Full wwPDB X-ray Structure Validation Report (i)

Feb 26, 2022 – 06:07 am GMT

PDB ID	:	6YQ4
Title	:	Crystal structure of Fusobacterium nucleatum tannase
Authors	:	Mancheno, J.M.; Anguita, J.; Rodriguez, H.
Deposited on	:	2020-04-16
Resolution	:	2.40 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

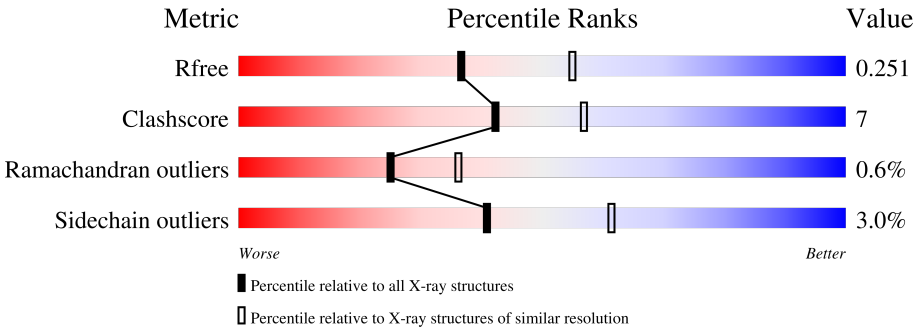
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.27
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	495	80% 15%
1	B	495	79% 17%
1	C	495	81% 14%

2 Entry composition (i)

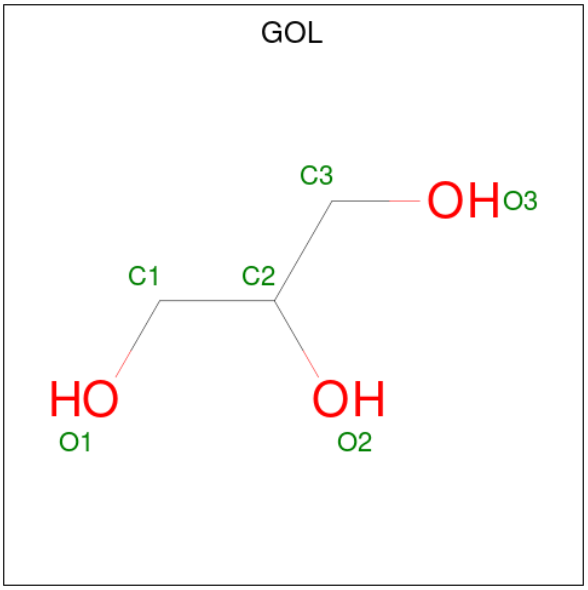
There are 5 unique types of molecules in this entry. The entry contains 11702 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Tannase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	478	Total	C	N	O	S	0	1	0
			3752	2377	635	729	11			
1	B	480	Total	C	N	O	S	0	0	0
			3763	2382	638	732	11			
1	C	478	Total	C	N	O	S	0	1	0
			3749	2374	635	729	11			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

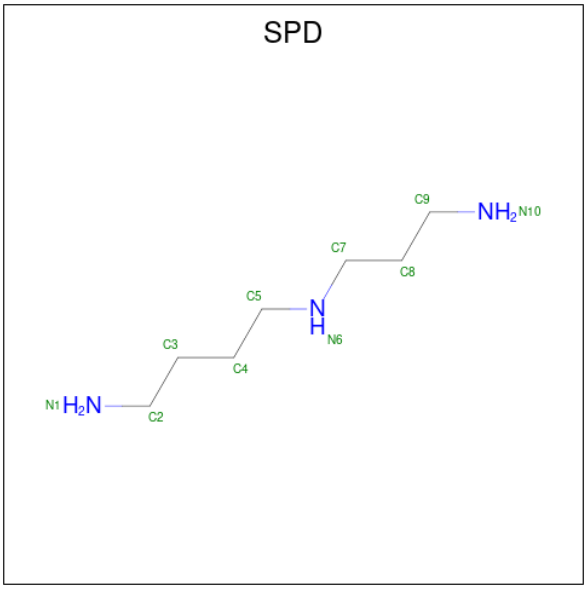


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is SPERMIDINE (three-letter code: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C N 10 7 3	0	0

- Molecule 5 is water.

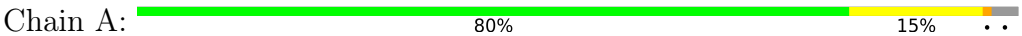
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	180	Total O 180 180	0	0
5	B	107	Total O 107 107	0	0
5	C	120	Total O 120 120	0	0

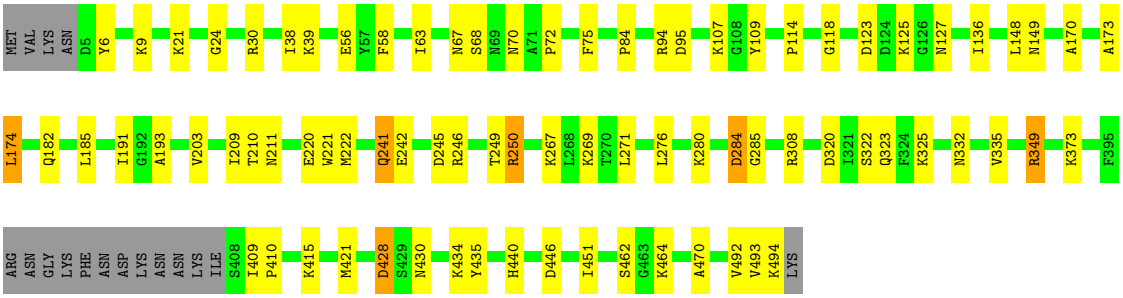
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: Tannase

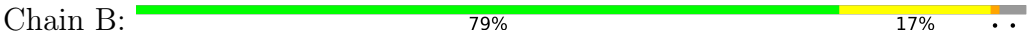
Chain A:

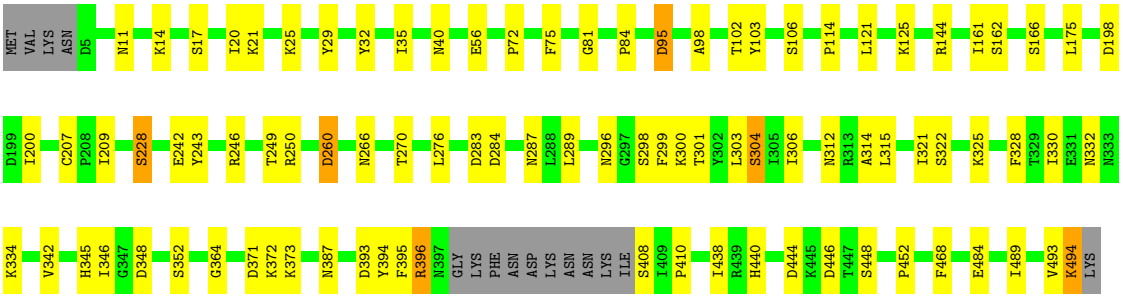




- Molecule 1: Tannase

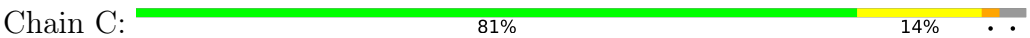
Chain B:

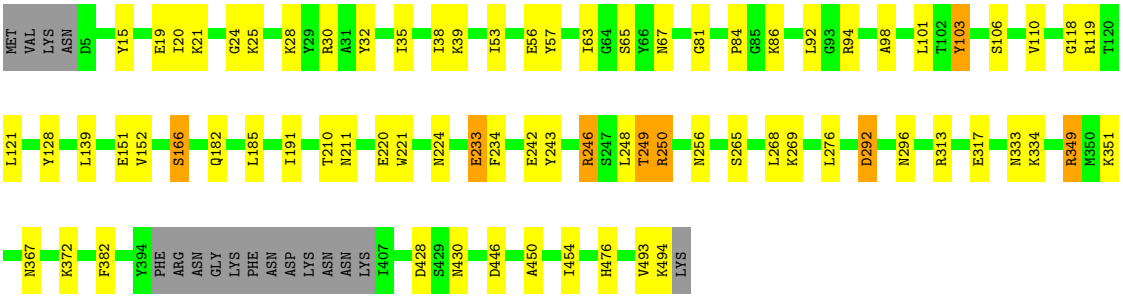




- Molecule 1: Tannase

Chain C:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	71.84Å 91.07Å 124.07Å 90.00° 101.70° 90.00°	Depositor
Resolution (Å)	47.79 – 2.40 47.79 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.0 (47.79-2.40) 98.9 (47.79-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.85 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.171 , 0.251 0.171 , 0.251	Depositor DCC
R_{free} test set	3103 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	33.6	Xtriage
Anisotropy	0.532	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	11702	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, SPD, MG

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	0.46	0/3831	0.61	1/5179 (0.0%)
1	B	0.42	0/3839	0.59	0/5190
1	C	0.43	0/3827	0.57	0/5174
All	All	0.43	0/11497	0.59	1/15543 (0.0%)

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

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	373	LYS	CD-CE-NZ	-6.57	96.58	111.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	393	ASP	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	3752	0	3696	58	0
1	B	3763	0	3702	52	0
1	C	3749	0	3698	47	0
2	A	6	0	8	1	0
2	B	6	0	8	1	0
2	C	6	0	8	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	B	10	0	19	3	0
5	A	180	0	0	4	0
5	B	107	0	0	5	0
5	C	120	0	0	1	0
All	All	11702	0	11139	155	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 (155) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:LYS:NZ	5:A:601:HOH:O	1.94	0.97
1:B:125:LYS:NZ	5:B:601:HOH:O	1.92	0.96
1:C:246:ARG:NH1	1:C:446:ASP:OD2	2.10	0.84
1:C:243:TYR:O	1:C:246:ARG:NH2	2.14	0.80
1:A:409:ILE:HD12	1:A:410:PRO:HD2	1.62	0.79
1:A:221:TRP:HA	1:A:269:LYS:HG3	1.67	0.76
1:C:210:THR:HG22	1:C:211:ASN:H	1.52	0.75
1:A:38:ILE:HD11	1:A:193:ALA:N	2.04	0.73
1:B:364:GLY:H	4:B:502:SPD:H21	1.54	0.72
1:A:38:ILE:HG13	1:A:191:ILE:O	1.89	0.72
1:A:38:ILE:HD12	1:A:193:ALA:HA	1.73	0.70
1:B:289:LEU:HA	1:B:298:SER:HB2	1.74	0.68
1:B:484:GLU:N	1:B:484:GLU:OE2	2.27	0.68
1:C:221:TRP:HA	1:C:269:LYS:HD2	1.77	0.67
1:A:242:GLU:O	5:A:602:HOH:O	2.12	0.66
1:B:303:LEU:HA	1:B:306:ILE:HD12	1.78	0.66
1:A:38:ILE:CD1	1:A:193:ALA:HA	2.26	0.65
1:B:408:SER:OG	5:B:602:HOH:O	2.15	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:THR:O	1:A:250:ARG:HD3	1.99	0.62
1:B:20:ILE:HG12	1:B:29:TYR:HE2	1.64	0.62
1:B:325:LYS:HE3	1:B:330:ILE:HD12	1.84	0.59
1:C:103:TYR:O	1:C:106:SER:OG	2.14	0.59
1:A:94:ARG:HD3	1:A:245:ASP:OD1	2.02	0.59
1:C:128:TYR:HB2	1:C:372:LYS:HA	1.85	0.59
1:A:241:GLN:H	1:A:241:GLN:CD	2.05	0.58
1:A:493:VAL:O	1:A:494:LYS:HB2	2.03	0.58
1:A:9:LYS:HD3	1:A:149:ASN:OD1	2.04	0.57
1:A:220:GLU:OE1	1:A:349[B]:ARG:NH2	2.27	0.57
1:C:15:TYR:CD1	1:C:30:ARG:HG2	2.40	0.57
1:C:233:GLU:H	1:C:233:GLU:CD	2.08	0.57
1:A:284:ASP:HB3	1:B:121:LEU:HD12	1.86	0.56
1:C:242:GLU:OE1	1:C:249:THR:HG21	2.05	0.55
1:A:38:ILE:CD1	1:A:193:ALA:CA	2.86	0.53
1:B:32:TYR:HB3	1:B:35:ILE:HD11	1.89	0.53
1:A:67:ASN:OD1	1:A:70:ASN:HB2	2.08	0.53
1:C:15:TYR:CE1	1:C:30:ARG:HG2	2.43	0.53
1:C:19:GLU:HG2	1:C:28:LYS:HG2	1.89	0.53
1:A:415:LYS:N	1:A:415:LYS:HD3	2.23	0.53
1:B:14:LYS:HD2	1:B:14:LYS:N	2.25	0.52
1:A:428:ASP:HB3	1:A:430:ASN:H	1.75	0.52
1:B:301:THR:HA	1:B:304:SER:HB3	1.90	0.52
1:C:56:GLU:OE2	1:C:63:ILE:HD11	2.10	0.52
1:A:38:ILE:CG1	1:A:191:ILE:O	2.56	0.52
1:A:75:PHE:CZ	1:A:114:PRO:HG3	2.45	0.52
1:C:210:THR:HG22	1:C:211:ASN:N	2.22	0.52
1:C:248:LEU:O	1:C:249:THR:OG1	2.27	0.52
1:C:38:ILE:HG21	1:C:191:ILE:HD12	1.91	0.52
1:C:65:SER:O	1:C:65:SER:OG	2.28	0.51
1:B:296:ASN:OD1	1:B:300:LYS:NZ	2.39	0.51
1:A:136:ILE:HG12	1:A:174:LEU:HD13	1.93	0.51
1:A:249:THR:C	1:A:250:ARG:HD3	2.31	0.50
1:A:332:ASN:N	5:A:609:HOH:O	2.38	0.50
1:C:292:ASP:HB2	1:C:296:ASN:O	2.11	0.50
1:B:321:ILE:HG23	1:B:328:PHE:HE2	1.76	0.50
1:A:280:LYS:NZ	5:A:611:HOH:O	2.44	0.50
1:C:15:TYR:HB3	1:C:32:TYR:CE2	2.47	0.50
1:B:364:GLY:N	4:B:502:SPD:H21	2.27	0.49
1:C:94:ARG:NH1	1:C:248:LEU:HG	2.28	0.49
1:B:161:ILE:HG21	1:B:489:ILE:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:322:SER:O	1:B:325:LYS:HG2	2.11	0.49
1:B:342:VAL:O	1:B:346:ILE:HG13	2.13	0.49
1:A:67:ASN:H	1:A:70:ASN:HB3	1.76	0.49
1:A:182:GLN:HA	1:A:185:LEU:HG	1.95	0.49
1:A:209:ILE:HG13	2:A:501:GOL:H12	1.95	0.48
1:C:32:TYR:HB3	1:C:35:ILE:HD11	1.96	0.48
1:C:166:SER:OG	1:C:476:HIS:NE2	2.33	0.48
1:C:333:ASN:O	1:C:334:LYS:HD2	2.14	0.48
1:B:11:ASN:CG	1:B:14:LYS:HD3	2.35	0.48
1:C:313:ARG:O	1:C:317:GLU:HG3	2.14	0.48
1:C:220:GLU:HG3	1:C:265:SER:HA	1.96	0.47
1:C:428:ASP:HB3	1:C:430:ASN:H	1.78	0.47
1:A:440:HIS:O	1:A:470:ALA:HA	2.14	0.47
1:C:81:GLY:HA3	1:C:243:TYR:CD2	2.49	0.47
1:B:440:HIS:NE2	1:B:444:ASP:HB3	2.30	0.47
1:C:39:LYS:NZ	5:C:610:HOH:O	2.48	0.47
1:A:72:PRO:HB2	1:A:109:TYR:CD2	2.49	0.47
1:C:20:ILE:HD12	1:C:21:LYS:H	1.79	0.47
1:B:72:PRO:HG3	1:B:493:VAL:HG11	1.97	0.47
1:A:38:ILE:CD1	1:A:193:ALA:N	2.76	0.46
1:B:56:GLU:OE2	1:B:56:GLU:N	2.43	0.46
1:C:53:ILE:HG12	1:C:110:VAL:HG13	1.97	0.46
1:B:81:GLY:HA3	1:B:243:TYR:CE2	2.50	0.46
1:C:57:TYR:CE1	1:C:67:ASN:HA	2.50	0.46
1:B:266:ASN:O	1:B:270:THR:HG23	2.16	0.46
1:A:308:ARG:HG3	1:A:335:VAL:HG12	1.98	0.46
1:B:387:ASN:OD1	1:B:410:PRO:HB3	2.16	0.46
1:B:75:PHE:CZ	1:B:114:PRO:HG3	2.51	0.46
1:B:98:ALA:HB1	1:B:102:THR:HB	1.98	0.46
1:C:151:GLU:HB3	1:C:152:VAL:HG13	1.98	0.46
1:C:450:ALA:O	1:C:454:ILE:HG12	2.16	0.46
1:A:415:LYS:HD3	1:A:415:LYS:H	1.79	0.46
1:B:371:ASP:HB2	5:B:673:HOH:O	2.15	0.46
1:C:92:LEU:HD23	1:C:98:ALA:HA	1.97	0.46
1:A:435:TYR:CD2	1:A:492:VAL:HG13	2.51	0.45
1:B:228:SER:OG	1:B:348:ASP:OD1	2.34	0.45
1:B:312:ASN:HA	1:B:315:LEU:HD12	1.98	0.45
1:A:222:MET:HE3	1:A:222:MET:HB2	1.86	0.45
1:B:246:ARG:HA	1:B:246:ARG:HD3	1.66	0.45
1:B:276:LEU:HD21	1:B:299:PHE:CG	2.51	0.45
1:C:493:VAL:O	1:C:494:LYS:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:GLN:H	1:A:323:GLN:HG3	1.54	0.45
1:A:246:ARG:HA	1:A:250:ARG:HH22	1.81	0.44
1:B:352:SER:H	4:B:502:SPD:H91	1.81	0.44
1:A:285:GLY:HA2	1:B:84:PRO:HG2	1.99	0.44
1:B:209:ILE:HG13	2:B:501:GOL:H2	1.99	0.44
1:B:314:ALA:CB	1:B:321:ILE:HD11	2.47	0.44
1:B:166:SER:HA	1:B:207:CYS:O	2.18	0.44
1:C:84:PRO:N	1:C:118:GLY:HA3	2.33	0.44
1:A:84:PRO:N	1:A:118:GLY:HA3	2.32	0.44
1:A:462:SER:O	1:A:464:LYS:HE2	2.17	0.44
1:B:283:ASP:OD1	1:B:287:ASN:HB2	2.19	0.43
1:B:325:LYS:HD2	1:B:325:LYS:HA	1.80	0.43
1:A:95:ASP:OD1	1:A:95:ASP:N	2.50	0.43
1:B:162:SER:HB2	1:B:200:ILE:HD12	2.00	0.43
1:A:123:ASP:OD1	1:A:127:ASN:N	2.51	0.43
1:A:30:ARG:HD2	1:A:58:PHE:CE2	2.53	0.43
1:B:332:ASN:O	1:B:334:LYS:N	2.52	0.43
1:B:81:GLY:HA3	1:B:243:TYR:CD2	2.53	0.43
1:C:182:GLN:HA	1:C:185:LEU:HD12	2.00	0.43
1:B:325:LYS:HE3	1:B:330:ILE:CD1	2.49	0.43
1:C:139:LEU:HD23	1:C:139:LEU:HA	1.81	0.43
1:A:250:ARG:HE	1:A:250:ARG:HB2	1.63	0.42
1:A:107:LYS:HA	1:A:107:LYS:HD3	1.88	0.42
1:A:170:ALA:CB	1:A:210:THR:HG23	2.49	0.42
1:A:6:TYR:O	1:A:39:LYS:HG2	2.19	0.42
1:A:56:GLU:CD	1:A:63:ILE:HD11	2.39	0.42
1:A:173:ALA:HA	1:A:203:VAL:HG11	2.01	0.42
1:A:322:SER:HA	1:A:325:LYS:HD2	2.02	0.42
1:B:438:ILE:O	1:B:468:PHE:HA	2.20	0.42
1:C:121:LEU:HD12	1:C:121:LEU:HA	1.85	0.42
1:A:435:TYR:CG	1:A:492:VAL:HG13	2.54	0.42
1:B:103:TYR:O	1:B:106:SER:HB3	2.20	0.42
1:B:242:GLU:CD	1:B:250:ARG:HD3	2.40	0.42
1:B:394:TYR:HA	5:B:610:HOH:O	2.19	0.42
1:C:234:PHE:HD1	1:C:234:PHE:HA	1.67	0.42
1:A:267:LYS:O	1:A:271:LEU:HD13	2.20	0.41
1:C:101:LEU:H	1:C:101:LEU:HD12	1.84	0.41
1:C:249:THR:HA	1:C:250:ARG:NE	2.34	0.41
1:C:334:LYS:HD2	1:C:334:LYS:HA	1.77	0.41
1:C:349[B]:ARG:NE	1:C:351:LYS:O	2.45	0.41
1:A:494:LYS:HD3	1:A:494:LYS:HA	1.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:119:ARG:HD2	1:C:367:ASN:HB3	2.03	0.41
1:C:220:GLU:O	1:C:224:ASN:HB2	2.20	0.41
1:A:170:ALA:HB1	1:A:210:THR:HG23	2.03	0.41
1:A:320:ASP:OD2	1:A:322:SER:HB3	2.21	0.41
1:C:25:LYS:HD2	1:C:25:LYS:HA	1.79	0.41
1:A:174:LEU:HD11	1:A:421:MET:HA	2.03	0.41
1:B:260:ASP:OD2	1:B:260:ASP:N	2.54	0.41
1:B:493:VAL:O	1:B:494:LYS:HD2	2.20	0.41
1:B:448:SER:O	1:B:452:PRO:HD2	2.21	0.41
1:A:38:ILE:HD11	1:A:193:ALA:CA	2.51	0.40
1:B:396:ARG:HG2	5:B:610:HOH:O	2.20	0.40
1:A:211:ASN:HB3	1:A:451:ILE:HD12	2.02	0.40
1:C:268:LEU:HD21	1:C:382:PHE:CD1	2.56	0.40
1:B:144:ARG:HG3	1:B:198:ASP:HB3	2.04	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	475/495 (96%)	455 (96%)	19 (4%)	1 (0%)	47 62
1	B	476/495 (96%)	450 (94%)	23 (5%)	3 (1%)	25 36
1	C	475/495 (96%)	447 (94%)	24 (5%)	4 (1%)	19 29
All	All	1426/1485 (96%)	1352 (95%)	66 (5%)	8 (1%)	25 36

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	395	PHE
1	C	233	GLU
1	B	95	ASP

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Mol	Chain	Res	Type
1	B	249	THR
1	C	249	THR
1	C	292	ASP
1	A	24	GLY
1	C	24	GLY

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	403/418 (96%)	390 (97%)	13 (3%)	39	59
1	B	404/418 (97%)	388 (96%)	16 (4%)	31	49
1	C	403/418 (96%)	394 (98%)	9 (2%)	52	71
All	All	1210/1254 (96%)	1172 (97%)	38 (3%)	41	60

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	LYS
1	A	68	SER
1	A	148	LEU
1	A	174	LEU
1	A	241	GLN
1	A	250	ARG
1	A	276	LEU
1	A	284	ASP
1	A	349[A]	ARG
1	A	349[B]	ARG
1	A	428	ASP
1	A	434	LYS
1	A	446	ASP
1	B	17	SER
1	B	21	LYS
1	B	25	LYS
1	B	40	ASN

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Mol	Chain	Res	Type
1	B	95	ASP
1	B	175	LEU
1	B	228	SER
1	B	260	ASP
1	B	284	ASP
1	B	304	SER
1	B	345	HIS
1	B	372	LYS
1	B	373	LYS
1	B	396	ARG
1	B	446	ASP
1	B	494	LYS
1	C	86	LYS
1	C	103	TYR
1	C	166	SER
1	C	246	ARG
1	C	250	ARG
1	C	256	ASN
1	C	276	LEU
1	C	349[A]	ARG
1	C	349[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	241	GLN
1	B	40	ASN
1	B	254	GLN
1	B	333	ASN
1	B	430	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	A	501	-	5,5,5	0.93	0	5,5,5	0.96	0
2	GOL	B	501	-	5,5,5	0.92	0	5,5,5	1.01	0
2	GOL	C	501	-	5,5,5	0.71	0	5,5,5	1.13	0
4	SPD	B	502	-	9,9,9	0.34	0	8,8,8	0.51	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	A	501	-	-	2/4/4/4	-
2	GOL	B	501	-	-	2/4/4/4	-
2	GOL	C	501	-	-	2/4/4/4	-
4	SPD	B	502	-	-	4/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	C1-C2-C3-O3
2	B	501	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
4	B	502	SPD	C8-C7-N6-C5
2	B	501	GOL	O1-C1-C2-O2
4	B	502	SPD	C4-C5-N6-C7
4	B	502	SPD	N6-C7-C8-C9
2	A	501	GOL	O2-C2-C3-O3
4	B	502	SPD	N1-C2-C3-C4
2	C	501	GOL	O2-C2-C3-O3
2	C	501	GOL	C1-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	GOL	1	0
2	B	501	GOL	1	0
4	B	502	SPD	3	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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.