



Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 02:07 am BST

PDB ID : 2ELC
Title : Crystal structure of TTHA1842 from *Thermus thermophilus* HB8
Authors : Shimizu, K.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2007-03-27
Resolution : 1.55 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

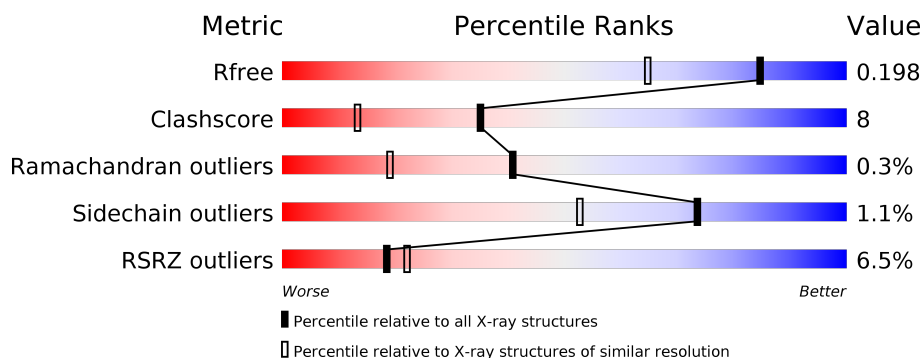
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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}	130704	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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 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	329	<div> <div>9%</div> <div> <div></div> <div>84%</div> <div>14%</div> <div>••</div> </div> </div>
1	B	329	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>13%</div> <div>•</div> </div> </div>
1	C	329	<div> <div>6%</div> <div> <div></div> <div>84%</div> <div>16%</div> <div>•</div> </div> </div>
1	D	329	<div> <div>6%</div> <div> <div></div> <div>86%</div> <div>13%</div> <div>•</div> </div> </div>

2 Entry composition [i](#)

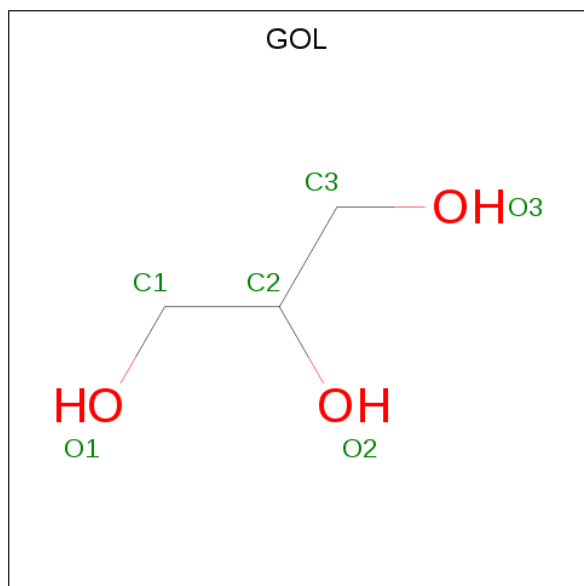
There are 4 unique types of molecules in this entry. The entry contains 11432 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Anthranilate phosphoribosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	329	Total	C	N	O	S	6	4	0
			2422	1530	437	447	8			
1	B	329	Total	C	N	O	S	1	7	0
			2442	1542	446	445	9			
1	C	329	Total	C	N	O	S	13	13	0
			2462	1555	446	452	9			
1	D	329	Total	C	N	O	S	17	12	0
			2463	1555	449	449	10			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

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

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Na	0	0
			1	1		
3	D	1	Total	Na	0	0
			1	1		

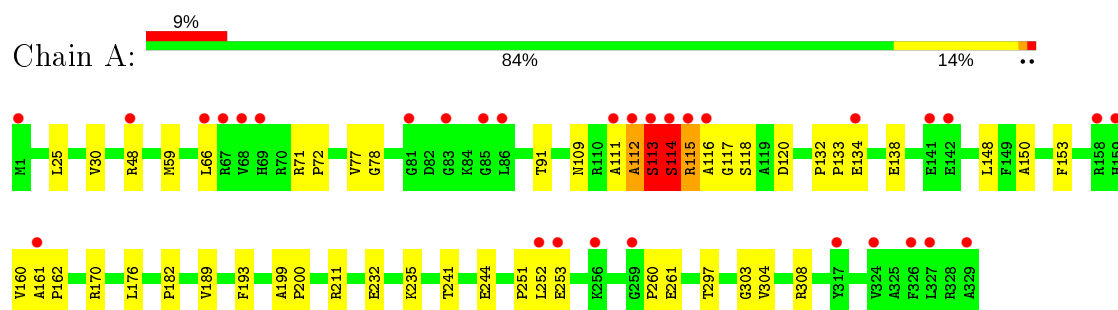
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	382	Total	O	0	0
			382	382		
4	B	449	Total	O	0	0
			449	449		
4	C	352	Total	O	0	0
			352	352		
4	D	386	Total	O	0	0
			386	386		

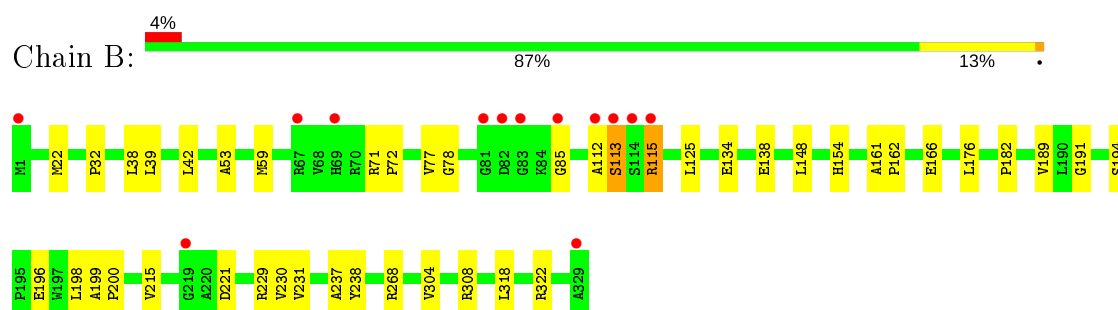
3 Residue-property plots [i](#)

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 ($RSRZ > 2$). 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.

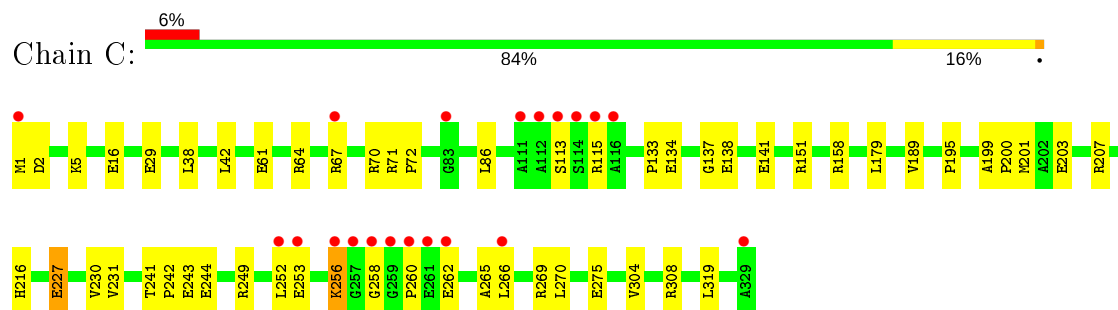
• Molecule 1: Anthranilate phosphoribosyltransferase



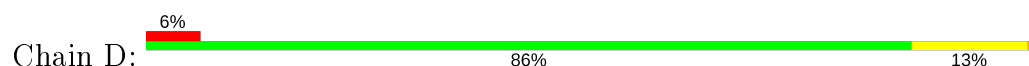
• Molecule 1: Anthranilate phosphoribosyltransferase

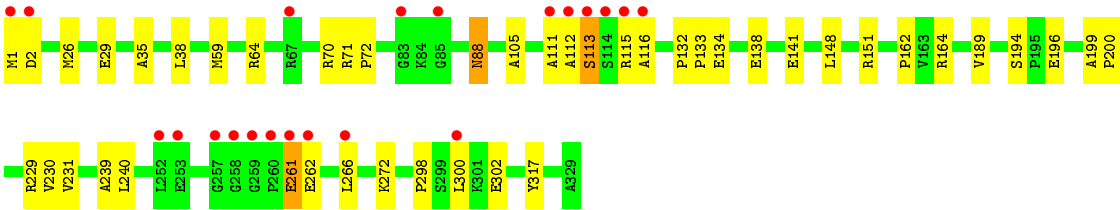


• Molecule 1: Anthranilate phosphoribosyltransferase



• Molecule 1: Anthranilate phosphoribosyltransferase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	165.32Å 72.91Å 141.26Å 90.00° 125.21° 90.00°	Depositor
Resolution (Å)	40.00 – 1.55 39.04 – 1.55	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.00-1.55) 100.0 (39.04-1.55)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.30 (at 1.55Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.187 , 0.202 0.183 , 0.198	Depositor DCC
R_{free} test set	9764 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	12.4	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.005 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11432	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.26 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.4240e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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, NA

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	0.37	0/2480	0.66	2/3355 (0.1%)
1	B	0.32	0/2515	0.61	1/3401 (0.0%)
1	C	0.35	0/2565	0.63	1/3468 (0.0%)
1	D	0.34	0/2561	0.63	1/3460 (0.0%)
All	All	0.35	0/10121	0.63	5/13684 (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	A	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	SER	O-C-N	-7.33	110.97	122.70
1	D	189	VAL	N-CA-C	-6.61	93.16	111.00
1	B	189	VAL	N-CA-C	-6.45	93.58	111.00
1	C	189	VAL	N-CA-C	-6.18	94.32	111.00
1	A	189	VAL	N-CA-C	-6.17	94.35	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	113	SER	Peptide

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Mol	Chain	Res	Type	Group
1	A	114	SER	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	2422	0	2492	53	0
1	B	2442	0	2525	40	0
1	C	2462	0	2548	40	0
1	D	2463	0	2552	31	0
2	A	24	0	32	0	0
2	B	18	0	24	5	0
2	C	18	0	24	0	0
2	D	12	0	16	1	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	A	382	0	0	2	0
4	B	449	0	0	5	0
4	C	352	0	0	4	0
4	D	386	0	0	3	0
All	All	11432	0	10213	164	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 8.

All (164) 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:318:LEU:HG	1:B:322:ARG:NH1	1.79	0.96
1:B:229[B]:ARG:HG3	1:B:229[B]:ARG:HH11	1.35	0.91
1:A:251:PRO:HB2	1:A:253:GLU:OE1	1.75	0.85
1:B:125:LEU:O	2:B:2013:GOL:H31	1.77	0.84
1:A:235:LYS:O	1:A:235:LYS:HD3	1.78	0.84
1:B:215:VAL:HG12	1:B:230[A]:VAL:HG22	1.57	0.84
1:A:111:ALA:HB1	1:A:113:SER:O	1.80	0.81
1:B:318:LEU:HG	1:B:322:ARG:HH11	1.44	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:LYS:C	1:A:235:LYS:HD3	2.01	0.80
1:C:227:GLU:OE1	1:C:249:ARG:NH2	2.17	0.76
1:A:253:GLU:H	1:A:253:GLU:CD	1.88	0.75
1:C:2:ASP:HB2	4:C:2293:HOH:O	1.87	0.75
1:B:115:ARG:HB2	1:B:115:ARG:HH11	1.53	0.74
1:B:229[B]:ARG:HG3	1:B:229[B]:ARG:NH1	2.00	0.73
1:C:2:ASP:HB3	4:C:2358:HOH:O	1.87	0.73
1:A:162:PRO:HB3	1:C:29:GLU:OE2	1.89	0.72
1:B:59[A]:MET:SD	1:B:176:LEU:HD13	2.30	0.71
1:A:114:SER:OG	1:A:260:PRO:HD3	1.93	0.68
1:A:115:ARG:O	1:A:120:ASP:HB3	1.95	0.66
1:B:38:LEU:C	1:B:38:LEU:HD12	2.16	0.66
1:D:261:GLU:OE1	1:D:262:GLU:HG3	1.96	0.65
1:A:232:GLU:HB3	1:A:235:LYS:HB3	1.77	0.65
1:C:258:GLY:HA3	1:C:262:GLU:OE1	1.97	0.65
1:D:240:LEU:HD21	1:D:300[B]:LEU:HD21	1.79	0.64
1:C:270:LEU:HD23	1:C:275:GLU:HB3	1.80	0.64
1:B:318:LEU:CG	1:B:322:ARG:NH1	2.57	0.64
1:C:64[B]:ARG:HD3	1:C:133:PRO:HG2	1.80	0.63
1:A:111:ALA:O	1:A:115:ARG:N	2.31	0.63
1:D:1:MET:HG2	1:D:2:ASP:H	1.63	0.62
1:A:111:ALA:CB	1:A:113:SER:O	2.46	0.62
1:A:114:SER:O	1:A:114:SER:OG	2.18	0.62
1:C:1:MET:HG3	1:C:5:LYS:HD3	1.80	0.62
1:A:235:LYS:CD	1:A:235:LYS:C	2.69	0.61
1:A:111:ALA:O	1:A:113:SER:N	2.33	0.61
1:A:161:ALA:HB3	1:A:162:PRO:HD3	1.83	0.61
1:A:253:GLU:N	1:A:253:GLU:CD	2.55	0.60
1:D:113:SER:C	1:D:115:ARG:H	2.05	0.60
1:B:268:ARG:HH21	2:B:2013:GOL:C1	2.14	0.60
1:A:114:SER:OG	1:A:260:PRO:CG	2.50	0.59
1:C:179:LEU:HD21	1:C:201[B]:MET:HE3	1.84	0.59
1:B:229[B]:ARG:HE	1:B:237:ALA:HB1	1.67	0.59
1:A:134:GLU:O	1:A:138:GLU:HG3	2.03	0.59
1:C:253:GLU:OE1	1:C:256:LYS:HE2	2.01	0.58
1:B:229[B]:ARG:HH11	1:B:229[B]:ARG:CG	2.08	0.58
1:C:179:LEU:HG	1:C:201[B]:MET:HE1	1.84	0.58
1:A:111:ALA:O	1:A:115:ARG:HA	2.04	0.58
1:A:115:ARG:O	1:A:120:ASP:CB	2.52	0.58
1:D:194:SER:HB3	1:D:196:GLU:OE1	2.05	0.57
1:B:85:GLY:HA3	1:B:115:ARG:NH2	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:179:LEU:HD21	1:C:201[B]:MET:CE	2.35	0.56
1:A:111:ALA:O	1:A:113:SER:O	2.23	0.56
1:A:114:SER:OG	1:A:260:PRO:HG3	2.06	0.56
1:B:268:ARG:HH21	2:B:2013:GOL:H12	1.68	0.56
1:C:199:ALA:HB3	1:C:200:PRO:HD3	1.86	0.56
1:A:170:ARG:NH2	1:A:193:PHE:CD2	2.74	0.56
1:A:111:ALA:O	1:A:115:ARG:CA	2.53	0.55
1:B:161:ALA:HB3	1:B:162:PRO:HD3	1.89	0.55
1:B:229[B]:ARG:NE	1:B:237:ALA:HB1	2.20	0.55
1:C:86:LEU:HD11	1:C:252[B]:LEU:HD11	1.88	0.54
1:B:318:LEU:HG	1:B:322:ARG:HH12	1.69	0.54
1:A:114:SER:OG	1:A:260:PRO:CD	2.55	0.54
1:C:241:THR:O	1:C:244:GLU:HB2	2.09	0.53
1:B:318:LEU:CG	1:B:322:ARG:HH12	2.21	0.53
1:D:164:ARG:NH1	4:D:2456:HOH:O	2.41	0.53
1:A:148:LEU:HD13	1:A:182:PRO:HG2	1.90	0.53
1:C:179:LEU:CG	1:C:201[B]:MET:HE1	2.39	0.53
1:D:199:ALA:HB3	1:D:200:PRO:HD3	1.90	0.53
2:D:2009:GOL:H31	4:D:2161:HOH:O	2.07	0.53
1:B:154:HIS:HE1	4:B:2164:HOH:O	1.92	0.52
1:D:113:SER:C	1:D:115:ARG:N	2.62	0.51
1:C:16:GLU:CD	1:C:16:GLU:H	2.13	0.51
1:A:199:ALA:HB3	1:A:200:PRO:HD3	1.93	0.51
2:B:2011:GOL:H12	4:B:2514:HOH:O	2.10	0.51
1:D:261:GLU:OE1	1:D:262:GLU:N	2.44	0.51
1:D:35:ALA:O	1:D:38[A]:LEU:HG	2.11	0.50
1:B:38:LEU:HD12	1:B:39:LEU:N	2.26	0.50
1:C:266:LEU:HD23	1:C:269:ARG:HH21	1.76	0.50
1:A:25[A]:LEU:HD23	1:A:30:VAL:HB	1.93	0.50
1:D:151:ARG:HG2	1:D:151:ARG:HH11	1.75	0.50
1:D:64[A]:ARG:HG3	4:D:2164:HOH:O	2.11	0.50
1:C:70:ARG:HG3	1:C:141[A]:GLU:OE1	2.12	0.49
1:C:67:ARG:HG3	1:C:67:ARG:HH11	1.77	0.49
1:C:134:GLU:O	1:C:138:GLU:HG3	2.12	0.49
1:B:166:GLU:HB2	1:D:29:GLU:HG2	1.95	0.49
1:D:26[B]:MET:SD	1:D:59:MET:HG2	2.52	0.49
1:B:148:LEU:HD13	1:B:182:PRO:HG2	1.95	0.49
1:D:240:LEU:CD2	1:D:300[B]:LEU:HD21	2.43	0.48
1:C:266:LEU:HD23	1:C:269:ARG:NH2	2.27	0.48
1:A:241:THR:OG1	1:A:244:GLU:HG3	2.14	0.48
1:C:265:ALA:HB1	1:C:269:ARG:HH12	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:229[B]:ARG:NH1	1:D:239:ALA:HB2	2.29	0.48
1:C:61:GLU:HG3	4:C:2231:HOH:O	2.14	0.48
1:A:116:ALA:HB2	4:A:2125:HOH:O	2.13	0.47
1:C:115:ARG:O	1:C:260:PRO:HB3	2.14	0.47
1:A:297:THR:HG21	1:A:303:GLY:HA2	1.96	0.47
1:B:230[B]:VAL:HG21	1:B:238:TYR:CE1	2.49	0.47
1:B:134:GLU:O	1:B:138:GLU:HG3	2.14	0.47
1:D:111:ALA:HB3	1:D:116:ALA:H	1.79	0.47
1:D:88:ASN:C	1:D:88:ASN:HD22	2.16	0.47
1:A:114:SER:O	1:A:260:PRO:HG3	2.14	0.47
1:B:112:ALA:O	1:B:113:SER:HB3	2.14	0.47
1:B:32:PRO:HD2	4:B:2388:HOH:O	2.14	0.47
1:A:111:ALA:HB3	1:A:117:GLY:N	2.30	0.47
1:A:111:ALA:O	1:A:112:ALA:C	2.53	0.47
1:C:304:VAL:O	1:C:308:ARG:HG3	2.15	0.47
1:A:114:SER:O	1:A:260:PRO:CG	2.64	0.46
1:D:112:ALA:HA	1:D:113:SER:HA	1.51	0.46
1:D:134:GLU:O	1:D:138:GLU:HG3	2.15	0.46
1:C:38:LEU:O	1:C:42:LEU:HG	2.15	0.46
1:C:64[B]:ARG:HG2	4:C:2136:HOH:O	2.15	0.46
1:B:199:ALA:HB3	1:B:200:PRO:HD3	1.98	0.46
1:D:105:ALA:HB1	1:D:148:LEU:HD11	1.98	0.46
1:A:25[B]:LEU:HG	1:A:160:VAL:CG1	2.46	0.45
1:A:25[B]:LEU:HG	1:A:160:VAL:HG11	1.98	0.45
1:B:115:ARG:CB	1:B:115:ARG:HH11	2.25	0.45
1:B:198:LEU:HD12	1:B:229[B]:ARG:NH1	2.32	0.45
1:C:230:VAL:HG12	1:C:231:VAL:N	2.32	0.45
2:B:2011:GOL:C1	4:B:2514:HOH:O	2.65	0.45
1:A:48:ARG:HH11	1:A:48:ARG:HD2	1.61	0.45
1:A:77:VAL:HG22	1:A:78:GLY:N	2.32	0.45
1:B:231:VAL:HG22	1:B:237:ALA:HB2	1.99	0.45
1:A:111:ALA:C	1:A:113:SER:N	2.70	0.44
1:A:111:ALA:HB3	1:A:117:GLY:H	1.82	0.44
1:A:91[B]:THR:CG2	1:A:118:SER:HB2	2.47	0.44
1:C:71:ARG:HA	1:C:72:PRO:C	2.37	0.44
1:C:64[B]:ARG:CD	1:C:133:PRO:HG2	2.47	0.44
1:B:77:VAL:HG22	1:B:78:GLY:N	2.33	0.44
1:D:272:LYS:HE2	1:D:317:TYR:CE2	2.54	0.43
1:A:261:GLU:CD	1:A:261:GLU:H	2.22	0.43
1:B:194:SER:OG	1:B:196:GLU:HG2	2.18	0.43
1:C:195:PRO:HG3	1:C:216:HIS:CD2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:304:VAL:O	1:B:308:ARG:HG3	2.19	0.43
1:A:59:MET:SD	1:A:176:LEU:HD13	2.59	0.43
1:A:252:LEU:HA	1:A:252:LEU:HD23	1.87	0.42
1:A:66:LEU:HD22	1:A:153:PHE:CE1	2.54	0.42
1:B:53:ALA:HB3	4:B:2245:HOH:O	2.20	0.42
1:A:111:ALA:O	1:A:113:SER:C	2.58	0.42
1:C:158[B]:ARG:HG2	1:D:162:PRO:HB3	2.00	0.42
1:D:230:VAL:HG12	1:D:231:VAL:N	2.34	0.42
1:C:151:ARG:CG	1:C:158[A]:ARG:HG2	2.50	0.42
1:D:70:ARG:HG2	1:D:141:GLU:OE1	2.19	0.42
1:D:1:MET:HG2	1:D:2:ASP:N	2.31	0.42
1:B:191:GLY:HA3	1:B:221:ASP:O	2.20	0.42
1:C:242:PRO:HD2	1:C:243[A]:GLU:OE2	2.20	0.42
1:C:203:GLU:O	1:C:207[B]:ARG:HG3	2.20	0.41
1:C:137:GLY:O	1:C:141[A]:GLU:HG2	2.20	0.41
1:A:304:VAL:O	1:A:308:ARG:HG3	2.19	0.41
1:B:38:LEU:O	1:B:42[A]:LEU:HG	2.21	0.41
1:C:151:ARG:HG2	1:C:151:ARG:NH1	2.36	0.41
1:A:114:SER:HG	1:A:260:PRO:CG	2.33	0.41
1:A:132:PRO:HA	1:A:133:PRO:HD3	1.98	0.41
1:C:86:LEU:HD11	1:C:252[B]:LEU:CD1	2.51	0.41
1:B:71:ARG:HA	1:B:72:PRO:C	2.41	0.41
1:D:64[B]:ARG:HH11	1:D:64[B]:ARG:HG3	1.85	0.41
1:D:132:PRO:HA	1:D:133:PRO:HD3	1.99	0.41
1:A:71:ARG:HA	1:A:72:PRO:C	2.42	0.41
1:D:71:ARG:HA	1:D:72:PRO:C	2.42	0.41
1:B:115:ARG:HB2	1:B:115:ARG:NH1	2.30	0.40
1:D:298:PRO:HG2	1:D:302:GLU:OE1	2.21	0.40
1:B:59[B]:MET:CE	1:B:176:LEU:HD13	2.52	0.40
1:A:109:ASN:ND2	1:A:150:ALA:HB3	2.37	0.40
1:A:211:ARG:NH1	4:A:2252:HOH:O	2.55	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	331/329 (101%)	322 (97%)	6 (2%)	3 (1%)	17	3
1	B	334/329 (102%)	327 (98%)	6 (2%)	1 (0%)	41	19
1	C	340/329 (103%)	333 (98%)	7 (2%)	0	100	100
1	D	339/329 (103%)	333 (98%)	6 (2%)	0	100	100
All	All	1344/1316 (102%)	1315 (98%)	25 (2%)	4 (0%)	41	19

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	ALA
1	B	113	SER
1	A	115	ARG
1	A	114	SER

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	233/229 (102%)	232 (100%)	1 (0%)	91	82
1	B	236/229 (103%)	234 (99%)	2 (1%)	81	66
1	C	242/229 (106%)	239 (99%)	3 (1%)	71	49
1	D	241/229 (105%)	237 (98%)	4 (2%)	60	32
All	All	952/916 (104%)	942 (99%)	10 (1%)	73	53

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	SER
1	B	22	MET
1	B	115	ARG
1	C	113	SER

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Mol	Chain	Res	Type
1	C	227	GLU
1	C	256	LYS
1	D	88	ASN
1	D	113	SER
1	D	261	GLU
1	D	266	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	88	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GOL	B	2013	-	5,5,5	0.30	0	5,5,5	0.28	0
2	GOL	D	2008	-	5,5,5	0.37	0	5,5,5	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	B	2000	-	5,5,5	0.28	0	5,5,5	0.28	0
2	GOL	A	2012	-	5,5,5	0.31	0	5,5,5	0.28	0
2	GOL	A	2003	-	5,5,5	0.27	0	5,5,5	0.31	0
2	GOL	A	2004	-	5,5,5	0.34	0	5,5,5	0.27	0
2	GOL	B	2011	-	5,5,5	0.31	0	5,5,5	0.23	0
2	GOL	C	2007	-	5,5,5	0.36	0	5,5,5	0.25	0
2	GOL	A	2010	-	5,5,5	0.35	0	5,5,5	0.25	0
2	GOL	D	2009	-	5,5,5	0.24	0	5,5,5	0.31	0
2	GOL	C	2001	-	5,5,5	0.31	0	5,5,5	0.30	0
2	GOL	C	2006	-	5,5,5	0.30	0	5,5,5	0.28	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	GOL	B	2013	-	-	0/4/4/4	-
2	GOL	D	2008	-	-	0/4/4/4	-
2	GOL	B	2000	-	-	0/4/4/4	-
2	GOL	A	2012	-	-	0/4/4/4	-
2	GOL	A	2003	-	-	0/4/4/4	-
2	GOL	A	2004	-	-	0/4/4/4	-
2	GOL	B	2011	-	-	0/4/4/4	-
2	GOL	C	2007	-	-	0/4/4/4	-
2	GOL	A	2010	-	-	0/4/4/4	-
2	GOL	D	2009	-	-	0/4/4/4	-
2	GOL	C	2001	-	-	0/4/4/4	-
2	GOL	C	2006	-	-	0/4/4/4	-

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.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2013	GOL	3	0
2	B	2011	GOL	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	2009	GOL	1	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	329/329 (100%)	0.49	31 (9%) 8 9	7, 14, 31, 44	3 (0%)
1	B	329/329 (100%)	0.18	13 (3%) 38 44	6, 12, 26, 35	1 (0%)
1	C	329/329 (100%)	0.33	20 (6%) 21 25	7, 15, 30, 42	4 (1%)
1	D	329/329 (100%)	0.29	21 (6%) 19 23	6, 13, 29, 39	5 (1%)
All	All	1316/1316 (100%)	0.32	85 (6%) 18 22	6, 14, 30, 44	13 (0%)

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	114	SER	10.3
1	A	113	SER	10.0
1	A	81	GLY	8.0
1	A	112	ALA	7.5
1	C	112	ALA	7.3
1	D	114	SER	7.1
1	A	115	ARG	6.6
1	A	83	GLY	6.6
1	C	113	SER	6.5
1	A	111	ALA	6.5
1	D	1	MET	5.9
1	C	1	MET	5.8
1	D	113	SER	5.6
1	D	257	GLY	5.4
1	D	112	ALA	5.3
1	B	69	HIS	5.3
1	D	83	GLY	5.1
1	A	329	ALA	5.1
1	D	115	ARG	5.1
1	B	112	ALA	5.1
1	C	115	ARG	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	85	GLY	4.6
1	B	114	SER	4.6
1	D	258	GLY	4.6
1	B	115	ARG	4.5
1	B	1	MET	4.2
1	D	259	GLY	4.2
1	A	67	ARG	4.1
1	A	116	ALA	4.1
1	A	69	HIS	4.1
1	B	67	ARG	3.6
1	D	260	PRO	3.5
1	C	83	GLY	3.4
1	C	257	GLY	3.4
1	A	1	MET	3.3
1	C	114	SER	3.3
1	D	262	GLU	3.3
1	C	266	LEU	3.3
1	C	261	GLU	3.3
1	C	116	ALA	3.2
1	C	329	ALA	3.2
1	B	113	SER	3.1
1	C	262	GLU	3.0
1	C	258	GLY	3.0
1	A	253	GLU	2.9
1	B	81	GLY	2.9
1	D	116	ALA	2.9
1	D	2	ASP	2.9
1	A	142	GLU	2.8
1	A	158	ARG	2.8
1	C	67	ARG	2.8
1	C	259	GLY	2.8
1	B	329	ALA	2.7
1	D	111	ALA	2.7
1	D	300[A]	LEU	2.7
1	A	134	GLU	2.7
1	D	261	GLU	2.7
1	A	66	LEU	2.6
1	A	141	GLU	2.6
1	C	256	LYS	2.6
1	A	259	GLY	2.6
1	A	86	LEU	2.6
1	A	252	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	161	ALA	2.5
1	C	253	GLU	2.4
1	C	260	PRO	2.4
1	A	317	TYR	2.4
1	D	85	GLY	2.4
1	A	324	VAL	2.4
1	C	252[A]	LEU	2.4
1	D	253	GLU	2.3
1	A	256	LYS	2.3
1	A	68	VAL	2.3
1	B	85	GLY	2.3
1	B	219	GLY	2.2
1	B	83	GLY	2.2
1	A	327	LEU	2.2
1	A	326	PHE	2.2
1	D	252	LEU	2.2
1	B	82	ASP	2.2
1	A	159	HIS	2.1
1	D	67	ARG	2.1
1	D	266	LEU	2.1
1	C	111	ALA	2.0
1	A	48	ARG	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 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. 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(\AA^2)	Q<0.9
2	GOL	A	2010	6/6	0.59	0.30	34,35,35,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	GOL	B	2013	6/6	0.64	0.31	35,38,39,39	0
2	GOL	C	2006	6/6	0.65	0.23	30,31,32,35	0
2	GOL	D	2009	6/6	0.70	0.28	37,39,40,41	0
2	GOL	C	2007	6/6	0.73	0.21	32,32,33,35	0
2	GOL	C	2001	6/6	0.74	0.19	28,29,29,32	0
2	GOL	B	2011	6/6	0.77	0.18	36,37,38,40	0
2	GOL	A	2003	6/6	0.77	0.23	35,36,37,38	0
2	GOL	A	2004	6/6	0.77	0.26	26,32,33,34	0
2	GOL	D	2008	6/6	0.81	0.20	30,31,32,32	0
2	GOL	A	2012	6/6	0.81	0.25	36,37,37,38	0
2	GOL	B	2000	6/6	0.86	0.15	11,20,23,29	0
3	NA	B	2100	1/1	0.95	0.20	35,35,35,35	0
3	NA	D	2101	1/1	0.97	0.36	40,40,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.