Full wwPDB X-ray Structure Validation Report ⓘ

Dec 16, 2020 – 12:12 pm GMT

PDB ID	:	6ZQ6
Title	:	Crystal structure of Chaetomium thermophilum Glycerol Kinase in complex with glycerol in P21212 space group
Authors	:	Wilk, P.; Wator, E.; Grudnik, P.
Deposited on	:	2020-07-09
Resolution	:	2.30 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:

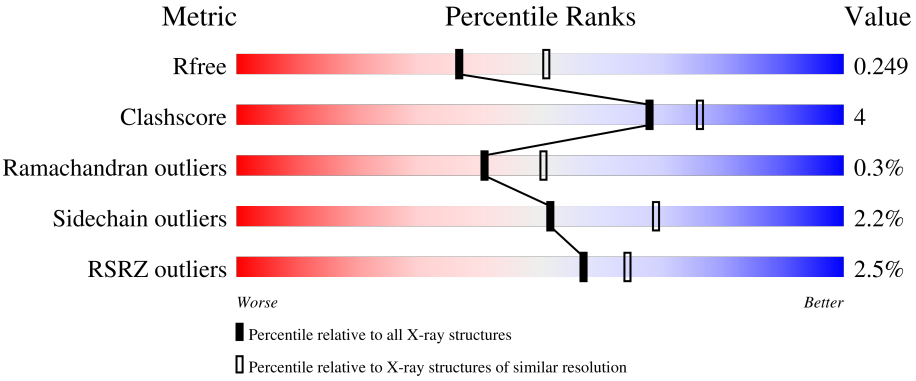
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.15.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.15.1

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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% 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	526	3% 87% 9%
1	B	526	3% 86% 11%
1	C	526	88% 8%
1	D	526	90% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 31410 atoms, of which 15389 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.

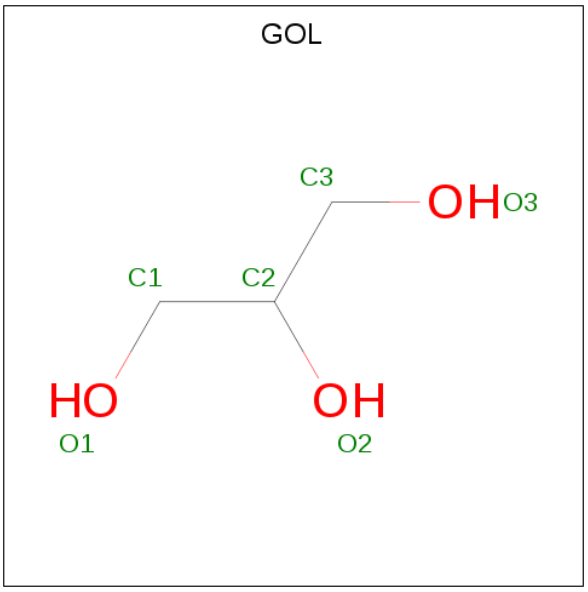
- Molecule 1 is a protein called Glycerol kinase-like protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	510	Total	C	H	N	O	S	0	0	0
			7738	2465	3846	671	740	16			
1	B	510	Total	C	H	N	O	S	0	0	0
			7728	2467	3831	674	740	16			
1	C	509	Total	C	H	N	O	S	0	2	0
			7730	2470	3831	673	740	16			
1	D	509	Total	C	H	N	O	S	0	1	0
			7726	2463	3838	669	739	17			

There are 8 discrepancies between the modelled and reference sequences:

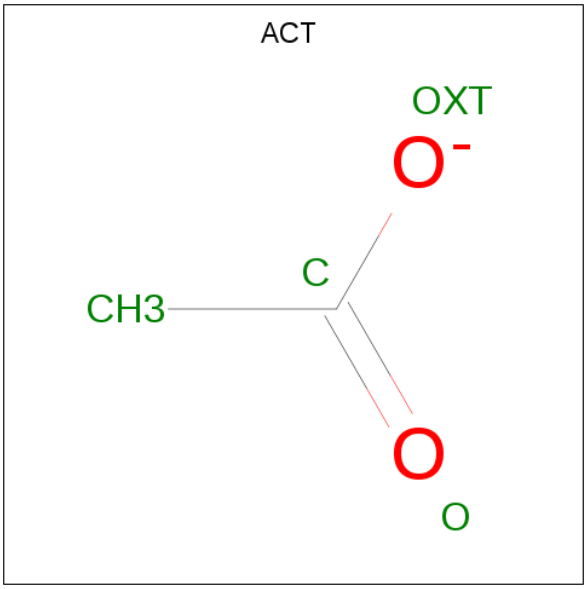
Chain	Residue	Modelled	Actual	Comment	Reference
A	65	GLY	-	expression tag	UNP G0SAG9
A	66	SER	-	expression tag	UNP G0SAG9
B	65	GLY	-	expression tag	UNP G0SAG9
B	66	SER	-	expression tag	UNP G0SAG9
C	65	GLY	-	expression tag	UNP G0SAG9
C	66	SER	-	expression tag	UNP G0SAG9
D	65	GLY	-	expression tag	UNP G0SAG9
D	66	SER	-	expression tag	UNP G0SAG9

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			14	3	8	3		
2	B	1	Total	C	H	O	0	0
			14	3	8	3		
2	C	1	Total	C	H	O	0	0
			14	3	8	3		
2	D	1	Total	C	H	O	0	0
			14	3	8	3		
2	D	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C H O 7 2 3 2	0	0

- Molecule 4 is water.

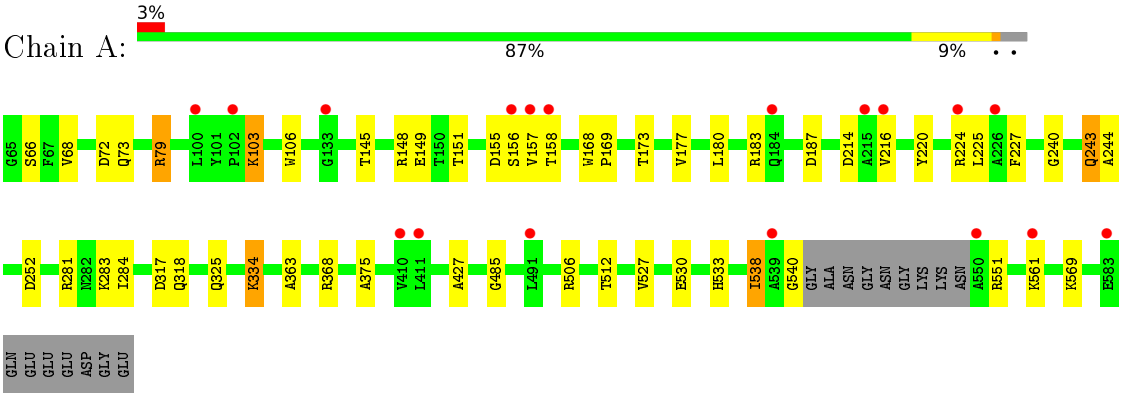
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	80	Total O 80 80	0	0
4	B	87	Total O 87 87	0	0
4	C	132	Total O 132 132	0	0
4	D	112	Total O 112 112	0	0

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 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.

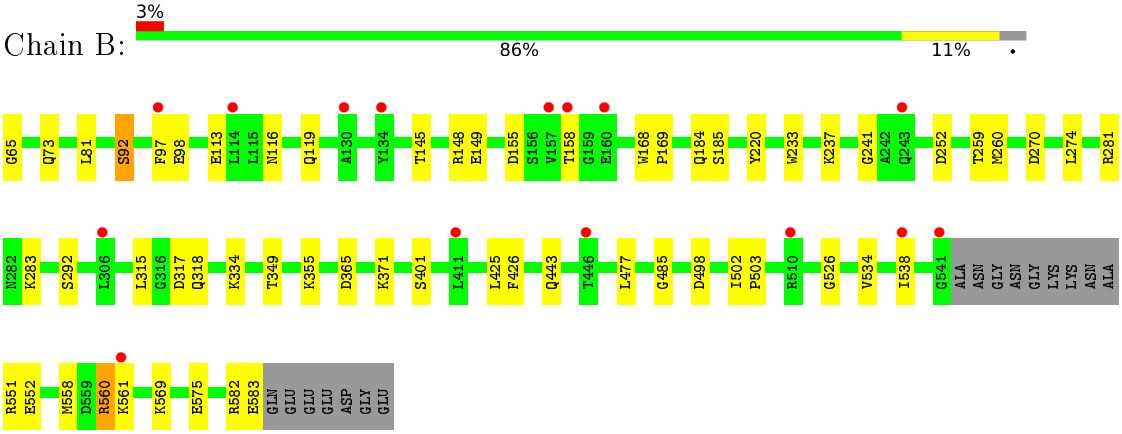
- Molecule 1: Glycerol kinase-like protein

Chain A:



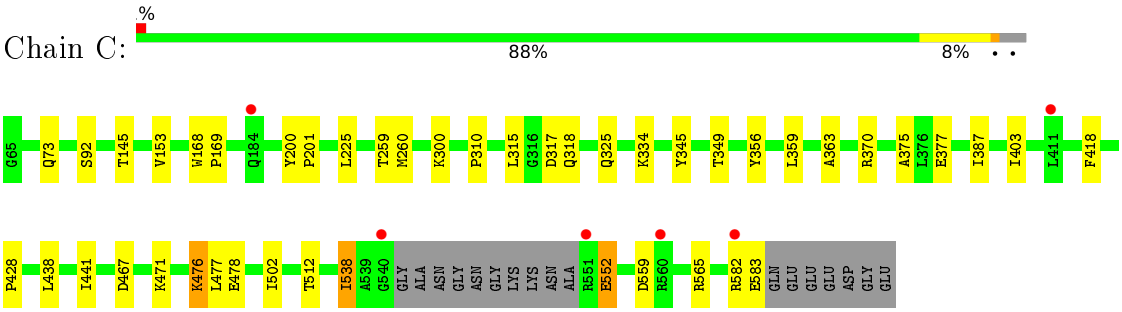
- Molecule 1: Glycerol kinase-like protein

Chain B:



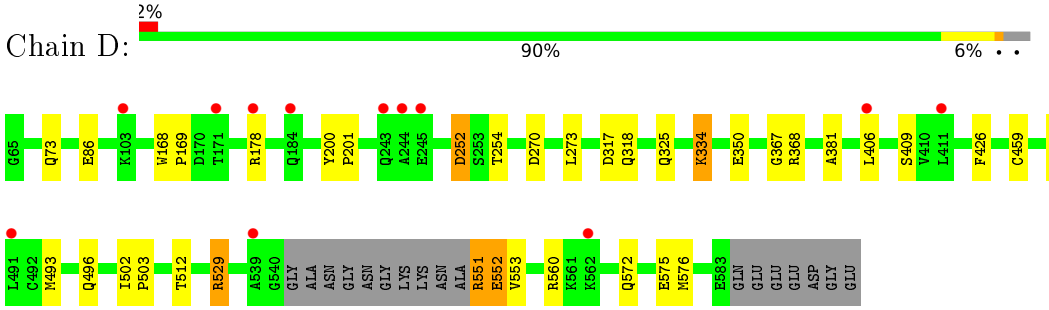
- Molecule 1: Glycerol kinase-like protein

Chain C:



• Molecule 1: Glycerol kinase-like protein

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	170.73Å 222.03Å 61.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.60 – 2.30 48.60 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.5 (48.60-2.30) 98.5 (48.60-2.30)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.11 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.214 , 0.249 0.215 , 0.249	Depositor DCC
R_{free} test set	2101 reflections (2.04%)	wwPDB-VP
Wilson B-factor (Å^2)	41.3	Xtriage
Anisotropy	0.236	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 40.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	31410	wwPDB-VP
Average B, all atoms (Å^2)	57.0	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 32.80 % 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 8.8572e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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, ACT

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	0.41	2/3974 (0.1%)	0.52	2/5388 (0.0%)
1	B	0.38	2/3979 (0.1%)	0.59	3/5393 (0.1%)
1	C	0.36	1/3987 (0.0%)	0.51	0/5405
1	D	0.36	1/3973 (0.0%)	0.51	0/5387
All	All	0.38	6/15913 (0.0%)	0.53	5/21573 (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

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	561	LYS	CE-NZ	-10.24	1.23	1.49
1	A	427	ALA	C-N	9.96	1.53	1.34
1	D	350	GLU	C-N	9.66	1.52	1.34
1	B	425	LEU	C-N	-7.81	1.16	1.34
1	B	65	GLY	C-O	-6.87	1.12	1.23
1	C	428	PRO	C-O	-5.26	1.12	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	425	LEU	C-N-CA	15.85	161.33	121.70
1	B	425	LEU	O-C-N	-12.13	103.29	122.70
1	A	561	LYS	CD-CE-NZ	-11.02	86.35	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	425	LEU	CA-C-N	8.82	136.61	117.20
1	A	103	LYS	CD-CE-NZ	-8.78	91.50	111.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	426	PHE	Mainchain

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	3892	3846	3846	33	0
1	B	3897	3831	3854	30	0
1	C	3899	3831	3861	25	0
1	D	3888	3838	3839	34	0
2	A	6	8	8	0	0
2	B	6	8	8	1	0
2	C	6	8	8	0	0
2	D	12	16	16	1	0
3	C	4	3	3	0	0
4	A	80	0	0	3	0
4	B	87	0	0	1	0
4	C	132	0	0	3	0
4	D	112	0	0	3	0
All	All	16021	15389	15443	117	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 4.

All (117) 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:D:482:VAL:HG21	1:D:493:MET:CE	1.77	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:482:VAL:HG21	1:D:493:MET:HE2	1.26	1.10
1:C:552:GLU:OE1	4:C:701:HOH:O	1.90	0.88
1:B:583:GLU:OE1	4:B:701:HOH:O	1.99	0.79
1:D:575:GLU:OE2	4:D:701:HOH:O	2.03	0.75
1:D:482:VAL:CG2	1:D:493:MET:CE	2.62	0.75
1:B:498:ASP:O	1:B:560:ARG:NH2	2.21	0.73
1:C:538:ILE:HD12	1:C:538:ILE:C	2.12	0.69
1:A:155:ASP:OD1	1:A:157:VAL:HG22	1.93	0.69
1:D:482:VAL:HG11	1:D:493:MET:HE3	1.74	0.69
1:C:559:ASP:OD1	4:C:702:HOH:O	2.13	0.67
1:A:151:THR:HG23	1:A:227:PHE:HE1	1.59	0.67
1:D:252:ASP:OD2	1:D:254:THR:OG1	2.11	0.65
1:A:368:ARG:NH2	1:B:270:ASP:OD1	2.30	0.64
1:D:178:ARG:NH2	4:D:705:HOH:O	2.30	0.63
1:A:151:THR:HG23	1:A:227:PHE:CE1	2.33	0.63
1:C:370:ARG:NH1	4:C:704:HOH:O	2.31	0.62
1:D:482:VAL:HG11	1:D:493:MET:CE	2.29	0.62
1:A:538:ILE:N	1:A:538:ILE:HD13	2.15	0.61
1:A:103:LYS:HD2	1:A:106:TRP:CE2	2.39	0.57
1:D:482:VAL:CB	1:D:493:MET:HE1	2.34	0.57
1:B:317:ASP:OD2	2:B:601:GOL:O3	2.22	0.57
1:C:259:THR:O	1:C:260:MET:HB2	2.06	0.56
1:B:233:TRP:CH2	1:B:237:LYS:HE3	2.40	0.56
1:C:477:LEU:HG	1:C:502:ILE:HD13	1.88	0.55
1:B:259:THR:O	1:B:260:MET:HB2	2.06	0.55
1:A:240:GLY:HA3	1:A:244:ALA:HB2	1.88	0.55
1:B:502:ILE:HG13	1:B:503:PRO:HD2	1.88	0.55
1:A:506:ARG:HH21	1:A:551:ARG:H	1.55	0.54
1:D:552:GLU:O	1:D:552:GLU:HG3	2.07	0.53
1:B:575:GLU:OE2	1:C:356:TYR:OH	2.23	0.52
1:D:482:VAL:HG21	1:D:493:MET:HE1	1.81	0.52
1:A:187:ASP:N	1:A:187:ASP:OD1	2.43	0.51
1:C:438:LEU:HD23	1:C:441:ILE:HD11	1.92	0.51
1:D:86:GLU:O	4:D:703:HOH:O	2.18	0.51
1:B:317:ASP:OD1	1:B:318:GLN:N	2.44	0.51
1:A:103:LYS:HD2	1:A:106:TRP:CD2	2.46	0.50
1:A:183:ARG:NH2	4:A:706:HOH:O	2.44	0.50
1:C:582:ARG:O	1:C:583:GLU:HB2	2.12	0.50
1:A:318:GLN:OE1	1:A:334:LYS:NZ	2.40	0.49
1:A:540:GLY:HA2	4:A:769:HOH:O	2.13	0.48
1:D:406:LEU:O	1:D:409:SER:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:GLU:HG2	1:A:533:HIS:H	1.79	0.48
1:B:582:ARG:O	1:B:583:GLU:CB	2.61	0.48
1:B:145:THR:HA	1:B:315:LEU:O	2.13	0.48
1:D:482:VAL:CG2	1:D:493:MET:HE1	2.39	0.48
1:B:292:SER:N	1:B:365:ASP:O	2.46	0.48
1:B:582:ARG:O	1:B:583:GLU:HB2	2.13	0.48
1:D:168:TRP:CG	1:D:169:PRO:HD3	2.49	0.48
1:D:502:ILE:HG13	1:D:503:PRO:HD2	1.96	0.48
1:C:317:ASP:OD1	1:C:318:GLN:N	2.47	0.47
1:D:318:GLN:OE1	1:D:334:LYS:NZ	2.45	0.47
1:C:168:TRP:CG	1:C:169:PRO:HD3	2.49	0.47
1:A:168:TRP:CG	1:A:169:PRO:HD3	2.50	0.47
1:D:551:ARG:HG3	1:D:551:ARG:HH11	1.79	0.47
1:B:477:LEU:HG	1:B:502:ILE:HD13	1.96	0.46
1:D:381:ALA:HB2	1:D:426:PHE:HE2	1.81	0.46
1:D:482:VAL:HB	1:D:493:MET:HE1	1.98	0.46
1:A:72:ASP:OD2	1:A:79:ARG:NH2	2.49	0.46
1:D:318:GLN:HE21	2:D:601:GOL:H12	1.81	0.46
1:C:325:GLN:HG2	1:C:512:THR:HG21	1.98	0.46
1:B:220:TYR:O	1:B:283:LYS:HG2	2.16	0.45
1:D:270:ASP:HB3	1:D:273:LEU:HD12	1.98	0.45
1:A:173:THR:O	1:A:177:VAL:HG23	2.17	0.45
1:C:387:ILE:HD12	1:C:403:ILE:HG21	1.98	0.45
1:D:381:ALA:HB2	1:D:426:PHE:CE2	2.52	0.45
1:A:363:ALA:HB2	1:A:375:ALA:HB2	1.98	0.45
1:B:168:TRP:CG	1:B:169:PRO:HD3	2.51	0.45
1:B:155:ASP:HB3	1:B:158:THR:OG1	2.16	0.44
1:C:345:TYR:HE2	1:C:477:LEU:HD13	1.83	0.44
1:C:476:LYS:NZ	1:C:478:GLU:OE2	2.44	0.44
1:D:551:ARG:HG3	1:D:551:ARG:NH1	2.32	0.44
1:A:220:TYR:CE1	1:A:284:ILE:HB	2.52	0.44
1:B:116:ASN:HA	1:B:119:GLN:OE1	2.18	0.44
1:A:368:ARG:HH22	1:B:270:ASP:CG	2.21	0.44
1:B:355:LYS:HZ1	1:C:349:THR:HG23	1.82	0.44
1:D:325:GLN:HG2	1:D:512:THR:HG21	1.99	0.44
1:A:220:TYR:CZ	1:A:283:LYS:HD2	2.52	0.44
1:B:274:LEU:HD13	1:B:281:ARG:HG2	2.00	0.44
1:B:526:GLY:HA3	1:D:529:ARG:HB3	2.00	0.44
1:D:560:ARG:HD2	1:D:560:ARG:HA	1.89	0.44
1:A:216:VAL:HG13	1:A:225:LEU:HD13	1.99	0.43
1:A:325:GLN:HG2	1:A:512:THR:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:145:THR:OG1	1:C:317:ASP:HA	2.18	0.43
1:B:502:ILE:HG13	1:B:503:PRO:CD	2.49	0.43
1:A:569:LYS:HA	1:A:569:LYS:HD2	1.83	0.43
1:A:317:ASP:OD1	1:A:318:GLN:N	2.52	0.42
1:C:300:LYS:HB3	1:C:310:PRO:HA	1.99	0.42
1:A:155:ASP:HB3	1:A:158:THR:CG2	2.49	0.42
1:C:582:ARG:O	1:C:583:GLU:CB	2.68	0.42
1:D:459:CYS:HA	1:D:496:GLN:OE1	2.19	0.42
1:A:68:VAL:CG2	1:A:527:VAL:HG21	2.50	0.42
1:B:534:VAL:O	1:B:538:ILE:HG12	2.20	0.42
1:D:482:VAL:CB	1:D:493:MET:CE	2.96	0.42
1:B:184:GLN:O	1:B:185:SER:HB2	2.20	0.42
1:B:498:ASP:HB3	1:B:558:MET:HB3	2.02	0.42
1:D:317:ASP:OD1	1:D:318:GLN:N	2.53	0.42
1:C:200:TYR:HB2	1:C:201:PRO:HD3	2.01	0.41
1:C:359:LEU:HB2	1:C:377:GLU:HB3	2.03	0.41
1:B:148:ARG:O	1:B:149:GLU:HB2	2.21	0.41
1:B:81:LEU:HG	1:B:92:SER:HB2	2.03	0.41
1:C:145:THR:HA	1:C:315:LEU:O	2.20	0.41
1:A:281:ARG:NH1	4:A:701:HOH:O	1.88	0.41
1:B:349:THR:HB	1:B:371:LYS:HE3	2.02	0.41
1:A:145:THR:OG1	1:A:317:ASP:HA	2.20	0.41
1:C:153:VAL:HB	1:C:225:LEU:HD11	2.02	0.41
1:A:103:LYS:HB2	1:A:106:TRP:CG	2.56	0.40
1:A:148:ARG:O	1:A:149:GLU:HB2	2.21	0.40
1:A:243:GLN:OE1	1:A:243:GLN:CA	2.69	0.40
1:C:467:ASP:O	1:C:471:LYS:HG3	2.21	0.40
1:A:180:LEU:HD23	1:A:183:ARG:HD2	2.03	0.40
1:C:363:ALA:HB2	1:C:375:ALA:HB2	2.03	0.40
1:D:200:TYR:HB2	1:D:201:PRO:HD3	2.04	0.40
1:D:529:ARG:HG2	1:D:529:ARG:HH11	1.87	0.40
1:D:553:VAL:HG13	1:D:553:VAL:O	2.22	0.40
1:D:572:GLN:HG2	1:D:576[B]:MET:HE3	2.03	0.40
1:B:97:PHE:HB2	1:B:113:GLU:HG3	2.03	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	506/526 (96%)	488 (96%)	17 (3%)	1 (0%)	47	58
1	B	506/526 (96%)	490 (97%)	14 (3%)	2 (0%)	34	42
1	C	507/526 (96%)	487 (96%)	20 (4%)	0	100	100
1	D	506/526 (96%)	492 (97%)	11 (2%)	3 (1%)	25	31
All	All	2025/2104 (96%)	1957 (97%)	62 (3%)	6 (0%)	41	50

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	368	ARG
1	A	485	GLY
1	B	485	GLY
1	D	367	GLY
1	D	485	GLY
1	B	241	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	408/420 (97%)	398 (98%)	10 (2%)	47	65
1	B	409/420 (97%)	397 (97%)	12 (3%)	42	58
1	C	410/420 (98%)	402 (98%)	8 (2%)	55	72
1	D	408/420 (97%)	402 (98%)	6 (2%)	65	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1635/1680 (97%)	1599 (98%)	36 (2%)	52 69

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	SER
1	A	73	GLN
1	A	79	ARG
1	A	156	SER
1	A	214	ASP
1	A	224	ARG
1	A	243	GLN
1	A	252	ASP
1	A	334	LYS
1	A	538	ILE
1	B	73	GLN
1	B	92	SER
1	B	98	GLU
1	B	252	ASP
1	B	334	LYS
1	B	401	SER
1	B	443	GLN
1	B	551	ARG
1	B	552	GLU
1	B	560	ARG
1	B	561	LYS
1	B	569	LYS
1	C	73	GLN
1	C	92	SER
1	C	334	LYS
1	C	418	PHE
1	C	476	LYS
1	C	538	ILE
1	C	552	GLU
1	C	565	ARG
1	D	73	GLN
1	D	252	ASP
1	D	334	LYS
1	D	529	ARG
1	D	551	ARG
1	D	552	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	GOL	D	602	-	5,5,5	0.84	0	5,5,5	0.97	0
3	ACT	C	602	-	1,3,3	4.39	1 (100%)	0,3,3	0.00	-
2	GOL	A	601	-	5,5,5	0.78	0	5,5,5	0.99	0
2	GOL	C	601	-	5,5,5	0.45	0	5,5,5	0.70	0
2	GOL	B	601	-	5,5,5	0.83	0	5,5,5	1.12	0
2	GOL	D	601	-	5,5,5	0.71	0	5,5,5	0.85	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	C	601	-	-	2/4/4/4	-
2	GOL	B	601	-	-	0/4/4/4	-
2	GOL	D	602	-	-	1/4/4/4	-
2	GOL	D	601	-	-	4/4/4/4	-
2	GOL	A	601	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	602	ACT	CH3-C	4.39	1.54	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	GOL	C1-C2-C3-O3
2	C	601	GOL	O1-C1-C2-C3
2	D	601	GOL	O1-C1-C2-C3
2	D	601	GOL	C1-C2-C3-O3
2	A	601	GOL	O2-C2-C3-O3
2	C	601	GOL	O1-C1-C2-O2
2	D	601	GOL	O1-C1-C2-O2
2	D	601	GOL	O2-C2-C3-O3
2	D	602	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	GOL	1	0
2	D	601	GOL	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	425:LEU	C	426:PHE	N	1.16

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, 95^{th} 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	510/526 (96%)	0.41	18 (3%) 44 51	34, 53, 83, 119	0
1	B	510/526 (96%)	0.32	15 (2%) 51 58	34, 50, 78, 105	0
1	C	509/526 (96%)	0.07	6 (1%) 79 83	29, 42, 65, 99	0
1	D	509/526 (96%)	0.14	12 (2%) 59 66	32, 47, 74, 135	0
All	All	2038/2104 (96%)	0.24	51 (2%) 57 64	29, 48, 77, 135	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	550	ALA	6.6
1	A	216	VAL	5.1
1	C	540	GLY	4.6
1	A	184	GLN	4.3
1	D	184	GLN	4.1
1	B	510	ARG	4.1
1	A	411	LEU	4.0
1	A	583	GLU	3.9
1	D	411	LEU	3.9
1	A	224	ARG	3.8
1	B	411	LEU	3.8
1	A	215	ALA	3.6
1	C	411	LEU	3.4
1	A	133	GLY	3.4
1	B	134	TYR	3.2
1	C	184	GLN	3.1
1	B	160	GLU	3.1
1	C	551	ARG	3.1
1	A	157	VAL	3.0
1	A	156	SER	3.0
1	B	97	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	538	ILE	2.9
1	D	406	LEU	2.8
1	B	130	ALA	2.8
1	A	226	ALA	2.8
1	A	539	ALA	2.7
1	B	158	THR	2.7
1	B	561	LYS	2.7
1	B	114	LEU	2.7
1	B	243	GLN	2.6
1	A	158	THR	2.6
1	D	171	THR	2.5
1	D	491	LEU	2.5
1	A	100	LEU	2.5
1	D	245	GLU	2.4
1	D	243	GLN	2.4
1	B	157	VAL	2.4
1	B	306	LEU	2.4
1	D	562	LYS	2.4
1	A	561	LYS	2.3
1	A	491	LEU	2.3
1	B	446	THR	2.2
1	D	244	ALA	2.2
1	D	178	ARG	2.2
1	A	410	VAL	2.2
1	B	541	GLY	2.2
1	D	103	LYS	2.1
1	C	582	ARG	2.1
1	D	539	ALA	2.1
1	A	102	PRO	2.1
1	C	560[A]	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 monosaccharides in this entry.

6.4 Ligands

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, 95^{th} 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(Å^2)	Q<0.9
2	GOL	D	602	6/6	0.77	0.18	73,88,93,96	0
3	ACT	C	602	4/4	0.85	0.22	57,60,68,68	0
2	GOL	D	601	6/6	0.93	0.18	39,48,57,58	0
2	GOL	B	601	6/6	0.94	0.17	42,50,55,58	0
2	GOL	A	601	6/6	0.95	0.14	37,44,53,53	0
2	GOL	C	601	6/6	0.95	0.17	37,44,49,50	0

6.5 Other polymers

There are no such residues in this entry.