



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:02 PM UTC

PDB ID : 4DDH / pdb_00004ddh
Title : Pantothenate synthetase in complex with 6-methoxy-1-benzofuran-3-yl acetic acid
Authors : Silvestre, H.L.
Deposited on : 2012-01-18
Resolution : 2.07 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

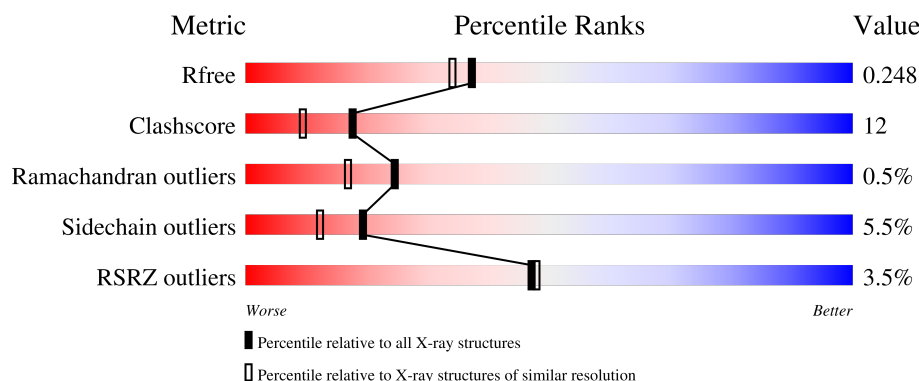
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

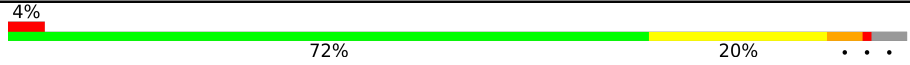
The reported resolution of this entry is 2.07 Å.

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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	301	
1	B	301	

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	EOH	A	401	-	-	X	-
5	GOL	B	404	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4786 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.

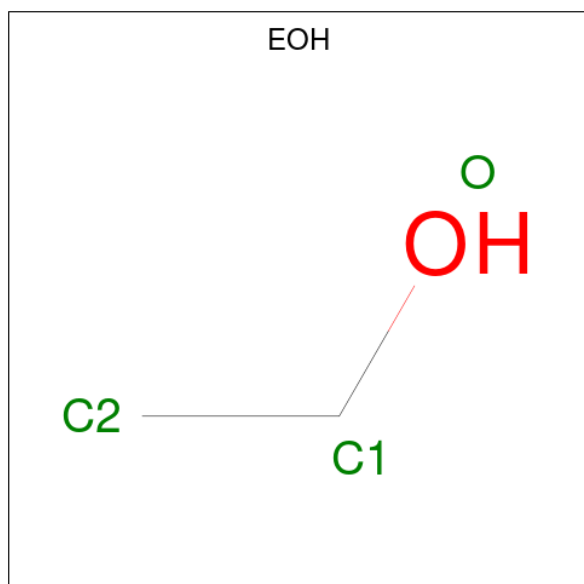
- Molecule 1 is a protein called Pantothenate synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	7	0
			2165	1369	390	400	6			
1	B	279	Total	C	N	O	S	0	9	0
			2116	1340	383	387	6			

There are 4 discrepancies between the modelled and reference sequences:

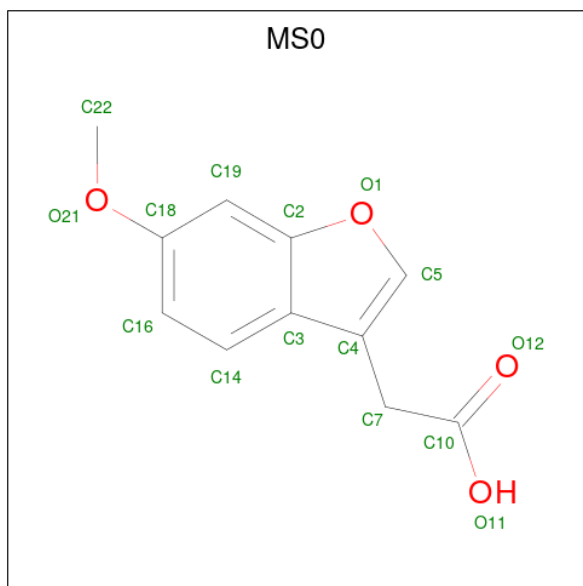
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	THR	engineered mutation	UNP P0A5R0
A	77	GLY	GLU	engineered mutation	UNP P0A5R0
B	2	ALA	THR	engineered mutation	UNP P0A5R0
B	77	GLY	GLU	engineered mutation	UNP P0A5R0

- Molecule 2 is ETHANOL (CCD ID: EOH) (formula: C₂H₆O).



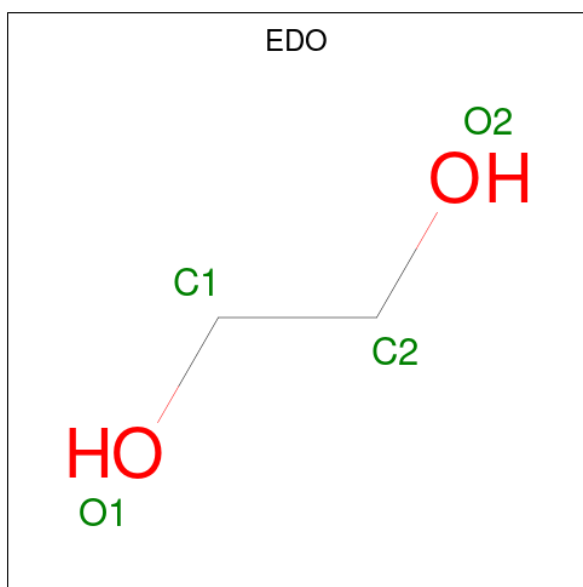
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			3	2	1		
2	A	1	Total	C	O	0	0
			3	2	1		
2	B	1	Total	C	O	0	0
			3	2	1		

- Molecule 3 is (6-methoxy-1-benzofuran-3-yl)acetic acid (CCD ID: MS0) (formula: $C_{11}H_{10}O_4$).



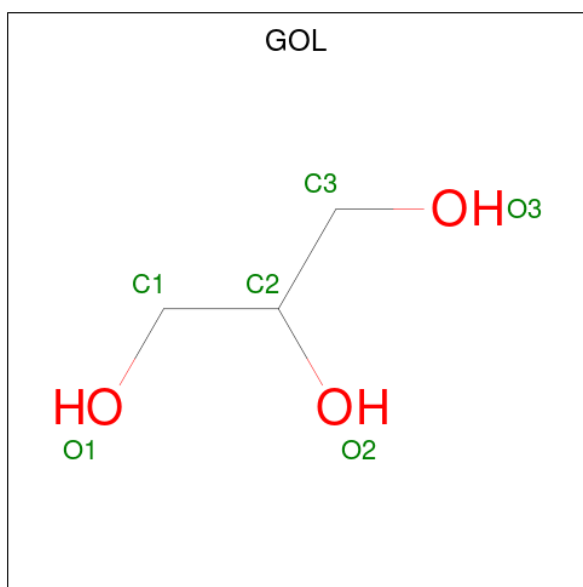
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			15	11	4		
3	B	1	Total	C	O	0	0
			15	11	4		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

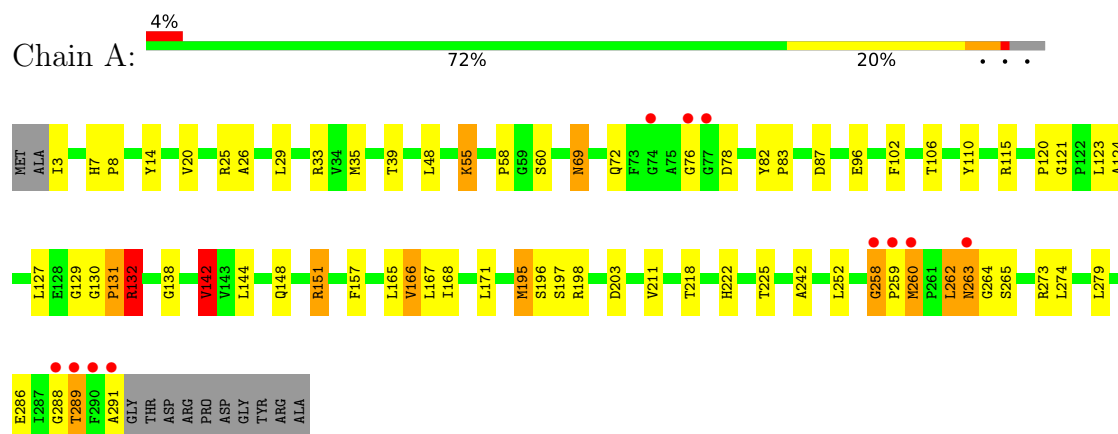
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	228	Total	O	0	0
			228	228		
6	B	202	Total	O	0	0
			202	202		

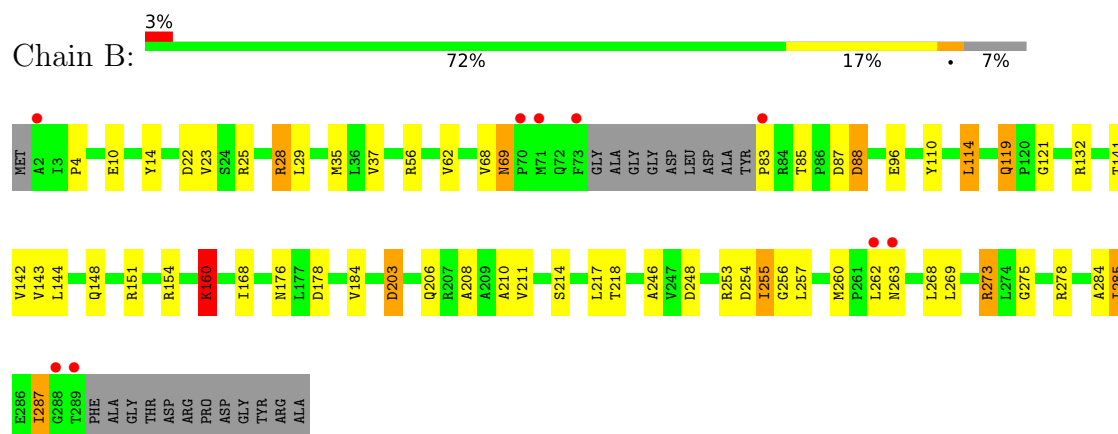
3 Residue-property plots

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: Pantothenate synthetase



• Molecule 1: Pantothenate synthetase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.58Å 70.93Å 82.01Å 90.00° 99.40° 90.00°	Depositor
Resolution (Å)	53.38 – 2.07 53.38 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.3 (53.38-2.07) 99.3 (53.38-2.07)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.68 (at 2.06Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.187 , 0.250 0.186 , 0.248	Depositor DCC
R_{free} test set	1702 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	22.8	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4786	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.61% 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: EDO, EOH, GOL, MSO

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	1.40	7/2207 (0.3%)	1.36	19/3014 (0.6%)
1	B	1.33	4/2157 (0.2%)	1.27	13/2946 (0.4%)
All	All	1.37	11/4364 (0.3%)	1.32	32/5960 (0.5%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	37	VAL	CA-CB	6.11	1.59	1.54
1	A	171	LEU	C-O	5.99	1.31	1.24
1	A	142	VAL	CA-CB	-5.99	1.46	1.54
1	B	151	ARG	N-CA	5.92	1.50	1.46
1	A	39	THR	CA-CB	5.67	1.64	1.53
1	B	210	ALA	N-CA	5.67	1.53	1.46
1	B	184	VAL	CA-C	5.59	1.57	1.52
1	A	165	LEU	C-O	5.55	1.30	1.24
1	A	166	VAL	CA-C	5.48	1.59	1.52
1	A	131	PRO	N-CA	-5.28	1.44	1.47
1	A	106	THR	C-O	5.02	1.29	1.24

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	121	GLY	CA-C-N	11.29	131.71	119.28
1	B	121	GLY	C-N-CA	11.29	131.71	119.28
1	A	121	GLY	CA-C-N	9.26	129.01	119.56
1	A	121	GLY	C-N-CA	9.26	129.01	119.56
1	A	69	ASN	CA-C-N	-7.18	112.40	119.87
1	A	69	ASN	C-N-CA	-7.18	112.40	119.87
1	A	130	GLY	CA-C-N	6.75	128.63	120.94
1	A	130	GLY	C-N-CA	6.75	128.63	120.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	141	THR	N-CA-C	-6.61	103.34	111.40
1	B	37	VAL	CA-C-N	-6.17	112.12	119.84
1	B	37	VAL	C-N-CA	-6.17	112.12	119.84
1	A	242	ALA	CA-C-N	6.07	127.43	119.84
1	A	242	ALA	C-N-CA	6.07	127.43	119.84
1	B	203	ASP	CA-C-N	-5.86	112.46	118.85
1	B	203	ASP	C-N-CA	-5.86	112.46	118.85
1	A	211	VAL	N-CA-C	-5.61	105.71	113.00
1	A	151	ARG	CA-C-N	-5.56	115.02	120.52
1	A	151	ARG	C-N-CA	-5.56	115.02	120.52
1	A	258	GLY	CA-C-N	5.32	126.49	119.84
1	A	258	GLY	C-N-CA	5.32	126.49	119.84
1	A	132	ARG	CA-C-N	-5.29	114.37	119.87
1	A	132	ARG	C-N-CA	-5.29	114.37	119.87
1	A	289	THR	N-CA-CB	5.24	119.35	110.49
1	B	160	LYS	N-CA-CB	5.20	117.69	109.94
1	A	127	LEU	CB-CA-C	-5.20	110.16	117.23
1	B	62	VAL	N-CA-C	5.19	115.57	107.99
1	B	69	ASN	CA-C-N	-5.18	114.48	119.87
1	B	69	ASN	C-N-CA	-5.18	114.48	119.87
1	A	260	MET	CA-C-N	-5.03	115.05	120.03
1	A	260	MET	C-N-CA	-5.03	115.05	120.03
1	B	132	ARG	CA-C-N	5.03	124.74	119.82
1	B	132	ARG	C-N-CA	5.03	124.74	119.82

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	2165	0	2207	59	0
1	B	2116	0	2177	49	0
2	A	6	0	12	3	0
2	B	3	0	6	0	0
3	A	15	0	9	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	15	0	9	1	0
4	A	12	0	18	5	0
4	B	12	0	18	3	0
5	B	12	0	16	5	0
6	A	228	0	0	14	0
6	B	202	0	0	9	0
All	All	4786	0	4472	110	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 (110) 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:273[A]:ARG:HD2	1:B:275:GLY:O	1.54	1.07
1:B:4:PRO:HB3	4:B:407:EDO:H12	1.41	1.03
1:A:263:ASN:CG	1:A:264:GLY:H	1.70	0.97
1:A:197[A]:SER:OG	1:A:198[A]:ARG:HD3	1.68	0.92
1:A:69:ASN:ND2	1:A:142:VAL:HG21	1.86	0.90
1:A:195:MET:HE2	6:A:725:HOH:O	1.69	0.90
1:A:69:ASN:HD22	1:A:72:GLN:HE21	1.22	0.87
1:A:69:ASN:CG	1:A:142:VAL:HG21	2.01	0.86
1:B:246:ALA:HB2	5:B:404:GOL:O1	1.78	0.84
1:B:273[A]:ARG:CD	1:B:275:GLY:O	2.27	0.83
1:B:218[B]:THR:HG21	6:B:506:HOH:O	1.76	0.82
1:B:28:ARG:HG3	1:B:28:ARG:HH11	1.44	0.82
1:A:69:ASN:ND2	1:A:142:VAL:CG2	2.42	0.81
1:A:263:ASN:CG	1:A:264:GLY:N	2.38	0.80
1:A:14:TYR:HB2	1:A:20[B]:VAL:HG23	1.66	0.78
1:B:83:PRO:HG2	6:B:676:HOH:O	1.84	0.77
1:B:22:ASP:OD1	1:B:25[A]:ARG:NH1	2.16	0.73
1:A:286:GLU:OE1	6:A:650:HOH:O	2.07	0.72
1:A:115:ARG:O	2:A:401:EOH:H22	1.90	0.71
1:A:263:ASN:ND2	1:A:265:SER:H	1.87	0.71
1:A:274:LEU:HD13	1:A:279:LEU:HD12	1.72	0.71
1:A:197[A]:SER:OG	1:A:198[A]:ARG:CD	2.39	0.71
1:A:258:GLY:HA3	6:A:726:HOH:O	1.90	0.70
1:A:110:TYR:HD1	4:A:404:EDO:H21	1.58	0.69
1:A:263:ASN:ND2	6:A:618:HOH:O	2.19	0.69
1:A:25:ARG:NH1	6:A:517:HOH:O	2.28	0.67
1:B:246:ALA:CB	5:B:404:GOL:O1	2.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198[B]:ARG:HD2	6:A:640:HOH:O	1.95	0.66
2:A:401:EOH:H21	1:B:119:GLN:HG2	1.78	0.66
1:B:28:ARG:HH11	1:B:28:ARG:CG	2.09	0.66
1:A:198[A]:ARG:HG2	1:A:198[A]:ARG:HH21	1.62	0.65
1:B:214:SER:O	1:B:218[B]:THR:HG22	1.96	0.65
1:A:258:GLY:CA	6:A:726:HOH:O	2.45	0.64
1:B:85:THR:HB	1:B:88:ASP:CG	2.22	0.64
1:B:248:ASP:HB3	6:B:531:HOH:O	1.97	0.63
1:A:33:ARG:NH2	1:A:58:PRO:O	2.32	0.62
1:A:3:ILE:HG21	1:A:26:ALA:HB2	1.83	0.60
1:B:10:GLU:HB2	6:B:631:HOH:O	2.03	0.59
1:B:143:VAL:HG11	1:B:168[A]:ILE:HD12	1.84	0.58
1:B:96:GLU:HB3	6:B:530:HOH:O	2.03	0.58
1:A:196:SER:OG	1:A:198[B]:ARG:HB2	2.04	0.57
1:A:291:ALA:HB1	6:A:655:HOH:O	2.04	0.56
1:A:33:ARG:HH22	1:A:58:PRO:HG2	1.70	0.56
1:A:218:THR:O	1:A:222:HIS:HD2	1.89	0.55
1:B:269:LEU:N	1:B:269:LEU:HD12	2.21	0.55
1:A:262:LEU:HB2	4:A:406:EDO:H22	1.90	0.54
1:B:203:ASP:OD1	1:B:203:ASP:C	2.51	0.52
1:B:88:ASP:OD2	1:B:88:ASP:N	2.30	0.52
1:B:35:MET:SD	1:B:154:ARG:HB2	2.50	0.52
1:A:72:GLN:HE22	4:A:405:EDO:C2	2.23	0.52
2:A:402:EOH:C2	6:A:719:HOH:O	2.59	0.52
1:B:69:ASN:CG	1:B:142[B]:VAL:HG21	2.35	0.52
1:A:198[A]:ARG:HG2	1:A:198[A]:ARG:NH2	2.23	0.51
1:B:85:THR:HB	1:B:88:ASP:OD1	2.10	0.51
1:A:110:TYR:CD1	4:A:404:EDO:H21	2.41	0.51
1:A:20[B]:VAL:HG21	1:A:102:PHE:HB2	1.94	0.50
1:B:176:ASN:HD22	4:B:406:EDO:H22	1.77	0.49
1:A:138:GLY:O	1:A:142:VAL:HG23	2.13	0.49
1:B:206:GLN:HG2	6:B:701:HOH:O	2.13	0.48
1:A:151:ARG:HD2	1:B:178[B]:ASP:OD2	2.13	0.48
1:A:273:ARG:HD2	6:A:680:HOH:O	2.13	0.48
1:A:131:PRO:HG2	1:A:132:ARG:NH2	2.29	0.47
1:A:124:ALA:O	1:A:129:GLY:HA3	2.15	0.47
1:A:69:ASN:CG	1:A:142:VAL:CG2	2.81	0.47
1:A:35:MET:HG2	1:A:60:SER:HB2	1.96	0.46
1:A:252:LEU:HG	1:A:262:LEU:HD23	1.97	0.46
1:B:28:ARG:CG	1:B:28:ARG:NH1	2.78	0.46
1:A:72:GLN:HE22	4:A:405:EDO:H21	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:PHE:CZ	1:A:168:ILE:HD13	2.52	0.45
1:B:4:PRO:CB	4:B:407:EDO:H12	2.28	0.45
1:B:114:LEU:HD22	1:B:114:LEU:HA	1.77	0.45
1:B:217:LEU:HD23	1:B:268:LEU:HD23	1.99	0.45
1:A:120:PRO:HB2	1:A:124:ALA:CB	2.46	0.45
1:A:263:ASN:ND2	1:A:264:GLY:N	2.64	0.45
1:B:160:LYS:HE3	6:B:615:HOH:O	2.16	0.45
1:A:262:LEU:HD12	1:A:263:ASN:N	2.33	0.44
1:B:246:ALA:HB3	1:B:273[B]:ARG:HG2	1.99	0.44
1:A:78:ASP:CG	6:A:534:HOH:O	2.60	0.44
1:B:56:ARG:NH1	6:B:669:HOH:O	2.51	0.44
1:B:256:GLY:O	1:B:257:LEU:HB2	2.18	0.44
1:A:87:ASP:HB3	6:A:653:HOH:O	2.17	0.44
1:B:28:ARG:HG3	1:B:28:ARG:NH1	2.23	0.44
1:A:203:ASP:OD1	1:A:203:ASP:C	2.61	0.43
1:B:110:TYR:OH	1:B:142[B]:VAL:CG2	2.67	0.43
1:B:273[B]:ARG:O	5:B:404:GOL:H31	2.18	0.43
1:A:225:THR:HA	1:A:288:GLY:HA3	2.01	0.42
1:B:14:TYR:CZ	1:B:23:VAL:HG21	2.54	0.42
1:A:144:LEU:O	1:A:148:GLN:HG2	2.19	0.42
1:A:166:VAL:HG13	6:A:687:HOH:O	2.18	0.42
1:B:284:ALA:O	1:B:285:ILE:HG12	2.20	0.42
1:B:246:ALA:CB	5:B:404:GOL:HO1	2.33	0.42
1:B:253:ARG:HB3	1:B:257:LEU:HA	2.02	0.41
1:A:274:LEU:CD1	1:A:279:LEU:HD12	2.47	0.41
1:B:208:ALA:O	1:B:211[A]:VAL:HG12	2.20	0.41
1:B:262:LEU:HD23	1:B:262:LEU:HA	1.95	0.41
1:A:55:LYS:HD2	6:A:654:HOH:O	2.20	0.41
1:A:263:ASN:HD21	1:A:265:SER:H	1.64	0.41
1:A:123:LEU:HD23	1:A:167:LEU:HG	2.03	0.41
1:A:48:LEU:HD22	1:A:96:GLU:HG3	2.03	0.41
1:B:144:LEU:O	1:B:148:GLN:HG2	2.20	0.41
1:A:33:ARG:O	1:A:60:SER:HA	2.20	0.41
1:B:255:ILE:HD12	1:B:255:ILE:HA	1.77	0.41
3:B:401:MS0:H22A	3:B:401:MS0:H19	1.80	0.41
5:B:405:GOL:H2	6:B:516:HOH:O	2.20	0.41
1:B:248:ASP:OD1	1:B:273[B]:ARG:NH2	2.54	0.41
1:A:7:HIS:HA	1:A:8:PRO:HD2	1.99	0.40
1:A:82:TYR:CG	1:A:83:PRO:HD2	2.57	0.40
1:B:260:MET:HE2	1:B:287:ILE:HG12	2.03	0.40
1:B:110:TYR:OH	1:B:142[B]:VAL:HG22	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:ILE:HA	1:B:287:ILE:HD13	1.72	0.40

There are no symmetry-related clashes.

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	292/301 (97%)	277 (95%)	12 (4%)	3 (1%)	12	5
1	B	284/301 (94%)	273 (96%)	11 (4%)	0	100	100
All	All	576/602 (96%)	550 (96%)	23 (4%)	3 (0%)	24	17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	76	GLY
1	A	289	THR
1	A	259	PRO

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	220/223 (99%)	212 (96%)	8 (4%)	31	25
1	B	216/223 (97%)	200 (93%)	16 (7%)	13	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	436/446 (98%)	412 (94%)	24 (6%)	19	12

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	LEU
1	A	55	LYS
1	A	132	ARG
1	A	142	VAL
1	A	195	MET
1	A	260	MET
1	A	262	LEU
1	A	263	ASN
1	B	28	ARG
1	B	29	LEU
1	B	68	VAL
1	B	87	ASP
1	B	88	ASP
1	B	114	LEU
1	B	119	GLN
1	B	160	LYS
1	B	254	ASP
1	B	255	ILE
1	B	263	ASN
1	B	273[A]	ARG
1	B	273[B]	ARG
1	B	278	ARG
1	B	285	ILE
1	B	287	ILE

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	69	ASN
1	A	72	GLN
1	A	148	GLN
1	A	222	HIS
1	A	263	ASN
1	B	7	HIS
1	B	119	GLN
1	B	148	GLN

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Mol	Chain	Res	Type
1	B	170	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 ⓘ

13 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	$\# Z > 2$
5	GOL	B	405	-	5,5,5	0.32	0	5,5,5	0.73	0
4	EDO	A	404	-	3,3,3	0.24	0	2,2,2	0.78	0
4	EDO	A	406	-	3,3,3	0.52	0	2,2,2	0.05	0
2	EOH	A	401	-	2,2,2	0.47	0	1,1,1	0.07	0
4	EDO	A	405	-	3,3,3	0.39	0	2,2,2	0.49	0
2	EOH	B	403	-	2,2,2	0.52	0	1,1,1	0.22	0
2	EOH	A	402	-	2,2,2	0.64	0	1,1,1	0.23	0
4	EDO	B	402	-	3,3,3	0.32	0	2,2,2	1.04	0
4	EDO	B	406	-	3,3,3	0.45	0	2,2,2	0.44	0
5	GOL	B	404	-	5,5,5	0.55	0	5,5,5	0.91	0
3	MS0	A	403	-	16,16,16	2.49	7 (43%)	19,22,22	3.11	6 (31%)
4	EDO	B	407	-	3,3,3	0.39	0	2,2,2	0.59	0
3	MS0	B	401	-	16,16,16	2.66	7 (43%)	19,22,22	2.54	8 (42%)

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
5	GOL	B	405	-	-	4/4/4/4	-
4	EDO	A	404	-	-	1/1/1/1	-
4	EDO	A	406	-	-	1/1/1/1	-
4	EDO	A	405	-	-	0/1/1/1	-
4	EDO	B	402	-	-	0/1/1/1	-
4	EDO	B	406	-	-	0/1/1/1	-
5	GOL	B	404	-	-	0/4/4/4	-
3	MS0	A	403	-	-	0/6/6/6	0/2/2/2
4	EDO	B	407	-	-	0/1/1/1	-
3	MS0	B	401	-	-	2/6/6/6	0/2/2/2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	403	MS0	C7-C4	5.75	1.57	1.50
3	B	401	MS0	C3-C4	-5.73	1.34	1.44
3	B	401	MS0	C7-C4	5.61	1.57	1.50
3	A	403	MS0	C3-C4	-4.19	1.37	1.44
3	A	403	MS0	C7-C10	-3.03	1.46	1.51
3	A	403	MS0	C3-C2	-2.95	1.35	1.39
3	B	401	MS0	C14-C3	-2.78	1.35	1.39
3	A	403	MS0	C14-C3	-2.70	1.35	1.39
3	B	401	MS0	O1-C2	2.62	1.41	1.37
3	A	403	MS0	O1-C2	2.61	1.41	1.37
3	B	401	MS0	O1-C5	-2.47	1.31	1.38
3	B	401	MS0	C3-C2	-2.44	1.36	1.39
3	A	403	MS0	C19-C18	2.03	1.42	1.39
3	B	401	MS0	C16-C14	2.01	1.42	1.38

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	403	MS0	O1-C5-C4	-9.12	106.92	112.91
3	A	403	MS0	C2-O1-C5	5.35	109.74	105.19
3	B	401	MS0	C22-O21-C18	-4.95	106.87	117.50
3	A	403	MS0	O1-C2-C3	-4.75	105.51	110.53
3	B	401	MS0	C7-C4-C3	4.35	132.10	126.43
3	A	403	MS0	O1-C2-C19	3.98	131.58	125.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	MS0	O1-C5-C4	-3.96	110.31	112.91
3	B	401	MS0	C10-C7-C4	3.80	120.76	114.93
3	A	403	MS0	C10-C7-C4	3.74	120.66	114.93
3	B	401	MS0	O1-C2-C19	3.53	130.82	125.01
3	B	401	MS0	C19-C2-C3	-3.30	120.93	124.70
3	B	401	MS0	C14-C16-C18	-2.83	116.50	119.73
3	A	403	MS0	C7-C4-C3	2.79	130.06	126.43
3	B	401	MS0	O1-C2-C3	-2.16	108.24	110.53

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	401	MS0	C3-C4-C7-C10
3	B	401	MS0	C5-C4-C7-C10
5	B	405	GOL	O1-C1-C2-C3
5	B	405	GOL	C1-C2-C3-O3
4	A	404	EDO	O1-C1-C2-O2
5	B	405	GOL	O2-C2-C3-O3
5	B	405	GOL	O1-C1-C2-O2
4	A	406	EDO	O1-C1-C2-O2

There are no ring outliers.

10 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	405	GOL	1	0
4	A	404	EDO	2	0
4	A	406	EDO	1	0
2	A	401	EOH	2	0
4	A	405	EDO	2	0
2	A	402	EOH	1	0
4	B	406	EDO	1	0
5	B	404	GOL	4	0
4	B	407	EDO	2	0
3	B	401	MS0	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	289/301 (96%)	-0.00	11 (3%) 44 44	11, 22, 42, 57	8 (2%)
1	B	279/301 (92%)	0.01	9 (3%) 50 50	7, 23, 47, 68	9 (3%)
All	All	568/602 (94%)	0.00	20 (3%) 47 48	7, 23, 43, 68	17 (2%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	76	GLY	4.6
1	B	289	THR	3.4
1	A	291	ALA	3.4
1	A	290	PHE	3.1
1	B	71	MET	3.0
1	B	73	PHE	2.9
1	B	288	GLY	2.9
1	A	289	THR	2.8
1	A	288	GLY	2.8
1	B	83	PRO	2.7
1	B	263	ASN	2.6
1	A	260	MET	2.5
1	B	2	ALA	2.5
1	A	258	GLY	2.4
1	A	74	GLY	2.4
1	A	263	ASN	2.1
1	B	70	PRO	2.1
1	B	262	LEU	2.0
1	A	77	GLY	2.0
1	A	259	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	B	407	4/4	0.74	0.13	59,60,60,60	0
5	GOL	B	404	6/6	0.77	0.16	44,46,48,51	0
2	EOH	A	402	3/3	0.78	0.18	24,24,27,28	0
2	EOH	B	403	3/3	0.78	0.17	43,43,44,45	0
5	GOL	B	405	6/6	0.79	0.16	54,58,59,61	0
3	MS0	B	401	15/15	0.83	0.13	29,39,45,46	0
2	EOH	A	401	3/3	0.85	0.16	41,41,44,44	0
4	EDO	A	405	4/4	0.88	0.10	40,40,41,41	0
4	EDO	B	406	4/4	0.89	0.11	37,39,40,44	0
3	MS0	A	403	15/15	0.89	0.09	15,28,31,31	0
4	EDO	A	406	4/4	0.94	0.08	36,36,38,39	0
4	EDO	A	404	4/4	0.95	0.08	18,18,20,27	0
4	EDO	B	402	4/4	0.95	0.07	21,23,25,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.