:HB2	1.89	0.55
1:A:401:GLY:O	1:A:405:VAL:HG23	2.05	0.55
1:A:578:ARG:NH1	1:B:399:ILE:O	2.33	0.55
1:A:252:ILE:HG12	1:A:445:LEU:HD13	1.87	0.55
1:B:216:PRO:HB2	1:B:219:ASP:HB2	1.89	0.55
1:A:407:SER:HB3	1:B:563:ILE:CG2	2.37	0.55
1:A:555:THR:HG23	1:A:702:LEU:HD22	1.88	0.54
1:B:293:PHE:HB3	1:B:445:LEU:HD21	1.88	0.54
1:B:526:ASP:HB3	1:B:534:VAL:HG22	1.89	0.54
1:A:414:MET:HB3	1:B:556:TYR:O	2.08	0.54
1:B:25:VAL:HB	1:B:97:MET:HE1	1.90	0.53
1:A:154:GLN:HA	1:A:157:ASN:HD21	1.74	0.53
1:B:539:MET:HE3	1:B:545:ILE:HG12	1.91	0.53
1:A:32:THR:O	1:A:36:LYS:N	2.28	0.53
1:A:340:THR:HG21	1:A:360:ILE:HA	1.90	0.53
1:A:536:LEU:HD21	1:B:536:LEU:HD11	1.90	0.53
1:A:201:ALA:HA	1:A:573:MET:HE1	1.90	0.53
1:A:663:LYS:NZ	1:A:688:ASP:OD2	2.42	0.53
1:A:144:VAL:HG13	1:A:148:PHE:HD2	1.72	0.52
1:A:548:ALA:HB1	1:B:643:LEU:HD11	1.90	0.52
1:A:180:ALA:HB2	1:A:253:VAL:HG21	1.92	0.52
1:B:119:LEU:HD13	1:B:317:PRO:HB3	1.92	0.52
1:A:248:PHE:CZ	1:A:252:ILE:HD11	2.45	0.52
1:B:344:LEU:HB2	1:B:359:ALA:HB1	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:SER:HB2	1:A:435:ALA:HB2	1.92	0.52
1:B:82:LEU:O	1:B:86:MET:HG2	2.10	0.51
1:B:206:ASP:O	1:B:210:LYS:HG2	2.10	0.51
1:B:639:ILE:O	1:B:643:LEU:HG	2.10	0.51
1:A:519:PHE:O	1:A:522:ILE:HB	2.10	0.51
1:A:540:LEU:HD11	1:B:518:MET:HB3	1.93	0.51
1:B:700:PRO:O	1:B:704:ILE:HG12	2.11	0.51
1:A:343:TYR:O	1:A:347:LEU:HG	2.11	0.51
1:B:32:THR:OG1	1:B:110:ARG:NH1	2.43	0.51
1:B:95:MET:SD	1:B:96:LYS:HG3	2.51	0.51
1:A:138:LEU:HD13	1:A:295:LEU:HD23	1.92	0.51
1:A:490:VAL:O	1:A:494:THR:HG23	2.11	0.50
1:A:571:MET:HA	1:B:404:MET:SD	2.51	0.50
1:A:647:MET:HG3	1:B:552:ALA:HB1	1.92	0.50
1:A:362:PRO:O	1:A:366:ALA:N	2.31	0.50
1:A:557:TYR:CD1	1:B:415:LYS:HA	2.46	0.50
1:B:306:LEU:HD12	1:B:309:ILE:HD11	1.93	0.50
1:A:415:LYS:HA	1:B:557:TYR:CD2	2.47	0.50
1:A:519:PHE:CE1	1:A:535:LEU:HD21	2.46	0.50
1:B:301:SER:HB3	1:B:453:THR:HG23	1.94	0.49
1:B:337:ALA:HB2	1:B:363:TRP:CE2	2.47	0.49
1:A:208:VAL:O	1:A:213:LEU:N	2.36	0.49
1:A:639:ILE:O	1:A:643:LEU:HG	2.12	0.49
1:A:82:LEU:HD23	1:A:144:VAL:HG23	1.94	0.49
1:A:537:LEU:HB3	1:B:539:MET:H	1.76	0.49
1:A:539:MET:HE3	1:B:539:MET:HB2	1.94	0.49
1:B:309:ILE:HG13	1:B:310:VAL:HG23	1.94	0.49
1:B:548:ALA:HA	1:B:636:GLY:O	2.12	0.49
1:A:80:PHE:HE2	1:A:185:ILE:HD12	1.77	0.49
1:B:337:ALA:HB2	1:B:363:TRP:CZ2	2.48	0.49
1:B:448:LEU:HD11	1:B:505:SER:HB2	1.93	0.49
1:B:263:PHE:HB2	1:B:283:ILE:HG13	1.94	0.49
1:B:518:MET:HE2	1:B:537:LEU:HB2	1.94	0.49
1:A:86:MET:HB3	1:A:136:PHE:HB3	1.95	0.48
1:A:563:ILE:O	1:A:567:THR:HG23	2.13	0.48
1:B:544:VAL:HG22	1:B:632:GLU:HB3	1.95	0.48
1:A:317:PRO:HG2	1:A:490:VAL:HG21	1.95	0.48
1:A:344:LEU:HD23	1:A:358:GLY:HA3	1.95	0.48
1:A:564:SER:HB2	1:B:411:SER:OG	2.12	0.48
1:A:539:MET:HB2	1:B:537:LEU:HB3	1.96	0.48
1:B:438:TYR:O	1:B:442:ILE:HG12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:VAL:HG13	1:A:245:LEU:HD12	1.96	0.48
1:B:167:ILE:HD13	1:B:719:ILE:HG12	1.96	0.48
1:B:52:HIS:NE2	1:B:601:GLU:HG2	2.29	0.48
1:A:413:GLY:HA3	1:A:655:SER:HB2	1.96	0.48
1:A:73:THR:HB	1:A:75:GLN:OE1	2.14	0.47
1:B:508:PHE:CD1	1:B:509:ALA:N	2.82	0.47
1:B:539:MET:HE3	1:B:545:ILE:HA	1.96	0.47
1:B:256:ILE:HG23	1:B:287:ILE:HG23	1.96	0.47
1:A:321:LEU:HD22	1:A:457:VAL:HG22	1.97	0.47
1:A:359:ALA:O	1:A:362:PRO:HD2	2.13	0.47
1:A:537:LEU:HD23	1:B:539:MET:HB3	1.96	0.47
1:B:414:MET:O	1:B:417:VAL:HG22	2.15	0.47
1:A:95:MET:HA	1:A:237:VAL:HG11	1.97	0.47
1:A:698:VAL:O	1:A:702:LEU:HG	2.14	0.47
1:B:262:MET:HG3	1:B:519:PHE:HE2	1.78	0.47
1:B:282:THR:HA	1:B:347:LEU:HD22	1.96	0.47
1:A:535:LEU:HB3	1:B:540:LEU:HD12	1.97	0.47
1:B:158:LEU:HD23	1:B:280:LYS:HG2	1.97	0.47
1:A:195:GLY:HA2	1:A:198:THR:HG22	1.97	0.47
1:A:396:LYS:O	1:A:400:GLU:HG2	2.15	0.46
1:B:517:TYR:HB2	1:B:714:VAL:HG22	1.96	0.46
1:B:198:THR:HG22	1:B:231:GLY:CA	2.45	0.46
1:A:97:MET:HE2	1:A:128:VAL:HG21	1.98	0.46
1:A:700:PRO:O	1:A:704:ILE:HG13	2.15	0.46
1:A:82:LEU:O	1:A:86:MET:HG2	2.15	0.46
1:B:199:LYS:HG3	1:B:693:PRO:HA	1.97	0.46
1:A:265:ILE:HG12	1:A:522:ILE:HG13	1.98	0.46
1:A:514:PHE:HE1	1:A:638:LEU:HB3	1.80	0.46
1:A:536:LEU:HD11	1:B:536:LEU:HD11	1.97	0.46
1:B:86:MET:HB3	1:B:136:PHE:HB3	1.97	0.46
1:B:332:THR:O	1:B:336:THR:OG1	2.16	0.46
1:A:258:LEU:HG	1:A:519:PHE:HE2	1.81	0.46
1:B:69:MET:HG2	1:B:74:TRP:HA	1.96	0.46
1:A:192:VAL:HG11	1:A:614:PRO:HG3	1.97	0.46
1:A:516:SER:HA	1:A:519:PHE:HB2	1.98	0.46
1:B:399:ILE:HG23	1:B:671:LEU:HD21	1.97	0.46
1:A:514:PHE:C	1:B:540:LEU:HD21	2.41	0.46
1:B:208:VAL:O	1:B:214:ASN:HA	2.16	0.46
1:B:643:LEU:O	1:B:647:MET:HG2	2.16	0.46
1:A:10:ILE:HG22	1:A:298:LEU:HD22	1.98	0.45
1:A:398:SER:HA	1:A:405:VAL:CG2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:643:LEU:HD11	1:B:548:ALA:HB1	1.98	0.45
1:A:119:LEU:HD13	1:A:317:PRO:HB3	1.97	0.45
1:B:107:GLU:OE1	1:B:110:ARG:NH2	2.49	0.45
1:B:664:LYS:O	1:B:668:ALA:N	2.46	0.45
1:B:710:SER:O	1:B:714:VAL:HG23	2.16	0.45
1:A:60:VAL:O	1:A:64:ILE:HG12	2.17	0.45
1:A:208:VAL:HG21	1:A:574:VAL:HG13	1.98	0.45
1:A:29:PRO:HG2	1:A:107:GLU:OE1	2.16	0.45
1:A:209:GLY:O	1:A:215:LEU:HB2	2.17	0.45
1:A:522:ILE:HD12	1:A:527:ILE:HG13	1.98	0.45
1:A:558:PHE:HE1	1:A:614:PRO:HB3	1.82	0.45
1:A:656:GLY:C	1:A:695:LYS:HD3	2.42	0.45
1:B:575:ASP:HA	1:B:578:ARG:HE	1.82	0.44
1:A:538:ASN:HD21	1:A:540:LEU:HB2	1.82	0.44
1:A:154:GLN:HA	1:A:157:ASN:ND2	2.32	0.44
1:A:80:PHE:CE2	1:A:185:ILE:HD12	2.51	0.44
1:A:336:THR:HG22	1:A:363:TRP:HD1	1.82	0.44
1:A:349:GLY:O	1:A:352:VAL:HG22	2.17	0.44
1:A:448:LEU:HD13	1:A:505:SER:HB2	2.00	0.44
1:A:560:GLY:HA3	1:B:414:MET:HB2	1.99	0.44
1:A:567:THR:O	1:A:571:MET:N	2.39	0.44
1:B:573:MET:HB2	1:B:603:THR:HG22	2.00	0.44
1:A:207:LEU:O	1:A:211:THR:HB	2.18	0.44
1:A:537:LEU:N	1:B:538:ASN:OD1	2.51	0.44
1:A:222:ASN:HB3	1:A:225:THR:HG23	1.99	0.44
1:A:700:PRO:HA	1:A:703:ASP:OD2	2.18	0.44
1:A:191:ARG:HD3	1:A:700:PRO:HB2	2.00	0.43
1:A:446:GLY:HA2	1:A:449:SER:HB3	2.00	0.43
1:B:247:SER:N	1:B:707:LYS:HZ2	2.16	0.43
1:B:524:PRO:O	1:B:527:ILE:HG12	2.18	0.43
1:A:266:TYR:HB3	1:A:277:GLN:HB2	1.99	0.43
1:B:97:MET:HE2	1:B:128:VAL:HG21	2.00	0.43
1:A:518:MET:HB2	1:B:540:LEU:HD11	1.99	0.43
1:B:233:ASN:O	1:B:237:VAL:HB	2.17	0.43
1:B:153:GLY:O	1:B:157:ASN:ND2	2.51	0.43
1:A:639:ILE:HG23	1:B:539:MET:HE2	2.01	0.43
1:B:188:MET:HA	1:B:704:ILE:HG21	2.00	0.43
1:B:413:GLY:O	1:B:417:VAL:HG13	2.19	0.43
1:A:69:MET:HG2	1:A:74:TRP:HA	2.00	0.43
1:A:267:VAL:HG21	1:A:527:ILE:HG23	2.01	0.43
1:A:399:ILE:HD11	1:A:671:LEU:HD21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:GLY:O	1:A:417:VAL:HG23	2.19	0.43
1:A:461:GLY:HA2	1:A:491:GLY:HA3	2.00	0.43
1:B:97:MET:HE3	1:B:125:GLY:HA2	2.00	0.43
1:A:333:VAL:HG22	1:A:367:ILE:HG12	2.00	0.43
1:A:429:LEU:HD11	1:B:629:LEU:HD11	2.00	0.43
1:B:401:GLY:O	1:B:405:VAL:HG23	2.18	0.43
1:B:461:GLY:N	1:B:462:PRO:HD2	2.34	0.43
1:B:613:TYR:HB3	1:B:614:PRO:HD3	2.00	0.43
1:B:517:TYR:CE1	1:B:717:VAL:HB	2.54	0.42
1:A:461:GLY:CA	1:A:491:GLY:HA3	2.49	0.42
1:B:151:TRP:CE3	1:B:152:MET:HG2	2.54	0.42
1:B:559:SER:OG	1:B:702:LEU:HD21	2.19	0.42
1:A:50:LEU:HD21	1:A:92:ILE:HG12	2.02	0.42
1:A:196:VAL:HA	1:A:566:VAL:HG22	2.02	0.42
1:B:499:LYS:O	1:B:503:ILE:HG13	2.20	0.42
1:A:418:PHE:HB3	1:A:419:PRO:HD3	2.01	0.42
1:A:557:TYR:HD1	1:B:415:LYS:HA	1.85	0.42
1:A:438:TYR:O	1:A:442:ILE:HG12	2.19	0.42
1:A:210:LYS:HD3	1:A:217:GLU:HB2	2.02	0.42
1:B:611:MET:HE2	1:B:611:MET:HB3	1.93	0.42
1:B:94:GLY:HA3	1:B:129:MET:SD	2.60	0.42
1:A:513:LEU:HD13	1:A:710:SER:OG	2.19	0.41
1:A:563:ILE:HB	1:B:411:SER:HB2	2.01	0.41
1:A:645:GLY:HA3	1:A:706:ILE:HD11	2.02	0.41
1:B:265:ILE:HG12	1:B:522:ILE:HD13	2.02	0.41
1:B:508:PHE:CD1	1:B:508:PHE:C	2.98	0.41
1:B:510:ALA:HB1	1:B:642:VAL:HG22	2.02	0.41
1:A:234:VAL:O	1:A:238:ALA:HB3	2.20	0.41
1:A:503:ILE:HD13	1:A:703:ASP:HB3	2.02	0.41
1:B:79:ALA:HB1	1:B:179:TYR:HB2	2.02	0.41
1:B:541[A]:ASP:HB3	1:B:544:VAL:HG23	2.02	0.41
1:A:160:ILE:HD11	1:A:168:ASN:HB2	2.02	0.41
1:A:233:ASN:O	1:A:237:VAL:HB	2.21	0.41
1:B:417:VAL:HA	1:B:650:ILE:HG21	2.02	0.41
1:B:483:ILE:O	1:B:487:LEU:HD13	2.20	0.41
1:A:539:MET:HE1	1:A:639:ILE:HD13	2.01	0.41
1:B:396:LYS:O	1:B:399:ILE:HG12	2.20	0.41
1:B:447:MET:SD	1:B:508:PHE:HE2	2.44	0.41
1:B:31:GLY:HA3	1:B:107:GLU:CD	2.46	0.41
1:B:237:VAL:HG23	1:B:462:PRO:HG3	2.03	0.41
1:B:319:ARG:O	1:B:323:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:370:ILE:HG23	1:B:450:PHE:HE1	1.86	0.41
1:A:520:SER:C	1:A:522:ILE:H	2.29	0.41
1:A:536:LEU:HD11	1:B:536:LEU:HD21	2.02	0.41
1:B:115:ILE:HG12	1:B:483:ILE:HG23	2.02	0.41
1:A:476:LEU:HD12	1:A:476:LEU:HA	1.86	0.41
1:B:252:ILE:HG23	1:B:290:PRO:HB2	2.03	0.41
1:B:634:VAL:O	1:B:638:LEU:HG	2.21	0.41
1:B:705:LEU:HA	1:B:708:ILE:HG22	2.02	0.41
1:B:399:ILE:CG2	1:B:671:LEU:HD21	2.51	0.40
1:B:508:PHE:HD1	1:B:509:ALA:N	2.20	0.40
1:A:138:LEU:HD12	1:A:298:LEU:HD13	2.02	0.40
1:A:540:LEU:HD21	1:B:518:MET:HB2	2.04	0.40
1:A:544:VAL:HG22	1:A:632:GLU:HB3	2.02	0.40
1:B:237:VAL:HG23	1:B:462:PRO:CG	2.51	0.40
1:B:248:PHE:HZ	1:B:294:ALA:HB1	1.86	0.40
1:B:693:PRO:O	1:B:697:THR:HB	2.21	0.40
1:B:158:LEU:HG	1:B:263:PHE:CD2	2.56	0.40
1:B:191:ARG:HA	1:B:191:ARG:HD3	1.72	0.40
1:A:53:GLU:O	1:A:57:ILE:HG12	2.22	0.40
1:B:418:PHE:HB3	1:B:419:PRO:HD3	2.02	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	706/735 (96%)	695 (98%)	11 (2%)	0	100	100
1	B	705/735 (96%)	696 (99%)	9 (1%)	0	100	100
All	All	1411/1470 (96%)	1391 (99%)	20 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	500/575 (87%)	493 (99%)	7 (1%)	59	71
1	B	526/575 (92%)	517 (98%)	9 (2%)	53	67
All	All	1026/1150 (89%)	1010 (98%)	16 (2%)	55	69

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	VAL
1	A	226	ILE
1	A	346	ASP
1	A	361	SER
1	A	522	ILE
1	A	527	ILE
1	A	623	LEU
1	B	103	VAL
1	B	152	MET
1	B	191	ARG
1	B	225	THR
1	B	353	LEU
1	B	487	LEU
1	B	508	PHE
1	B	540	LEU
1	B	579	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	168	ASN
1	A	276	HIS
1	B	154	GLN
1	B	277	GLN
1	B	492	ASN
1	B	606	ASN

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Mol	Chain	Res	Type
1	B	670	ASN
1	B	681	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 11 are monoatomic - leaving 3 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	$\# Z > 2$
5	PO4	B	802	3	4,4,4	0.97	0	6,6,6	0.46	0
5	PO4	B	801	3	4,4,4	0.95	0	6,6,6	0.45	0
2	DPO	A	801	4,3	6,8,8	0.66	0	12,13,13	0.85	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
2	DPO	A	801	4,3	-	0/6/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

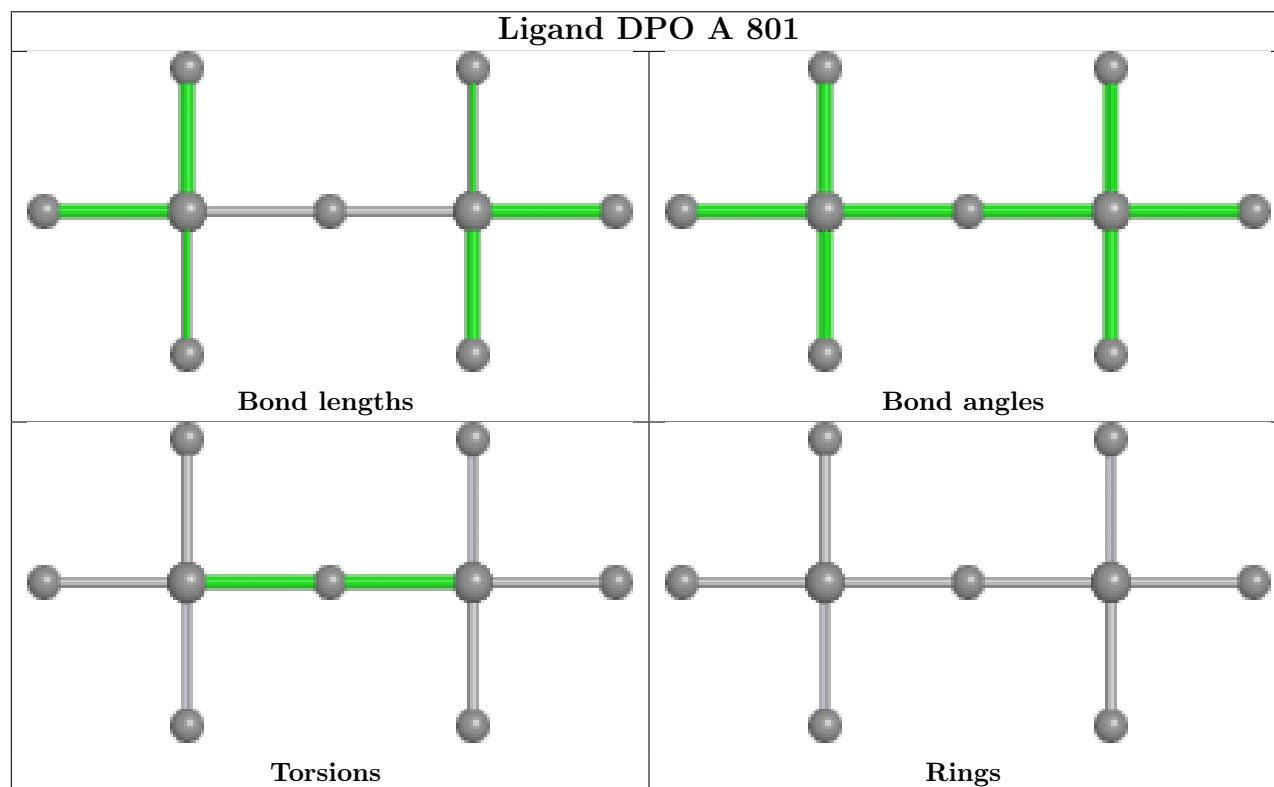
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

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	710/735 (96%)	0.34	64 (9%)	15	19	219, 383, 516, 644	0
1	B	705/735 (95%)	0.17	43 (6%)	27	28	125, 381, 531, 728	4 (0%)
All	All	1415/1470 (96%)	0.25	107 (7%)	20	23	125, 382, 523, 728	4 (0%)

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	422	LEU	8.6
1	B	418	PHE	8.3
1	B	214	ASN	8.2
1	A	559	SER	7.7
1	A	563	ILE	7.6
1	A	698	VAL	6.9
1	A	694	LEU	6.7
1	B	489	ALA	6.3
1	A	612	GLY	6.2
1	A	679	GLU	6.1
1	A	57	ILE	6.1
1	A	690	VAL	5.9
1	A	683	ALA	5.7
1	A	614	PRO	5.7
1	A	557	TYR	5.5
1	B	348[A]	GLN	5.5
1	A	700	PRO	5.4
1	A	53	GLU	5.3
1	B	211	THR	5.1
1	B	210	LYS	5.0
1	B	410	LEU	4.9
1	A	615	ALA	4.8
1	A	558	PHE	4.8
1	A	191	ARG	4.8

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Mol	Chain	Res	Type	RSRZ
1	B	57	ILE	4.6
1	A	617	ILE	4.6
1	A	402	THR	4.5
1	A	639	ILE	4.5
1	B	272	GLU	4.5
1	A	549	LEU	4.4
1	B	321	LEU	4.4
1	A	611	MET	4.4
1	A	188	MET	4.4
1	A	562	LEU	4.2
1	B	614	PRO	4.2
1	A	670	ASN	4.0
1	A	410	LEU	3.9
1	A	697	THR	3.9
1	B	212	GLU	3.7
1	A	550	LEU	3.6
1	A	351	ASP	3.6
1	A	548	ALA	3.5
1	B	53	GLU	3.5
1	B	700	PRO	3.4
1	B	419	PRO	3.3
1	A	561	TYR	3.3
1	B	694	LEU	3.3
1	A	693	PRO	3.2
1	B	652	THR	3.2
1	A	684	LEU	3.2
1	A	680	PRO	3.2
1	B	699	GLY	3.0
1	B	682	LYS	3.0
1	B	698	VAL	3.0
1	B	123	TYR	2.9
1	B	549	LEU	2.9
1	A	545	ILE	2.9
1	B	639	ILE	2.9
1	A	4	ALA	2.9
1	B	559	SER	2.8
1	A	610	GLN	2.8
1	B	141	LEU	2.8
1	A	521	GLN	2.7
1	A	386	TYR	2.7
1	A	616	PHE	2.7
1	A	406	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	320	GLU	2.6
1	A	141	LEU	2.6
1	B	562	LEU	2.6
1	A	699	GLY	2.6
1	A	702	LEU	2.6
1	A	32	THR	2.6
1	A	189	PHE	2.6
1	A	482	LYS	2.6
1	A	271	GLY	2.5
1	B	88	ALA	2.5
1	B	425	VAL	2.5
1	B	54	THR	2.5
1	B	191	ARG	2.5
1	B	511	LEU	2.5
1	B	457	VAL	2.5
1	A	643	LEU	2.4
1	B	490	VAL	2.4
1	A	486	HIS	2.4
1	B	690	VAL	2.4
1	A	677	GLY	2.4
1	A	682	LYS	2.4
1	A	316	ASN	2.4
1	A	628	LEU	2.3
1	A	336	THR	2.3
1	A	701	SER	2.3
1	B	213	LEU	2.3
1	B	414	MET	2.3
1	B	209	GLY	2.2
1	A	696	ASP	2.2
1	B	426	LEU	2.1
1	A	401	GLY	2.1
1	B	545	ILE	2.1
1	A	564	SER	2.1
1	B	240	LEU	2.1
1	A	372	SER	2.1
1	A	405	VAL	2.1
1	A	613	TYR	2.0
1	A	110	ARG	2.0
1	A	243	ASP	2.0
1	A	632	GLU	2.0
1	B	192	VAL	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](#)

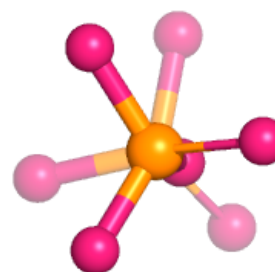
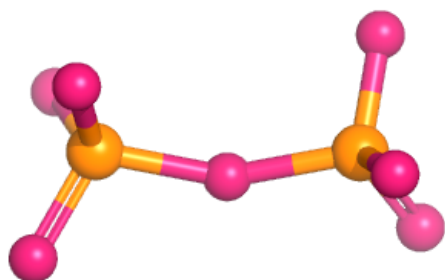
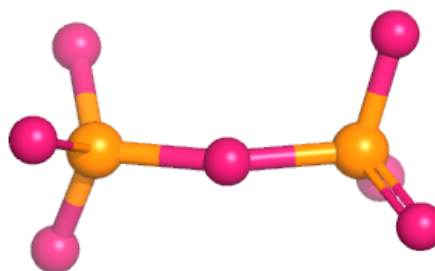
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	MG	B	805	1/1	0.64	0.10	368,368,368,368	0
3	MG	B	806	1/1	0.80	0.08	387,387,387,387	0
5	PO4	B	802	5/5	0.80	0.08	406,406,406,406	0
3	MG	B	803	1/1	0.84	0.12	352,352,352,352	0
4	K	A	807	1/1	0.85	0.12	331,331,331,331	0
5	PO4	B	801	5/5	0.93	0.05	389,389,389,389	0
3	MG	A	804	1/1	0.93	0.12	440,440,440,440	0
3	MG	A	802	1/1	0.94	0.05	474,474,474,474	0
3	MG	B	804	1/1	0.94	0.05	379,379,379,379	0
3	MG	B	807	1/1	0.94	0.06	381,381,381,381	0
3	MG	A	803	1/1	0.95	0.05	472,472,472,472	0
2	DPO	A	801	9/9	0.96	0.04	436,436,436,436	0
3	MG	A	806	1/1	0.96	0.11	404,404,404,404	0
3	MG	A	805	1/1	0.97	0.10	450,450,450,450	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around DPO A 801:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.