



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 10:55 pm GMT

PDB ID : 2VC7
Title : STRUCTURAL BASIS FOR NATURAL LACTONASE AND PROMISCUOUS PHOSPHOTRIESTERASE ACTIVITIES
Authors : Elias, M.; Dupuy, J.; Merone, L.; Mandrich, L.; Moniot, S.; Rochu, D.; Lecomte, C.; Rossi, M.; Masson, P.; Manco, G.; Chabriere, E.
Deposited on : 2007-09-19
Resolution : 2.05 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

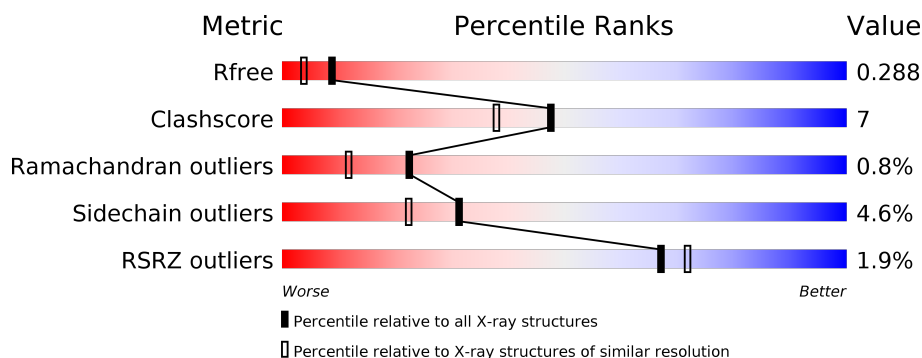
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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}	100719	1316 (2.04-2.04)
Clashscore	112137	1394 (2.04-2.04)
Ramachandran outliers	110173	1383 (2.04-2.04)
Sidechain outliers	110143	1383 (2.04-2.04)
RSRZ outliers	101464	1319 (2.04-2.04)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	314	<div> <div>2%</div> <div>84%</div> <div>14%</div> <div>•</div> </div>
1	B	314	<div> <div>2%</div> <div>86%</div> <div>12%</div> <div>••</div> </div>
1	C	314	<div> <div>2%</div> <div>81%</div> <div>16%</div> <div>•</div> </div>
1	D	314	<div> <div>2%</div> <div>86%</div> <div>12%</div> <div>•</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	A	1319	-	-	-	X
4	GOL	A	1321	-	-	-	X
4	GOL	A	1324	-	-	-	X
4	GOL	A	1325[A]	-	-	-	X
4	GOL	A	1325[B]	-	-	-	X
4	GOL	A	1328	-	-	-	X
4	GOL	A	1329	-	-	-	X
4	GOL	A	1333	-	-	-	X
4	GOL	B	1317	-	-	-	X
4	GOL	B	1321	-	-	-	X
4	GOL	B	1327	-	-	-	X
4	GOL	C	1319[A]	-	-	-	X
4	GOL	C	1324	-	-	-	X
4	GOL	C	1325	-	-	-	X
4	GOL	D	1317	-	-	-	X
4	GOL	D	1321	-	-	-	X
5	EDO	A	1318	-	-	-	X
5	EDO	A	1320	-	-	-	X
5	EDO	A	1322	-	-	-	X
5	EDO	A	1330	-	-	-	X
5	EDO	B	1318	-	-	-	X
5	EDO	B	1319	-	-	-	X
5	EDO	C	1323	-	-	-	X
5	EDO	D	1319	-	-	-	X
5	EDO	D	1328	-	-	-	X
6	HT5	A	1335	-	-	-	X
6	HT5	B	1328	-	-	-	X
6	HT5	D	1329	X	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 11719 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 ARYLDIALKYLPHOSPHATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	18	0
			2673	1701	464	500	8			
1	B	314	Total	C	N	O	S	0	13	0
			2641	1689	454	491	7			
1	C	314	Total	C	N	O	S	0	15	0
			2639	1685	452	494	8			
1	D	314	Total	C	N	O	S	0	15	0
			2640	1686	455	492	7			

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Fe	0	0
			1	1		
2	A	1	Total	Fe	0	0
			1	1		
2	D	1	Total	Fe	0	0
			1	1		
2	C	1	Total	Fe	0	0
			1	1		

- Molecule 3 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Co	0	0
			1	1		
3	A	1	Total	Co	0	0
			1	1		
3	D	1	Total	Co	0	0
			1	1		
3	C	1	Total	Co	0	0
			1	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	1
			12	6	6		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	1
			12	6	6		
4	C	1	Total	C	O	0	1
			12	6	6		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



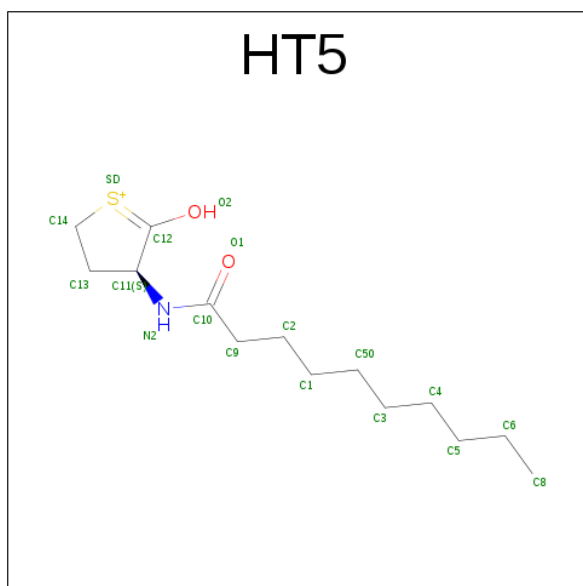
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is (4S)-4-(DECANOYLAMINO)-5-HYDROXY-3,4-DIHYDRO-2H-THIOPHEN IUM (three-letter code: HT5) (formula: C₁₄H₂₆NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	S	0	0
			18	14	1	2	1		
6	B	1	Total	C	N	O	S	0	0
			18	14	1	2	1		
6	C	1	Total	C	N	O	S	0	0
			18	14	1	2	1		
6	D	1	Total	C	N	O	S	0	0
			18	14	1	2	1		

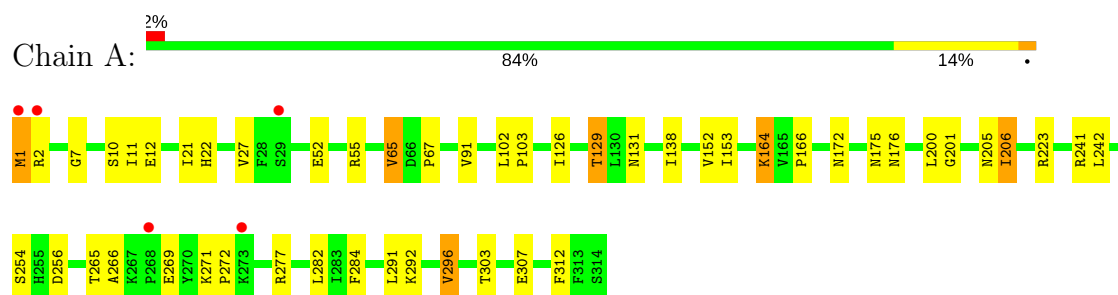
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	218	Total	O	0	0
			218	218		
7	B	162	Total	O	0	0
			162	162		
7	C	204	Total	O	0	0
			204	204		
7	D	176	Total	O	0	0
			176	176		

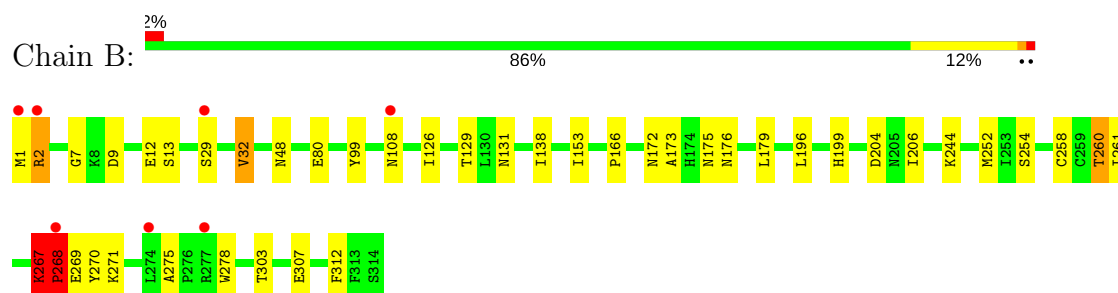
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 ($\text{RSRZ} > 2$). 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.

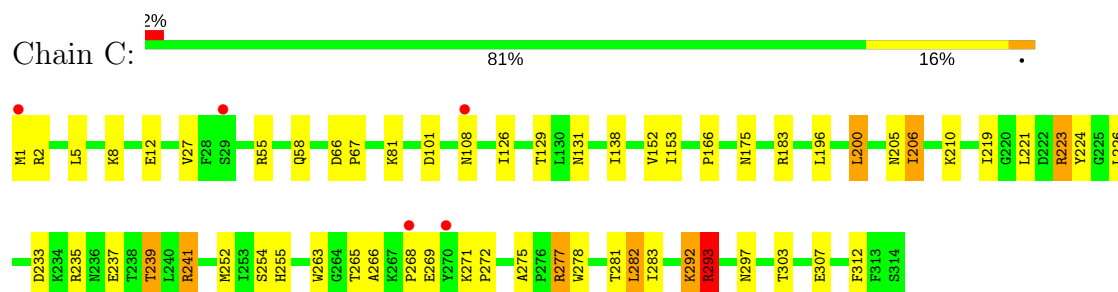
• Molecule 1: ARYLDIALKYLPHOSPHATASE



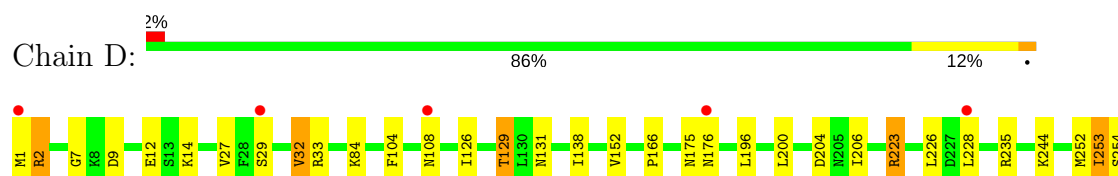
• Molecule 1: ARYLDIALKYLPHOSPHATASE

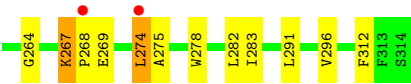


• Molecule 1: ARYLDIALKYLPHOSPHATASE



• Molecule 1: ARYLDIALKYLPHOSPHATASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.38Å 104.12Å 153.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	61.66 – 2.05 57.28 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.9 (61.66-2.05) 99.9 (57.28-2.05)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.237 , 0.287 0.238 , 0.288	Depositor DCC
R_{free} test set	4370 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.0	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	0.93	EDS
Total number of atoms	11719	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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: GOL, CO, EDO, HT5, FE, KCX

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	1.64	2/2711 (0.1%)	0.54	2/3655 (0.1%)
1	B	0.44	1/2683 (0.0%)	0.56	1/3620 (0.0%)
1	C	0.35	0/2677	0.53	1/3612 (0.0%)
1	D	0.39	0/2681	0.53	0/3614
All	All	0.89	3/10752 (0.0%)	0.54	4/14501 (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	1	2
1	C	1	0
All	All	2	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1[A]	MET	CG-SD	59.01	3.34	1.81
1	A	1[B]	MET	CG-SD	59.01	3.34	1.81
1	B	268	PRO	CG-CD	8.56	1.78	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1[A]	MET	CG-SD-CE	6.46	110.54	100.20
1	A	1[B]	MET	CG-SD-CE	6.46	110.54	100.20
1	B	268	PRO	N-CD-CG	-6.00	94.20	103.20
1	C	292	LYS	C-N-CA	5.12	134.51	121.70

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	129	THR	CB
1	C	129	THR	CB

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	267	LYS	Peptide
1	B	268	PRO	Peptide

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	2673	0	2685	39	0
1	B	2641	0	2660	33	0
1	C	2639	0	2651	42	0
1	D	2640	0	2656	33	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	78	0	104	6	0
4	B	36	0	48	0	0
4	C	48	0	64	4	0
4	D	24	0	32	0	0
5	A	24	0	36	4	0
5	B	20	0	30	4	0
5	C	24	0	36	1	0
5	D	32	0	48	1	0
6	A	18	0	25	6	0
6	B	18	0	25	6	0
6	C	18	0	25	7	0
6	D	18	0	24	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	218	0	0	2	0
7	B	162	0	0	0	0
7	C	204	0	0	5	0
7	D	176	0	0	1	0
All	All	11719	0	11149	156	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 7.

All (156) 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:268:PRO:CD	1:B:268:PRO:CG	1.78	1.57
1:D:268:PRO:HD2	1:D:269:GLU:OE2	1.40	1.19
1:C:265:THR:HG22	1:D:108:ASN:HD22	1.12	1.11
1:D:2[A]:ARG:HB2	1:D:2[A]:ARG:NH2	1.71	1.06
1:D:2[A]:ARG:HH21	1:D:2[A]:ARG:CB	1.72	1.03
6:D:1329:HT5:H131	6:D:1329:HT5:O1	1.59	1.02
1:C:1[B]:MET:CE	7:C:2001:HOH:O	2.06	1.02
6:B:1328:HT5:H131	6:B:1328:HT5:O1	1.56	1.01
1:C:241[A]:ARG:HG3	1:C:241[A]:ARG:HH11	1.21	1.01
1:D:2[A]:ARG:HB2	1:D:2[A]:ARG:HH21	0.85	0.98
1:C:1[B]:MET:HE1	7:C:2001:HOH:O	1.60	0.96
6:A:1335:HT5:SD	7:A:2200:HOH:O	2.26	0.93
1:B:99:TYR:H	5:B:1319:EDO:H22	1.33	0.92
1:D:223[A]:ARG:HG3	1:D:226:LEU:HD12	1.53	0.88
1:C:126:ILE:O	1:C:129:THR:HG22	1.76	0.85
1:A:103:PRO:HA	4:A:1328:GOL:H11	1.59	0.85
1:C:265:THR:HG22	1:D:108:ASN:ND2	1.93	0.84
1:B:126:ILE:O	1:B:129:THR:HG22	1.78	0.83
6:B:1328:HT5:O1	6:B:1328:HT5:C13	2.29	0.80
1:D:129:THR:HG23	1:D:131:ASN:H	1.48	0.79
6:C:1329:HT5:SD	7:C:2189:HOH:O	2.42	0.76
1:C:292:LYS:N	1:C:293:ARG:HB3	2.00	0.75
1:C:266:ALA:HA	6:C:1329:HT5:H6C1	1.68	0.75
1:C:241[A]:ARG:HG3	1:C:241[A]:ARG:NH1	1.99	0.74
6:D:1329:HT5:C13	6:D:1329:HT5:O1	2.36	0.74
1:A:201:GLY:HA2	5:A:1318:EDO:H22	1.70	0.73
1:B:175[A]:ASN:O	1:B:176[A]:ASN:HB2	1.88	0.71
1:C:223[A]:ARG:HG3	1:C:226:LEU:HD12	1.73	0.71
6:A:1335:HT5:O1	6:A:1335:HT5:H1C2	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:196:LEU:HD13	1:C:252:MET:HE3	1.72	0.70
1:D:175:ASN:O	1:D:176:ASN:HB2	1.94	0.66
1:A:21:ILE:HA	1:A:65:VAL:HG13	1.77	0.66
1:C:235:ARG:O	1:C:239:THR:HG22	1.96	0.65
6:C:1329:HT5:H131	6:C:1329:HT5:O1	1.97	0.64
6:C:1329:HT5:C13	6:C:1329:HT5:O1	2.45	0.63
1:C:1[B]:MET:HE3	7:C:2001:HOH:O	1.79	0.63
1:A:277:ARG:HA	4:C:1320:GOL:H11	1.80	0.63
1:B:129:THR:HG23	1:B:131:ASN:H	1.64	0.61
1:D:253:ILE:CD1	1:D:283:ILE:HG21	2.30	0.61
1:C:271:LYS:HG2	6:C:1329:HT5:H8C3	1.81	0.61
1:D:2[B]:ARG:HH12	1:D:14:LYS:HD3	1.65	0.61
1:C:129:THR:HG23	1:C:131:ASN:H	1.66	0.61
1:C:241[A]:ARG:HH11	1:C:241[A]:ARG:CG	2.03	0.61
1:D:253:ILE:HD11	1:D:283:ILE:HG21	1.82	0.60
1:C:206:ILE:HD11	1:C:210:LYS:HE3	1.83	0.59
1:A:201:GLY:CA	5:A:1318:EDO:H22	2.33	0.59
1:B:99:TYR:N	5:B:1319:EDO:H22	2.12	0.58
1:D:267:LYS:O	1:D:269:GLU:N	2.36	0.58
1:A:1[A]:MET:CE	1:A:10:SER:O	2.52	0.58
1:C:233:ASP:O	1:C:237[B]:GLU:HG2	2.03	0.58
1:C:255:HIS:CE1	1:C:283:ILE:HG12	2.39	0.58
1:D:1[A]:MET:HG2	1:D:12:GLU:HG2	1.86	0.58
1:C:292:LYS:H	1:C:293:ARG:HB3	1.69	0.57
1:B:2[B]:ARG:HH21	1:B:2[B]:ARG:HB2	1.69	0.57
1:C:275:ALA:HB1	1:C:278:TRP:HB2	1.87	0.57
1:A:266:ALA:HB2	6:A:1335:HT5:C50	2.35	0.56
1:B:261:ILE:HD12	6:B:1328:HT5:H132	1.87	0.56
1:B:29:SER:HB2	1:B:32:VAL:HG13	1.87	0.56
1:B:206[B]:ILE:HD13	1:B:206[B]:ILE:H	1.72	0.55
1:D:126:ILE:O	1:D:129:THR:HG22	2.07	0.55
1:C:224:TYR:OH	1:C:239:THR:HG21	2.08	0.54
1:C:303:THR:HA	1:C:307[A]:GLU:HB2	1.90	0.54
1:C:129:THR:O	5:C:1321:EDO:H11	2.07	0.54
1:D:33:ARG:HH21	5:D:1325:EDO:H11	1.73	0.54
1:A:172:ASN:HB3	1:A:175[B]:ASN:ND2	2.22	0.54
1:D:267:LYS:C	1:D:269:GLU:H	2.12	0.54
1:A:284:PHE:HD2	4:A:1324:GOL:H11	1.74	0.53
1:A:1[A]:MET:HA	1:A:1[A]:MET:SD	2.48	0.53
1:C:265:THR:CG2	1:D:108:ASN:HD22	2.03	0.53
1:C:221:LEU:HD13	1:C:239:THR:HB	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:ILE:HD13	1:A:241:ARG:HG2	1.92	0.52
1:A:175[A]:ASN:O	1:A:176:ASN:HB2	2.09	0.52
1:B:244:LYS:O	5:B:1326:EDO:H22	2.09	0.52
1:C:81:LYS:HE2	4:C:1324:GOL:H32	1.92	0.52
1:A:126:ILE:O	1:A:129:THR:HB	2.08	0.52
4:A:1328:GOL:H2	5:B:1319:EDO:H11	1.90	0.52
1:A:1[A]:MET:HE2	1:A:10:SER:O	2.11	0.51
1:B:175[A]:ASN:O	1:B:176[A]:ASN:CB	2.59	0.51
1:A:1[A]:MET:O	1:A:2[A]:ARG:C	2.50	0.51
1:D:138:ILE:HG22	1:D:152:VAL:HG12	1.93	0.51
1:A:138:ILE:HD13	1:A:153:ILE:HG12	1.93	0.50
1:A:2[A]:ARG:HH12	1:A:164[A]:LYS:HB3	1.76	0.50
1:A:52:GLU:OE2	1:A:55[A]:ARG:NH2	2.42	0.50
1:D:268:PRO:CD	1:D:269:GLU:OE2	2.34	0.50
1:B:129:THR:HG23	1:B:131:ASN:N	2.26	0.50
1:A:1[A]:MET:HE3	1:A:10:SER:O	2.12	0.49
1:C:138:ILE:HG22	1:C:152:VAL:HG12	1.94	0.49
1:A:11:ILE:CG2	5:A:1327:EDO:H11	2.42	0.49
1:A:271:LYS:HB3	1:A:272:PRO:HD3	1.95	0.49
1:A:201:GLY:HA2	5:A:1318:EDO:C2	2.40	0.48
1:A:266:ALA:HB2	6:A:1335:HT5:H502	1.94	0.48
1:B:7:GLY:H	1:B:131:ASN:ND2	2.11	0.48
1:C:277:ARG:O	1:C:282:LEU:HG	2.13	0.48
1:B:271:LYS:HA	6:B:1328:HT5:H8C2	1.96	0.48
1:C:303:THR:HA	1:C:307[B]:GLU:HB2	1.94	0.48
1:C:241[A]:ARG:NH1	1:C:241[A]:ARG:CG	2.67	0.48
1:A:266:ALA:HB2	6:A:1335:HT5:H501	1.95	0.47
1:B:267:LYS:O	1:B:267:LYS:HG2	2.13	0.47
1:D:291:LEU:O	1:D:296:VAL:HG13	2.14	0.47
7:A:2183:HOH:O	4:C:1320:GOL:H12	2.13	0.47
1:A:7:GLY:H	1:A:131:ASN:ND2	2.13	0.47
1:B:172:ASN:HB3	1:B:175[B]:ASN:OD1	2.15	0.47
1:D:275:ALA:HB1	1:D:278:TRP:HB2	1.97	0.47
1:A:129:THR:CG2	1:A:131:ASN:H	2.28	0.46
1:A:303:THR:HA	1:A:307[B]:GLU:HB2	1.98	0.46
1:D:29:SER:HB2	1:D:32:VAL:HG13	1.96	0.46
1:B:80:GLU:OE2	1:B:131:ASN:OD1	2.34	0.46
1:C:271:LYS:HB3	1:C:272:PRO:HD3	1.98	0.46
1:B:267:LYS:O	1:B:270:TYR:HB2	2.16	0.45
1:A:102:LEU:O	4:A:1329:GOL:H11	2.15	0.45
1:A:22:HIS:CD2	1:A:67:PRO:HG2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2[B]:ARG:HH22	1:B:12:GLU:HA	1.82	0.45
6:D:1329:HT5:C12	7:D:2166:HOH:O	2.64	0.45
1:D:228:LEU:HD13	1:D:274:LEU:HD12	1.97	0.45
1:B:2[B]:ARG:NH2	1:B:13:SER:H	2.14	0.45
1:C:200:LEU:HD23	1:C:219:ILE:HG22	1.98	0.45
1:B:204[A]:ASP:O	1:B:206[A]:ILE:N	2.50	0.45
1:B:268:PRO:HD3	1:B:271:LYS:HB2	1.99	0.45
1:D:223[A]:ARG:HB3	1:D:235:ARG:NH1	2.32	0.45
1:D:27:VAL:HG11	6:D:1329:HT5:H141	1.98	0.45
1:C:1[B]:MET:HG3	1:C:12:GLU:HG2	1.98	0.45
1:D:264:GLY:O	1:D:267:LYS:HG2	2.17	0.44
1:D:166:PRO:HB2	1:D:312:PHE:CZ	2.53	0.44
1:C:138:ILE:HD13	1:C:153:ILE:HG12	1.99	0.44
1:C:263:TRP:CH2	6:C:1329:HT5:H11	2.53	0.44
1:A:206:ILE:HD11	1:A:242:LEU:HG	1.99	0.44
1:B:303:THR:HA	1:B:307:GLU:HB2	1.99	0.43
1:A:265:THR:HG22	1:B:108:ASN:HD22	1.84	0.43
1:B:166:PRO:HB2	1:B:312:PHE:CZ	2.53	0.43
1:A:65:VAL:HB	1:A:91:VAL:HB	2.01	0.43
1:D:223[A]:ARG:CG	1:D:226:LEU:HD12	2.38	0.43
6:A:1335:HT5:H2C1	6:A:1335:HT5:H3C2	1.87	0.43
1:A:138:ILE:HG22	1:A:152:VAL:HG12	2.00	0.43
1:A:1[A]:MET:O	1:A:10:SER:HB2	2.19	0.43
1:C:263:TRP:CE2	1:D:104:PHE:HB3	2.54	0.42
1:A:223[A]:ARG:HD3	1:A:256:ASP:OD1	2.19	0.42
1:B:196:LEU:HD13	1:B:252:MET:HE3	2.00	0.42
1:B:275:ALA:HB1	1:B:278:TRP:HB2	2.01	0.42
1:D:2[A]:ARG:HH21	1:D:2[A]:ARG:CG	2.31	0.42
1:A:291:LEU:O	1:A:296:VAL:HG13	2.19	0.41
1:C:8:LYS:HD3	4:C:1319[A]:GOL:H32	2.03	0.41
1:A:166:PRO:HB2	1:A:312:PHE:CZ	2.56	0.41
1:B:258:CYS:SG	6:B:1328:HT5:H141	2.61	0.41
1:B:138:ILE:HD13	1:B:153:ILE:HG12	2.02	0.41
1:D:196:LEU:HD22	1:D:252:MET:HE3	2.03	0.41
1:C:166:PRO:HB2	1:C:312:PHE:CZ	2.55	0.41
1:B:48:ASN:HD22	1:B:260:THR:HG23	1.86	0.41
1:A:164[A]:LYS:HE2	4:A:1323:GOL:H11	2.03	0.41
1:C:55[B]:ARG:HD2	1:C:281:THR:HG21	2.03	0.41
1:C:66:ASP:HA	1:C:67:PRO:HD3	1.87	0.41
1:D:7:GLY:H	1:D:131:ASN:ND2	2.18	0.41
1:B:173:ALA:HB2	1:B:199:HIS:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:1329:HT5:C12	7:C:2189:HOH:O	2.67	0.40
1:A:2[B]:ARG:HG3	1:A:12:GLU:HA	2.03	0.40
1:B:271:LYS:HG3	6:B:1328:HT5:H8C1	2.04	0.40
4:A:1324:GOL:H32	1:C:58:GLN:HB3	2.02	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	328/314 (104%)	315 (96%)	11 (3%)	2 (1%)	28	17
1	B	325/314 (104%)	306 (94%)	15 (5%)	4 (1%)	15	6
1	C	324/314 (103%)	311 (96%)	7 (2%)	6 (2%)	9	2
1	D	325/314 (104%)	314 (97%)	11 (3%)	0	100	100
All	All	1302/1256 (104%)	1246 (96%)	44 (3%)	12 (1%)	22	10

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	269	GLU
1	B	2[A]	ARG
1	B	2[B]	ARG
1	B	268	PRO
1	C	293	ARG
1	A	205	ASN
1	C	2	ARG
1	C	205	ASN
1	C	269[A]	GLU
1	C	269[B]	GLU
1	B	267	LYS

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Mol	Chain	Res	Type
1	C	268[A]	PRO

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	290/272 (107%)	279 (96%)	11 (4%)	38	30
1	B	286/272 (105%)	277 (97%)	9 (3%)	45	38
1	C	285/272 (105%)	266 (93%)	19 (7%)	19	10
1	D	286/272 (105%)	268 (94%)	18 (6%)	21	11
All	All	1147/1088 (105%)	1090 (95%)	57 (5%)	31	19

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	VAL
1	A	65	VAL
1	A	129	THR
1	A	164[A]	LYS
1	A	164[B]	LYS
1	A	200	LEU
1	A	206	ILE
1	A	254	SER
1	A	282	LEU
1	A	292	LYS
1	A	296	VAL
1	B	1	MET
1	B	9	ASP
1	B	32	VAL
1	B	179	LEU
1	B	254	SER
1	B	260	THR
1	B	267	LYS
1	B	268	PRO
1	B	269	GLU

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Mol	Chain	Res	Type
1	C	5	LEU
1	C	27	VAL
1	C	101[A]	ASP
1	C	101[B]	ASP
1	C	108	ASN
1	C	175	ASN
1	C	183	ARG
1	C	200	LEU
1	C	206	ILE
1	C	223[A]	ARG
1	C	223[B]	ARG
1	C	239	THR
1	C	241[A]	ARG
1	C	241[B]	ARG
1	C	254	SER
1	C	277	ARG
1	C	282	LEU
1	C	293	ARG
1	C	297	ASN
1	D	2[A]	ARG
1	D	2[B]	ARG
1	D	9	ASP
1	D	32	VAL
1	D	84	LYS
1	D	129	THR
1	D	200	LEU
1	D	204[A]	ASP
1	D	204[B]	ASP
1	D	206	ILE
1	D	223[A]	ARG
1	D	223[B]	ARG
1	D	244	LYS
1	D	253	ILE
1	D	254	SER
1	D	267	LYS
1	D	274	LEU
1	D	282	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN

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Mol	Chain	Res	Type
1	A	182	GLN
1	A	236	ASN
1	B	58	GLN
1	B	108	ASN
1	B	131	ASN
1	B	160	ASN
1	B	236	ASN
1	C	160	ASN
1	C	175	ASN
1	C	236	ASN
1	D	108	ASN
1	D	131	ASN
1	D	160	ASN
1	D	236	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	KCX	A	137	1,3,2	8,11,12	1.26	1 (12%)	6,12,14	1.28	1 (16%)
1	KCX	B	137	1,3,2	8,11,12	1.12	1 (12%)	6,12,14	0.78	0
1	KCX	C	137	1,3,2	8,11,12	1.14	1 (12%)	6,12,14	0.97	0
1	KCX	D	137	1,3,2	8,11,12	1.09	1 (12%)	6,12,14	0.83	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
1	KCX	A	137	1,3,2	-	0/6/10/12	0/0/0/0
1	KCX	B	137	1,3,2	-	0/6/10/12	0/0/0/0
1	KCX	C	137	1,3,2	-	0/6/10/12	0/0/0/0
1	KCX	D	137	1,3,2	-	0/6/10/12	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	137	KCX	CA-C	2.17	1.53	1.50
1	D	137	KCX	CA-C	2.32	1.53	1.50
1	C	137	KCX	CA-C	2.40	1.53	1.50
1	A	137	KCX	CA-C	2.64	1.53	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	KCX	CD-CE-NZ	2.16	117.21	111.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 68 ligands modelled in this entry, 8 are monoatomic - leaving 60 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	A	1317	-	5,5,5	0.36	0	5,5,5	0.29	0
5	EDO	A	1318	-	3,3,3	0.46	0	2,2,2	0.24	0
4	GOL	A	1319	-	5,5,5	0.30	0	5,5,5	0.26	0
5	EDO	A	1320	-	3,3,3	0.45	0	2,2,2	0.37	0
4	GOL	A	1321	-	5,5,5	0.35	0	5,5,5	0.20	0
5	EDO	A	1322	-	3,3,3	0.44	0	2,2,2	0.40	0
4	GOL	A	1323	-	5,5,5	0.35	0	5,5,5	0.25	0
4	GOL	A	1324	-	5,5,5	0.34	0	5,5,5	0.23	0
4	GOL	A	1325[A]	-	5,5,5	0.34	0	5,5,5	0.28	0
4	GOL	A	1325[B]	-	5,5,5	0.35	0	5,5,5	0.20	0
4	GOL	A	1326	-	5,5,5	0.33	0	5,5,5	0.23	0
5	EDO	A	1327	-	3,3,3	0.43	0	2,2,2	0.33	0
4	GOL	A	1328	-	5,5,5	0.36	0	5,5,5	0.22	0
4	GOL	A	1329	-	5,5,5	0.34	0	5,5,5	0.18	0
5	EDO	A	1330	-	3,3,3	0.46	0	2,2,2	0.38	0
5	EDO	A	1331	-	3,3,3	0.45	0	2,2,2	0.37	0
4	GOL	A	1332	-	5,5,5	0.32	0	5,5,5	0.29	0
4	GOL	A	1333	-	5,5,5	0.34	0	5,5,5	0.24	0
4	GOL	A	1334	-	5,5,5	0.33	0	5,5,5	0.33	0
6	HT5	A	1335	-	16,18,18	1.45	2 (12%)	14,21,21	3.16	6 (42%)
4	GOL	B	1317	-	5,5,5	0.36	0	5,5,5	0.30	0
5	EDO	B	1318	-	3,3,3	0.46	0	2,2,2	0.32	0
5	EDO	B	1319	-	3,3,3	0.43	0	2,2,2	0.31	0
5	EDO	B	1320	-	3,3,3	0.44	0	2,2,2	0.36	0
4	GOL	B	1321	-	5,5,5	0.33	0	5,5,5	0.23	0
4	GOL	B	1322	-	5,5,5	0.35	0	5,5,5	0.24	0
4	GOL	B	1323	-	5,5,5	0.33	0	5,5,5	0.30	0
5	EDO	B	1324	-	3,3,3	0.44	0	2,2,2	0.38	0
4	GOL	B	1325	-	5,5,5	0.33	0	5,5,5	0.25	0
5	EDO	B	1326	-	3,3,3	0.45	0	2,2,2	0.34	0
4	GOL	B	1327	-	5,5,5	0.37	0	5,5,5	0.25	0
6	HT5	B	1328	-	16,18,18	1.25	2 (12%)	14,21,21	2.23	3 (21%)
4	GOL	C	1317[A]	-	5,5,5	0.34	0	5,5,5	0.31	0
4	GOL	C	1317[B]	-	5,5,5	0.36	0	5,5,5	0.18	0
5	EDO	C	1318	-	3,3,3	0.47	0	2,2,2	0.37	0
4	GOL	C	1319[A]	-	5,5,5	0.37	0	5,5,5	0.18	0
4	GOL	C	1319[B]	-	5,5,5	0.34	0	5,5,5	0.34	0
4	GOL	C	1320	-	5,5,5	0.35	0	5,5,5	0.31	0
5	EDO	C	1321	-	3,3,3	0.44	0	2,2,2	0.38	0
5	EDO	C	1322	-	3,3,3	0.46	0	2,2,2	0.35	0
5	EDO	C	1323	-	3,3,3	0.47	0	2,2,2	0.35	0
4	GOL	C	1324	-	5,5,5	0.35	0	5,5,5	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	C	1325	-	5,5,5	0.36	0	5,5,5	0.21	0
5	EDO	C	1326	-	3,3,3	0.45	0	2,2,2	0.37	0
4	GOL	C	1327	-	5,5,5	0.34	0	5,5,5	0.22	0
5	EDO	C	1328	-	3,3,3	0.46	0	2,2,2	0.36	0
6	HT5	C	1329	-	16,18,18	1.67	3 (18%)	14,21,21	1.46	2 (14%)
4	GOL	D	1317	-	5,5,5	0.34	0	5,5,5	0.21	0
5	EDO	D	1318	-	3,3,3	0.47	0	2,2,2	0.31	0
5	EDO	D	1319	-	3,3,3	0.45	0	2,2,2	0.35	0
4	GOL	D	1320	-	5,5,5	0.34	0	5,5,5	0.25	0
4	GOL	D	1321	-	5,5,5	0.34	0	5,5,5	0.17	0
5	EDO	D	1322	-	3,3,3	0.44	0	2,2,2	0.35	0
5	EDO	D	1323	-	3,3,3	0.45	0	2,2,2	0.36	0
4	GOL	D	1324	-	5,5,5	0.31	0	5,5,5	0.35	0
5	EDO	D	1325	-	3,3,3	0.47	0	2,2,2	0.30	0
5	EDO	D	1326	-	3,3,3	0.47	0	2,2,2	0.25	0
5	EDO	D	1327	-	3,3,3	0.46	0	2,2,2	0.36	0
5	EDO	D	1328	-	3,3,3	0.44	0	2,2,2	0.39	0
6	HT5	D	1329	-	16,18,18	1.39	3 (18%)	14,21,21	3.73	6 (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
4	GOL	A	1317	-	-	0/4/4/4	0/0/0/0
5	EDO	A	1318	-	-	0/1/1/1	0/0/0/0
4	GOL	A	1319	-	-	0/4/4/4	0/0/0/0
5	EDO	A	1320	-	-	0/1/1/1	0/0/0/0
4	GOL	A	1321	-	-	0/4/4/4	0/0/0/0
5	EDO	A	1322	-	-	0/1/1/1	0/0/0/0
4	GOL	A	1323	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1324	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1325[A]	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1325[B]	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1326	-	-	0/4/4/4	0/0/0/0
5	EDO	A	1327	-	-	0/1/1/1	0/0/0/0
4	GOL	A	1328	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1329	-	-	0/4/4/4	0/0/0/0
5	EDO	A	1330	-	-	0/1/1/1	0/0/0/0
5	EDO	A	1331	-	-	0/1/1/1	0/0/0/0
4	GOL	A	1332	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	1333	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1334	-	-	0/4/4/4	0/0/0/0
6	HT5	A	1335	-	-	0/13/23/23	0/0/1/1
4	GOL	B	1317	-	-	0/4/4/4	0/0/0/0
5	EDO	B	1318	-	-	0/1/1/1	0/0/0/0
5	EDO	B	1319	-	-	0/1/1/1	0/0/0/0
5	EDO	B	1320	-	-	0/1/1/1	0/0/0/0
4	GOL	B	1321	-	-	0/4/4/4	0/0/0/0
4	GOL	B	1322	-	-	0/4/4/4	0/0/0/0
4	GOL	B	1323	-	-	0/4/4/4	0/0/0/0
5	EDO	B	1324	-	-	0/1/1/1	0/0/0/0
4	GOL	B	1325	-	-	0/4/4/4	0/0/0/0
5	EDO	B	1326	-	-	0/1/1/1	0/0/0/0
4	GOL	B	1327	-	-	0/4/4/4	0/0/0/0
6	HT5	B	1328	-	-	0/13/23/23	0/0/1/1
4	GOL	C	1317[A]	-	-	0/4/4/4	0/0/0/0
4	GOL	C	1317[B]	-	-	0/4/4/4	0/0/0/0
5	EDO	C	1318	-	-	0/1/1/1	0/0/0/0
4	GOL	C	1319[A]	-	-	0/4/4/4	0/0/0/0
4	GOL	C	1319[B]	-	-	0/4/4/4	0/0/0/0
4	GOL	C	1320	-	-	0/4/4/4	0/0/0/0
5	EDO	C	1321	-	-	0/1/1/1	0/0/0/0
5	EDO	C	1322	-	-	0/1/1/1	0/0/0/0
5	EDO	C	1323	-	-	0/1/1/1	0/0/0/0
4	GOL	C	1324	-	-	0/4/4/4	0/0/0/0
4	GOL	C	1325	-	-	0/4/4/4	0/0/0/0
5	EDO	C	1326	-	-	0/1/1/1	0/0/0/0
4	GOL	C	1327	-	-	0/4/4/4	0/0/0/0
5	EDO	C	1328	-	-	0/1/1/1	0/0/0/0
6	HT5	C	1329	-	-	0/13/23/23	0/0/1/1
4	GOL	D	1317	-	-	0/4/4/4	0/0/0/0
5	EDO	D	1318	-	-	0/1/1/1	0/0/0/0
5	EDO	D	1319	-	-	0/1/1/1	0/0/0/0
4	GOL	D	1320	-	-	0/4/4/4	0/0/0/0
4	GOL	D	1321	-	-	0/4/4/4	0/0/0/0
5	EDO	D	1322	-	-	0/1/1/1	0/0/0/0
5	EDO	D	1323	-	-	0/1/1/1	0/0/0/0
4	GOL	D	1324	-	-	0/4/4/4	0/0/0/0
5	EDO	D	1325	-	-	0/1/1/1	0/0/0/0
5	EDO	D	1326	-	-	0/1/1/1	0/0/0/0
5	EDO	D	1327	-	-	0/1/1/1	0/0/0/0
5	EDO	D	1328	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	HT5	D	1329	-	1/1/3/4	0/13/23/23	0/0/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1329	HT5	O2-C12	-5.31	1.17	1.31
6	A	1335	HT5	O2-C12	-4.81	1.18	1.31
6	B	1328	HT5	O2-C12	-4.38	1.19	1.31
6	C	1329	HT5	C11-C12	-2.39	1.46	1.51
6	A	1335	HT5	C9-C10	-2.39	1.46	1.51
6	C	1329	HT5	O1-C10	-2.24	1.18	1.23
6	B	1328	HT5	O1-C10	-2.13	1.18	1.23
6	D	1329	HT5	O1-C10	2.55	1.28	1.23
6	D	1329	HT5	C10-N2	3.01	1.40	1.34
6	D	1329	HT5	C11-N2	3.51	1.53	1.45

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1335	HT5	C13-C11-N2	-7.81	98.22	115.23
6	B	1328	HT5	C13-C11-N2	-6.57	100.92	115.23
6	D	1329	HT5	C2-C9-C10	-5.12	98.95	113.32
6	D	1329	HT5	O1-C10-C9	-4.84	112.92	122.01
6	A	1335	HT5	C2-C9-C10	-4.08	101.85	113.32
6	A	1335	HT5	C11-N2-C10	-4.04	110.95	121.62
6	D	1329	HT5	C11-N2-C10	-3.66	111.96	121.62
6	A	1335	HT5	O1-C10-C9	-3.48	115.47	122.01
6	B	1328	HT5	O1-C10-C9	-3.01	116.34	122.01
6	C	1329	HT5	C2-C9-C10	-2.69	105.77	113.32
6	D	1329	HT5	C9-C10-N2	2.14	119.58	115.82
6	B	1328	HT5	C12-C11-N2	2.50	117.20	112.06
6	D	1329	HT5	O1-C10-N2	2.62	127.49	122.97
6	A	1335	HT5	C12-C11-N2	3.62	119.50	112.06
6	C	1329	HT5	C12-C11-N2	4.12	120.51	112.06
6	A	1335	HT5	C9-C10-N2	4.40	123.57	115.82
6	D	1329	HT5	C12-C11-N2	10.75	134.12	112.06

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	D	1329	HT5	C11

There are no torsion outliers.

There are no ring outliers.

17 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1318	EDO	3	0
4	A	1323	GOL	1	0
4	A	1324	GOL	2	0
5	A	1327	EDO	1	0
4	A	1328	GOL	2	0
4	A	1329	GOL	1	0
6	A	1335	HT5	6	0
5	B	1319	EDO	3	0
5	B	1326	EDO	1	0
6	B	1328	HT5	6	0
4	C	1319[A]	GOL	1	0
4	C	1320	GOL	2	0
5	C	1321	EDO	1	0
4	C	1324	GOL	1	0
6	C	1329	HT5	7	0
5	D	1325	EDO	1	0
6	D	1329	HT5	4	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	313/314 (99%)	0.09	5 (1%) 72 75	17, 24, 34, 46	5 (1%)
1	B	313/314 (99%)	0.21	7 (2%) 62 67	22, 29, 39, 50	5 (1%)
1	C	313/314 (99%)	0.18	5 (1%) 72 75	17, 25, 36, 49	8 (2%)
1	D	313/314 (99%)	0.22	7 (2%) 62 67	19, 29, 38, 52	8 (2%)
All	All	1252/1256 (99%)	0.18	24 (1%) 67 72	17, 27, 39, 52	26 (2%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	268	PRO	4.9
1	D	1[A]	MET	4.6
1	D	29	SER	4.6
1	B	29	SER	4.6
1	C	29	SER	4.2
1	A	268	PRO	3.8
1	B	1	MET	3.8
1	A	29	SER	3.7
1	C	268[A]	PRO	3.2
1	B	108	ASN	3.2
1	C	108	ASN	3.1
1	C	1[A]	MET	2.9
1	D	108	ASN	2.9
1	C	270	TYR	2.8
1	D	268	PRO	2.7
1	D	274	LEU	2.6
1	A	2[A]	ARG	2.5
1	A	1[A]	MET	2.4
1	A	273	LYS	2.3
1	D	176	ASN	2.2
1	D	228	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	2[A]	ARG	2.2
1	B	274	LEU	2.1
1	B	277[A]	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	KCX	C	137	12/13	0.93	0.13	-	17,17,18,18	0
1	KCX	A	137	12/13	0.93	0.13	-	16,17,18,19	0
1	KCX	D	137	12/13	0.93	0.12	-	22,23,24,25	0
1	KCX	B	137	12/13	0.94	0.12	-	18,22,24,24	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	GOL	A	1325[B]	6/6	0.78	0.33	10.24	24,24,24,24	6
4	GOL	A	1325[A]	6/6	0.78	0.33	10.01	39,39,39,39	6
5	EDO	A	1318	4/4	0.90	0.37	8.80	30,31,31,31	0
5	EDO	A	1330	4/4	0.76	0.20	7.60	36,37,37,37	0
4	GOL	C	1319[A]	6/6	0.84	0.27	6.99	7,7,7,8	6
4	GOL	A	1329	6/6	0.72	0.28	6.65	41,41,41,41	0
4	GOL	A	1321	6/6	0.76	0.20	5.74	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	GOL	C	1324	6/6	0.71	0.32	5.66	56,56,56,56	0
4	GOL	A	1328	6/6	0.70	0.28	4.75	52,52,52,52	0
4	GOL	C	1325	6/6	0.65	0.26	4.35	56,56,56,56	0
4	GOL	D	1317	6/6	0.84	0.20	4.34	42,43,43,43	0
6	HT5	A	1335	18/18	0.74	0.27	4.22	46,48,49,49	18
4	GOL	A	1333	6/6	0.78	0.22	3.60	44,45,45,45	0
5	EDO	B	1318	4/4	0.74	0.20	3.60	46,46,46,46	0
5	EDO	A	1322	4/4	0.87	0.20	3.54	50,50,50,50	0
4	GOL	A	1319	6/6	0.58	0.21	3.53	38,38,38,38	0
4	GOL	A	1324	6/6	0.83	0.20	3.32	45,45,45,45	0
5	EDO	B	1319	4/4	0.89	0.21	3.31	43,43,43,43	0
5	EDO	C	1323	4/4	0.82	0.20	3.25	34,34,34,35	0
4	GOL	B	1321	6/6	0.86	0.23	3.02	35,35,35,35	0
4	GOL	B	1317	6/6	0.85	0.19	3.01	33,33,33,33	0
5	EDO	D	1328	4/4	0.82	0.22	2.67	52,52,52,52	0
4	GOL	B	1327	6/6	0.89	0.21	2.48	34,35,36,36	0
6	HT5	B	1328	18/18	0.64	0.32	2.47	52,54,55,55	18
4	GOL	D	1321	6/6	0.82	0.21	2.40	52,52,52,52	0
5	EDO	D	1319	4/4	0.90	0.13	2.35	44,44,45,45	0
5	EDO	A	1320	4/4	0.74	0.20	2.18	43,43,43,43	0
6	HT5	D	1329	18/18	0.67	0.27	2.12	39,43,44,44	18
5	EDO	B	1324	4/4	0.75	0.20	1.95	53,53,53,53	0
4	GOL	A	1326	6/6	0.74	0.19	1.65	52,52,52,52	0
4	GOL	C	1317[A]	6/6	0.94	0.17	1.46	15,15,15,15	6
4	GOL	B	1322	6/6	0.77	0.19	1.44	54,54,54,54	0
4	GOL	C	1317[B]	6/6	0.94	0.17	1.40	33,33,33,33	6
5	EDO	A	1327	4/4	0.93	0.15	1.38	27,27,27,28	0
5	EDO	B	1326	4/4	0.58	0.30	1.38	62,62,62,62	0
5	EDO	D	1326	4/4	0.79	0.23	1.29	44,44,44,44	0
6	HT5	C	1329	18/18	0.80	0.22	1.09	39,42,42,42	18
4	GOL	A	1332	6/6	0.79	0.19	0.98	46,47,47,47	0
4	GOL	C	1320	6/6	0.86	0.20	0.90	51,51,51,51	0
5	EDO	D	1323	4/4	0.91	0.15	0.63	51,51,51,51	0
5	EDO	D	1318	4/4	0.95	0.16	0.62	19,19,19,20	0
5	EDO	C	1321	4/4	0.91	0.16	0.54	37,37,37,37	0
4	GOL	D	1320	6/6	0.87	0.17	0.53	55,55,55,55	0
4	GOL	C	1327	6/6	0.89	0.16	0.52	56,56,56,56	0
4	GOL	D	1324	6/6	0.84	0.14	0.31	53,53,53,54	0
5	EDO	C	1328	4/4	0.87	0.14	0.25	28,29,29,29	0
5	EDO	B	1320	4/4	0.81	0.14	0.24	50,50,50,50	0
4	GOL	A	1323	6/6	0.89	0.15	0.19	30,30,30,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	GOL	B	1325	6/6	0.85	0.21	0.16	46,47,47,47	0
4	GOL	B	1323	6/6	0.84	0.17	0.06	45,45,45,45	0
5	EDO	A	1331	4/4	0.78	0.18	0.01	57,57,57,57	0
4	GOL	A	1334	6/6	0.81	0.21	0.01	60,60,61,61	0
5	EDO	C	1326	4/4	0.80	0.17	-0.41	43,44,44,44	0
5	EDO	D	1327	4/4	0.82	0.14	-0.76	57,58,58,58	0
5	EDO	D	1322	4/4	0.93	0.12	-0.76	42,42,42,42	0
5	EDO	C	1318	4/4	0.95	0.13	-0.78	24,25,25,25	0
3	CO	B	1316	1/1	0.99	0.12	-0.89	25,25,25,25	0
3	CO	A	1316	1/1	0.99	0.11	-0.95	21,21,21,21	0
3	CO	C	1316	1/1	0.99	0.11	-1.15	20,20,20,20	0
3	CO	D	1316	1/1	1.00	0.08	-1.76	27,27,27,27	0
4	GOL	A	1317	6/6	0.94	0.12	-1.82	28,28,28,28	0
2	FE	B	1315	1/1	0.99	0.09	-	19,19,19,19	0
2	FE	A	1315	1/1	0.98	0.12	-	18,18,18,18	0
2	FE	C	1315	1/1	0.99	0.13	-	18,18,18,18	0
4	GOL	C	1319[B]	6/6	0.84	0.27	-	43,43,43,43	6
5	EDO	D	1325	4/4	0.82	0.16	-	47,47,47,47	0
2	FE	D	1315	1/1	1.00	0.11	-	25,25,25,25	0
5	EDO	C	1322	4/4	0.78	0.27	-	47,47,47,47	0

6.5 Other polymers ⓘ

There are no such residues in this entry.