



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:44 PM UTC

PDB ID : 6OHO / pdb_00006oho
Title : Structure of human Phospholipase D2 catalytic domain
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Deposited on : 2019-04-06
Resolution : 2.00 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

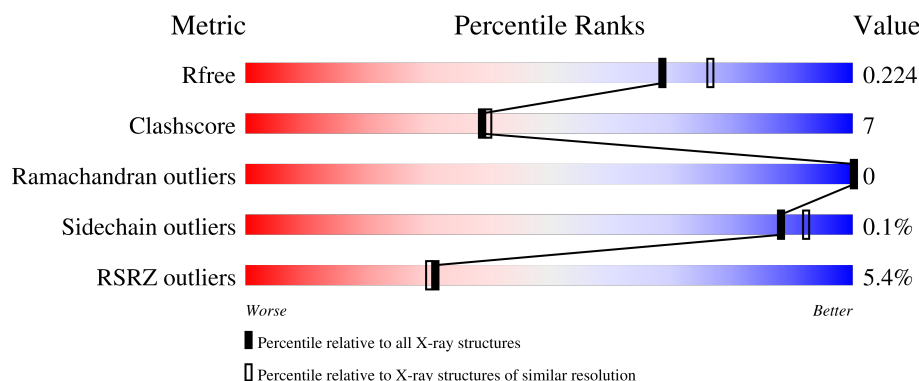
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	640	4% 78% 12% 9%
1	B	640	6% 78% 12% 10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	1005	-	-	X	-
3	GOL	A	1009	-	-	X	-
3	GOL	B	1010	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9866 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 Phospholipase D2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	580	Total	C	N	O	S	0	0	0
			4671	2998	817	840	16			
1	B	579	Total	C	N	O	S	0	0	0
			4660	2990	815	840	15			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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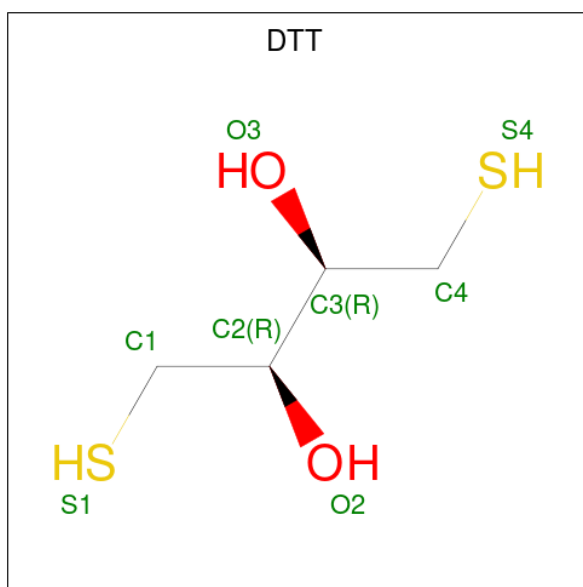
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (CCD ID: DTT) (formula: $C_4H_{10}O_2S_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	O	S	0	0
			8	4	2	2		

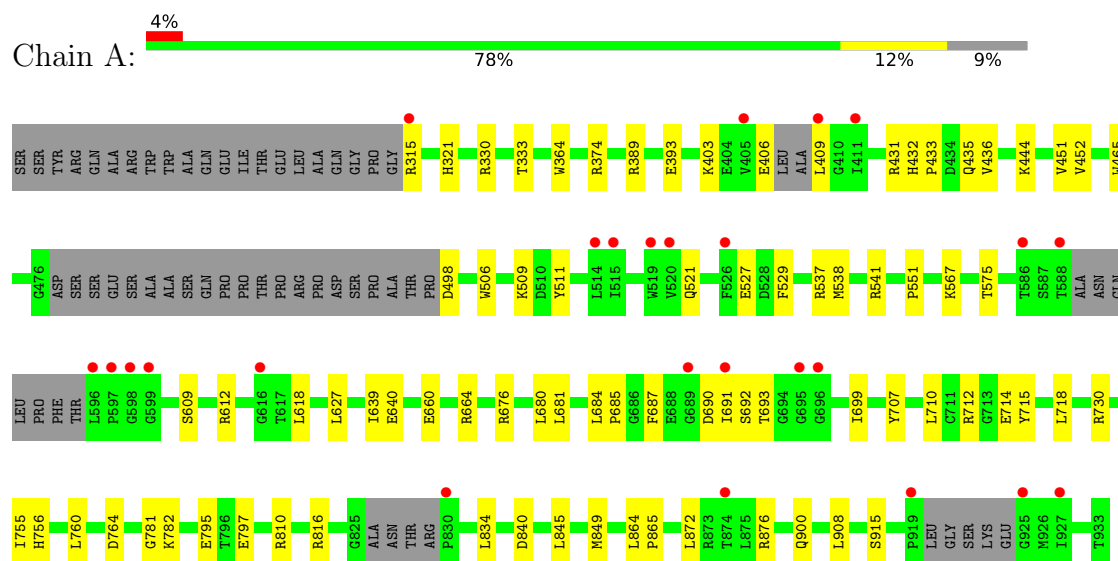
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	217	Total	O	0	0
			217	217		
5	B	177	Total	O	0	0
			177	177		

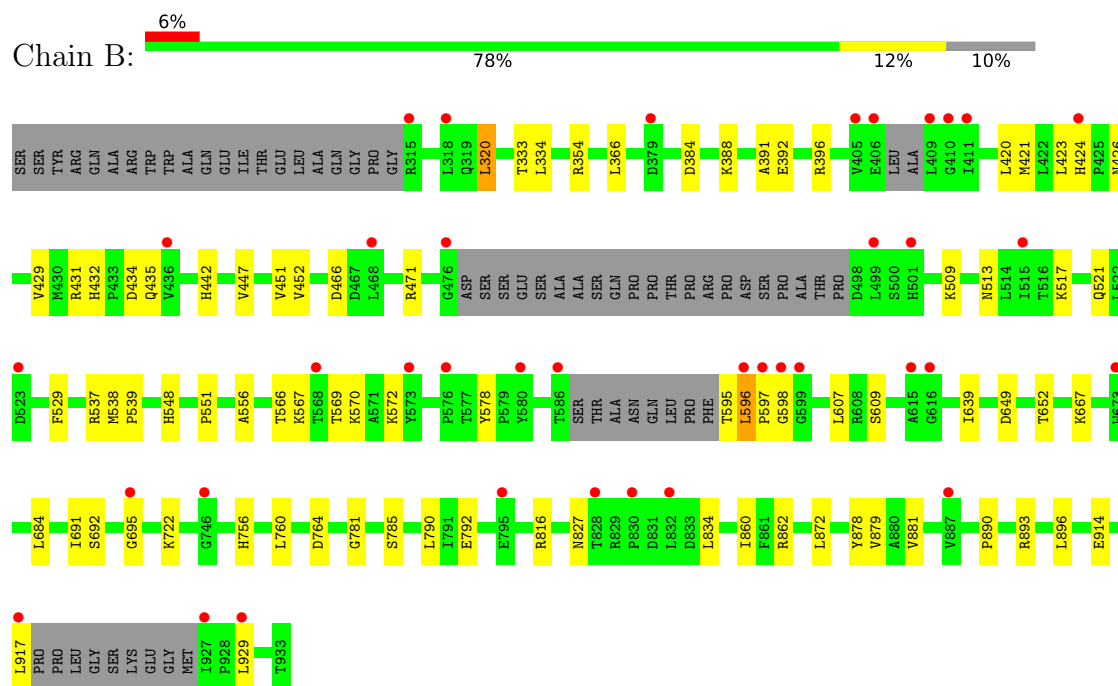
3 Residue-property plots [i](#)

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: Phospholipase D2



• Molecule 1: Phospholipase D2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	91.70Å 131.34Å 107.29Å 90.00° 111.77° 90.00°	Depositor
Resolution (Å)	48.57 – 2.00 48.57 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.57-2.00) 99.6 (48.57-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.181 , 0.224 0.183 , 0.224	Depositor DCC
R_{free} test set	4142 reflections (5.21%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.072	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9866	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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: SO4, GOL, DTT

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	0.26	0/4791	0.49	1/6507 (0.0%)
1	B	0.24	0/4779	0.45	0/6497
All	All	0.25	0/9570	0.47	1/13004 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	612	ARG	NE-CZ-NH2	6.97	125.47	119.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	596	LEU	Peptide

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	4671	0	4603	66	0
1	B	4660	0	4586	61	0
2	A	40	0	0	2	0
2	B	45	0	0	3	0
3	A	24	0	32	10	0
3	B	24	0	30	7	0
4	B	8	0	9	1	0
5	A	217	0	0	5	0
5	B	177	0	0	9	1
All	All	9866	0	9260	128	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 7.

All (128) 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:471:ARG:O	1:B:537:ARG:NH1	1.80	1.15
1:A:693:THR:HA	1:A:876:ARG:HH12	1.20	1.05
1:A:693:THR:HA	1:A:876:ARG:NH1	1.78	0.98
1:B:424:HIS:HD2	1:B:426:ASN:H	1.08	0.95
1:B:466:ASP:OD2	1:B:537:ARG:NH2	2.01	0.93
1:B:442:HIS:NE2	3:B:1010:GOL:O2	2.07	0.88
1:B:388:LYS:O	5:B:1101:HOH:O	1.93	0.87
1:A:908:LEU:HD12	3:A:1010:GOL:H32	1.58	0.85
1:A:730:ARG:HH22	3:A:1010:GOL:H31	1.43	0.82
1:A:693:THR:CA	1:A:876:ARG:HH12	1.91	0.82
1:B:537:ARG:NH2	1:B:539:PRO:HA	1.97	0.79
1:B:424:HIS:CD2	1:B:426:ASN:H	1.96	0.79
1:B:792:GLU:OE1	5:B:1102:HOH:O	2.03	0.75
1:B:756:HIS:NE2	3:B:1010:GOL:H2	2.03	0.72
1:A:498:ASP:O	5:A:1101:HOH:O	2.08	0.72
1:B:639:ILE:HG12	1:B:760:LEU:HD12	1.71	0.72
1:A:756:HIS:CE1	3:A:1009:GOL:H12	2.25	0.71
1:B:692:SER:HB2	1:B:879:VAL:HG21	1.72	0.70
1:A:406:GLU:O	5:A:1102:HOH:O	2.09	0.70
1:B:396:ARG:O	5:B:1103:HOH:O	2.09	0.70
4:B:1014:DTT:S1	4:B:1014:DTT:O3	2.45	0.69
1:A:575:THR:OG1	5:A:1103:HOH:O	2.13	0.67
1:A:409:LEU:O	5:A:1102:HOH:O	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:860:ILE:HG21	1:B:896:LEU:HD11	1.78	0.65
1:B:435:GLN:HG2	3:B:1013:GOL:O2	1.98	0.64
1:B:695:GLY:O	5:B:1105:HOH:O	2.14	0.64
2:B:1001:SO4:O2	5:B:1104:HOH:O	2.09	0.63
1:B:872:LEU:N	1:B:914:GLU:OE2	2.32	0.62
1:A:915:SER:O	3:A:1011:GOL:O3	2.14	0.62
1:A:764:ASP:OD1	1:A:816:ARG:HD3	2.00	0.62
1:A:364:TRP:CE3	3:A:1009:GOL:H31	2.35	0.62
1:B:434:ASP:N	3:B:1013:GOL:O2	2.33	0.61
1:A:872:LEU:O	1:A:876:ARG:HD3	2.01	0.61
1:B:384:ASP:HB2	1:B:423:LEU:HD11	1.83	0.60
1:A:509:LYS:NZ	1:A:521:GLN:O	2.35	0.59
1:B:421:MET:HE3	1:B:429:VAL:H	1.67	0.59
1:A:693:THR:O	1:A:876:ARG:CZ	2.51	0.59
1:A:627:LEU:HD22	1:A:660:GLU:HG3	1.84	0.59
1:B:890:PRO:HA	1:B:893:ARG:HD2	1.84	0.58
1:A:664:ARG:HH22	3:A:1012:GOL:H31	1.70	0.57
1:B:509:LYS:NZ	1:B:521:GLN:O	2.36	0.57
1:A:618:LEU:HD13	1:A:782:LYS:HE3	1.87	0.57
1:B:764:ASP:OD1	1:B:816:ARG:HD3	2.04	0.57
1:A:693:THR:O	1:A:876:ARG:NH2	2.37	0.57
1:A:509:LYS:HE2	1:A:529:PHE:HB3	1.88	0.56
1:A:389:ARG:O	1:A:393:GLU:HG3	2.06	0.56
1:B:609:SER:HB3	1:B:781:GLY:HA2	1.88	0.56
1:A:845:LEU:HD21	1:A:849:MET:HE3	1.88	0.55
1:B:334:LEU:HD21	1:B:598:GLY:HA2	1.87	0.55
1:B:391:ALA:N	5:B:1101:HOH:O	2.39	0.55
1:A:840:ASP:OD2	5:A:1104:HOH:O	2.19	0.54
1:B:862:ARG:NH1	1:B:881:VAL:HB	2.23	0.54
1:B:392:GLU:N	5:B:1101:HOH:O	2.02	0.54
1:A:511:TYR:CE2	1:A:537:ARG:HG3	2.42	0.54
1:A:690:ASP:OD1	1:A:692:SER:OG	2.26	0.54
1:A:315:ARG:N	1:A:330:ARG:HH12	2.06	0.54
1:A:707:TYR:HB3	1:A:712:ARG:HD2	1.90	0.53
1:A:693:THR:CA	1:A:876:ARG:NH1	2.56	0.53
1:B:756:HIS:CE1	3:B:1010:GOL:H2	2.44	0.52
1:A:432:HIS:CD2	1:A:433:PRO:HA	2.45	0.51
1:A:374:ARG:HG3	1:A:465:TRP:CE2	2.45	0.51
1:A:691:ILE:HG23	1:A:864:LEU:HD12	1.94	0.50
1:A:756:HIS:NE2	3:A:1009:GOL:H12	2.26	0.50
1:B:572:LYS:NZ	2:B:1005:SO4:O4	2.35	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:432:HIS:CG	1:A:433:PRO:HA	2.47	0.49
1:A:321:HIS:HB3	2:A:1003:SO4:O1	2.13	0.49
1:A:712:ARG:HD3	3:A:1011:GOL:H12	1.94	0.49
1:B:567:LYS:NZ	1:B:578:TYR:O	2.43	0.49
1:B:595:THR:O	1:B:596:LEU:HD13	2.12	0.49
1:B:354:ARG:HH11	1:B:595:THR:HG23	1.77	0.49
1:A:849:MET:SD	1:A:900:GLN:HG3	2.54	0.48
1:B:860:ILE:HG21	1:B:896:LEU:CD1	2.43	0.48
1:B:392:GLU:HA	1:B:424:HIS:CE1	2.49	0.48
1:A:403:LYS:HB2	1:A:431:ARG:HB3	1.96	0.47
1:A:609:SER:HB3	1:A:781:GLY:HA2	1.95	0.47
1:B:517:LYS:HD3	1:B:529:PHE:HD2	1.80	0.47
1:A:451:VAL:HG23	1:A:452:VAL:HG23	1.97	0.46
1:A:693:THR:O	1:A:876:ARG:NH1	2.48	0.46
1:B:513:ASN:HA	1:B:538:MET:HB3	1.97	0.46
1:A:435:GLN:HG3	1:A:436:VAL:N	2.30	0.46
1:B:862:ARG:NH1	1:B:878:TYR:O	2.49	0.46
1:B:862:ARG:NH2	5:B:1125:HOH:O	2.49	0.46
1:A:639:ILE:HG12	1:A:760:LEU:HD12	1.97	0.46
1:A:816:ARG:NH2	1:A:834:LEU:O	2.36	0.46
1:B:431:ARG:NH2	2:B:1005:SO4:O3	2.49	0.46
1:B:424:HIS:HD2	1:B:426:ASN:N	1.92	0.45
1:B:827:ASN:N	1:B:827:ASN:OD1	2.49	0.45
1:A:687:PHE:HB2	1:A:699:ILE:HD11	1.98	0.45
1:A:618:LEU:HD11	1:B:722:LYS:HB3	1.98	0.45
1:B:451:VAL:HG23	1:B:452:VAL:HG23	1.99	0.45
1:B:570:LYS:NZ	5:B:1114:HOH:O	2.40	0.45
1:B:816:ARG:NH2	1:B:834:LEU:O	2.29	0.45
1:A:567:LYS:HB3	1:A:567:LYS:HE3	1.73	0.45
1:A:664:ARG:HA	1:A:664:ARG:HD2	1.71	0.45
1:A:684:LEU:HG	1:A:865:PRO:HD3	2.00	0.44
1:A:444:LYS:NZ	3:A:1009:GOL:H32	2.32	0.44
1:A:333:THR:HG21	1:A:551:PRO:HG2	1.99	0.44
1:B:569:THR:HB	3:B:1013:GOL:H31	2.00	0.44
1:B:447:VAL:HG11	1:B:556:ALA:HB2	2.00	0.43
1:A:797:GLU:HG2	1:A:810:ARG:HG2	2.01	0.43
1:A:693:THR:C	1:A:876:ARG:NH1	2.76	0.43
1:B:517:LYS:HD3	1:B:529:PHE:CD2	2.54	0.43
1:B:917:LEU:HD21	1:B:929:LEU:HD11	2.00	0.43
1:B:684:LEU:HD11	1:B:691:ILE:HG12	2.01	0.43
1:A:714:GLU:HG3	1:A:715:TYR:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:384:ASP:N	1:B:384:ASP:OD1	2.50	0.43
1:A:685:PRO:HD2	1:A:699:ILE:HG23	2.01	0.42
1:B:649:ASP:OD2	1:B:652:THR:HG22	2.19	0.42
1:A:712:ARG:HH11	3:A:1011:GOL:H12	1.84	0.42
1:A:432:HIS:NE2	2:A:1005:SO4:O3	2.42	0.42
1:A:509:LYS:HE3	1:A:527:GLU:O	2.19	0.42
1:B:609:SER:O	1:B:785:SER:HA	2.19	0.42
1:A:795:GLU:OE1	1:A:810:ARG:NH1	2.52	0.42
1:B:548:HIS:NE2	1:B:597:PRO:HD2	2.35	0.42
1:A:506:TRP:CE3	1:A:537:ARG:HD2	2.55	0.41
1:A:541:ARG:HE	1:A:640:GLU:CD	2.28	0.41
1:B:320:LEU:HD12	1:B:320:LEU:HA	1.84	0.41
1:B:432:HIS:CD2	1:B:566:THR:HG23	2.55	0.41
1:A:681:LEU:C	1:A:755:ILE:HD12	2.46	0.41
1:A:538:MET:HE2	1:A:538:MET:HB3	1.97	0.41
1:A:710:LEU:O	1:A:718:LEU:HG	2.21	0.41
1:B:442:HIS:HE2	3:B:1010:GOL:C2	2.31	0.41
1:B:667:LYS:HE2	1:B:667:LYS:HB2	1.79	0.41
1:A:640:GLU:HG3	1:A:680:LEU:HD23	2.03	0.40
1:A:676:ARG:NH2	1:A:840:ASP:OD1	2.47	0.40
1:B:333:THR:HG21	1:B:551:PRO:HG3	2.03	0.40
1:B:366:LEU:HD22	1:B:420:LEU:HD11	2.03	0.40
1:B:607:LEU:HD11	1:B:790:LEU:HB2	2.04	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:B:1270:HOH:O	5:B:1273:HOH:O[2_556]	2.05	0.15

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	568/640 (89%)	545 (96%)	23 (4%)	0	100	100
1	B	569/640 (89%)	551 (97%)	18 (3%)	0	100	100
All	All	1137/1280 (89%)	1096 (96%)	41 (4%)	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	501/554 (90%)	501 (100%)	0	100	100
1	B	499/554 (90%)	498 (100%)	1 (0%)	87	92
All	All	1000/1108 (90%)	999 (100%)	1 (0%)	88	92

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	320	LEU

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	642	GLN
1	A	847	GLN
1	A	902	HIS
1	B	424	HIS
1	B	501	HIS
1	B	642	GLN
1	B	719	HIS
1	B	807	GLN

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 ⓘ

26 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	$\# Z > 2$
2	SO4	B	1008	-	4,4,4	0.22	0	6,6,6	0.10	0
3	GOL	B	1013	-	5,5,5	1.30	1 (20%)	5,5,5	0.75	0
2	SO4	B	1009	-	4,4,4	0.22	0	6,6,6	0.10	0
2	SO4	B	1006	-	4,4,4	0.26	0	6,6,6	0.05	0
2	SO4	B	1004	-	4,4,4	0.25	0	6,6,6	0.14	0
3	GOL	B	1011	-	5,5,5	0.94	0	5,5,5	1.03	0
2	SO4	B	1001	-	4,4,4	0.22	0	6,6,6	0.15	0
3	GOL	A	1009	-	5,5,5	0.70	0	5,5,5	1.16	1 (20%)
2	SO4	A	1006	-	4,4,4	0.23	0	6,6,6	0.08	0
3	GOL	A	1010	-	5,5,5	0.81	0	5,5,5	1.14	1 (20%)
2	SO4	A	1008	-	4,4,4	0.23	0	6,6,6	0.09	0
2	SO4	B	1005	-	4,4,4	0.23	0	6,6,6	0.09	0
4	DTT	B	1014	1	7,7,7	0.57	0	4,8,8	0.75	0
3	GOL	A	1011	-	5,5,5	0.87	0	5,5,5	1.14	0
3	GOL	B	1010	-	5,5,5	1.24	1 (20%)	5,5,5	1.08	0
2	SO4	A	1007	-	4,4,4	0.23	0	6,6,6	0.06	0
2	SO4	B	1003	-	4,4,4	0.19	0	6,6,6	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	1012	-	5,5,5	1.00	0	5,5,5	1.19	1 (20%)
3	GOL	B	1012	-	5,5,5	0.95	0	5,5,5	1.07	0
2	SO4	A	1001	-	4,4,4	0.21	0	6,6,6	0.33	0
2	SO4	A	1002	-	4,4,4	0.23	0	6,6,6	0.14	0
2	SO4	B	1007	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	A	1005	-	4,4,4	0.23	0	6,6,6	0.06	0
2	SO4	A	1004	-	4,4,4	0.24	0	6,6,6	0.06	0
2	SO4	B	1002	-	4,4,4	0.24	0	6,6,6	0.18	0
2	SO4	A	1003	-	4,4,4	0.22	0	6,6,6	0.14	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	1013	-	-	0/4/4/4	-
3	GOL	B	1011	-	-	4/4/4/4	-
4	DTT	B	1014	1	-	6/8/8/8	-
3	GOL	A	1011	-	-	0/4/4/4	-
3	GOL	B	1010	-	-	2/4/4/4	-
3	GOL	B	1012	-	-	4/4/4/4	-
3	GOL	A	1009	-	-	0/4/4/4	-
3	GOL	A	1012	-	-	0/4/4/4	-
3	GOL	A	1010	-	-	4/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1010	GOL	O2-C2	-2.61	1.35	1.43
3	B	1013	GOL	O2-C2	-2.54	1.36	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1010	GOL	C3-C2-C1	-2.11	104.04	111.80
3	A	1009	GOL	C3-C2-C1	-2.10	104.08	111.80
3	A	1012	GOL	C3-C2-C1	-2.04	104.31	111.80

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1010	GOL	O1-C1-C2-C3
3	A	1010	GOL	C1-C2-C3-O3
3	B	1011	GOL	O1-C1-C2-C3
3	B	1011	GOL	C1-C2-C3-O3
3	B	1011	GOL	O2-C2-C3-O3
3	B	1012	GOL	C1-C2-C3-O3
4	B	1014	DTT	C1-C2-C3-O3
4	B	1014	DTT	C1-C2-C3-C4
4	B	1014	DTT	O2-C2-C3-O3
4	B	1014	DTT	O2-C2-C3-C4
4	B	1014	DTT	C2-C3-C4-S4
4	B	1014	DTT	O3-C3-C4-S4
3	A	1010	GOL	O2-C2-C3-O3
3	B	1011	GOL	O1-C1-C2-O2
3	B	1012	GOL	O1-C1-C2-C3
3	B	1012	GOL	O2-C2-C3-O3
3	A	1010	GOL	O1-C1-C2-O2
3	B	1010	GOL	O1-C1-C2-O2
3	B	1012	GOL	O1-C1-C2-O2
3	B	1010	GOL	O1-C1-C2-C3

There are no ring outliers.

11 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1013	GOL	3	0
2	B	1001	SO4	1	0
3	A	1009	GOL	4	0
3	A	1010	GOL	2	0
2	B	1005	SO4	2	0
4	B	1014	DTT	1	0
3	A	1011	GOL	3	0
3	B	1010	GOL	4	0
3	A	1012	GOL	1	0
2	A	1005	SO4	1	0
2	A	1003	SO4	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	580/640 (90%)	0.03	25 (4%) 40 39	23, 37, 78, 95	0
1	B	579/640 (90%)	0.33	38 (6%) 24 23	23, 46, 85, 104	0
All	All	1159/1280 (90%)	0.18	63 (5%) 31 30	23, 41, 83, 104	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	925	GLY	4.3
1	A	689	GLY	4.0
1	A	597	PRO	4.0
1	B	405	VAL	3.8
1	A	598	GLY	3.7
1	A	691	ILE	3.7
1	B	917	LEU	3.4
1	A	919	PRO	3.3
1	B	596	LEU	3.3
1	B	409	LEU	3.2
1	B	832	LEU	3.2
1	A	830	PRO	3.1
1	A	596	LEU	3.0
1	B	476	GLY	3.0
1	B	315	ARG	3.0
1	B	568	THR	3.0
1	A	927	ILE	2.9
1	A	315	ARG	2.9
1	A	515	ILE	2.9
1	B	830	PRO	2.9
1	B	673	TRP	2.9
1	B	746	GLY	2.8
1	B	580	TYR	2.8
1	B	468	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	576	PRO	2.6
1	B	597	PRO	2.6
1	B	523	ASP	2.6
1	B	929	LEU	2.5
1	B	501	HIS	2.5
1	B	406	GLU	2.4
1	B	828	THR	2.4
1	B	499	LEU	2.4
1	A	526	PHE	2.4
1	B	411	ILE	2.4
1	A	616	GLY	2.4
1	B	515	ILE	2.4
1	B	573	TYR	2.3
1	B	616	GLY	2.3
1	A	586	THR	2.3
1	A	599	GLY	2.3
1	B	927	ILE	2.3
1	B	318	LEU	2.3
1	B	410	GLY	2.3
1	B	599	GLY	2.3
1	B	795	GLU	2.2
1	B	436	VAL	2.2
1	A	520	VAL	2.2
1	A	874	THR	2.2
1	A	695	GLY	2.2
1	A	409	LEU	2.2
1	A	519	TRP	2.2
1	B	379	ASP	2.2
1	B	887	VAL	2.1
1	B	598	GLY	2.1
1	A	514	LEU	2.1
1	B	586	THR	2.1
1	A	411	ILE	2.1
1	A	405	VAL	2.1
1	B	424	HIS	2.1
1	B	695	GLY	2.1
1	B	615	ALA	2.1
1	A	588	THR	2.1
1	A	696	GLY	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
2	SO4	B	1009	5/5	0.52	0.17	161,161,162,162	0
3	GOL	A	1012	6/6	0.57	0.23	94,99,105,109	0
2	SO4	B	1008	5/5	0.63	0.21	170,172,173,174	0
2	SO4	B	1003	5/5	0.69	0.17	71,71,88,88	0
2	SO4	A	1007	5/5	0.71	0.15	135,135,137,138	0
3	GOL	B	1012	6/6	0.74	0.16	73,80,83,85	0
2	SO4	B	1006	5/5	0.75	0.12	89,91,93,93	0
3	GOL	B	1010	6/6	0.77	0.22	56,70,76,77	0
2	SO4	B	1007	5/5	0.77	0.16	127,128,130,131	0
3	GOL	B	1013	6/6	0.77	0.20	76,79,87,92	0
3	GOL	A	1010	6/6	0.79	0.18	72,73,78,78	0
2	SO4	B	1004	5/5	0.81	0.12	83,84,85,88	0
3	GOL	A	1011	6/6	0.81	0.19	87,94,95,96	0
2	SO4	A	1005	5/5	0.83	0.16	108,109,112,113	0
3	GOL	B	1011	6/6	0.83	0.12	65,67,69,71	0
2	SO4	B	1005	5/5	0.83	0.11	95,96,97,101	0
2	SO4	A	1006	5/5	0.83	0.14	117,119,120,123	0
4	DTT	B	1014	8/8	0.84	0.26	53,114,136,140	0
3	GOL	A	1009	6/6	0.87	0.13	47,53,55,60	0
2	SO4	A	1008	5/5	0.87	0.14	123,125,126,129	0
2	SO4	A	1004	5/5	0.87	0.09	83,84,90,92	0
2	SO4	A	1001	5/5	0.90	0.12	60,60,68,69	0
2	SO4	A	1003	5/5	0.91	0.08	65,68,79,81	0
2	SO4	B	1001	5/5	0.93	0.08	54,55,60,61	0
2	SO4	B	1002	5/5	0.94	0.07	56,60,64,66	0
2	SO4	A	1002	5/5	0.95	0.06	59,67,67,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.