



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 02:47 PM GMT

PDB ID : 1VB9
Title : Crystal structure of Thermoactinomyces vulgaris R-47 alpha-amylase II (TVA II) complexed with transglycosylated product
Authors : Mizuno, M.; Tonozuka, T.; Uechi, A.; Ohtaki, A.; Ichikawa, K.; Kamitori, S.; Nishikawa, A.; Sakano, Y.
Deposited on : 2004-02-25
Resolution : 2.20 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

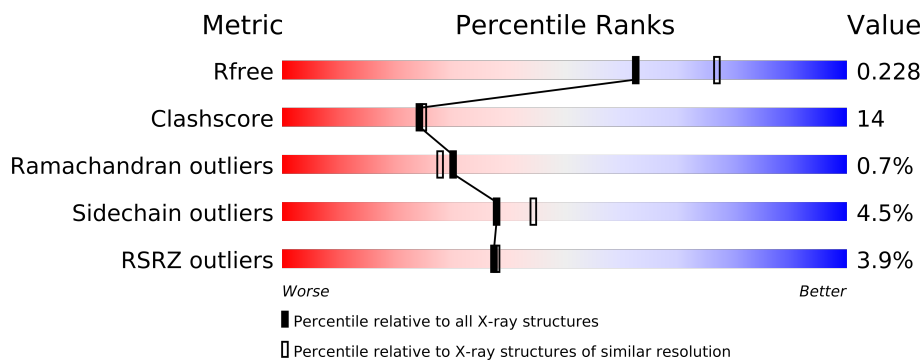
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.20 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}	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	585	
1	B	585	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10196 atoms, of which 0 are hydrogen and 0 are deuterium.

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 alpha-amylase II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	585	Total	C	N	O	S	0	0	0
			4776	3056	832	873	15			
1	B	585	Total	C	N	O	S	0	0	0
			4776	3056	832	873	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	325	ASN	ASP	ENGINEERED	UNP Q08751
B	325	ASN	ASP	ENGINEERED	UNP Q08751

- Molecule 2 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	6	Total	C	O	0	0
			67	36	31		
2	B	6	Total	C	O	0	0
			67	36	31		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	325	ASN	ASP	ENGINEERED	UNP Q08751
B	325	ASN	ASP	ENGINEERED	UNP Q08751

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	249	Total 249	O 249	0	0
4	B	259	Total 259	O 259	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	113.05Å 118.27Å 112.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.99 – 2.20 33.98 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (33.99-2.20) 99.9 (33.98-2.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.29 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.194 , 0.233 0.191 , 0.228	Depositor DCC
R_{free} test set	7737 reflections (11.21%)	DCC
Wilson B-factor (Å ²)	29.2	Xtriage
Anisotropy	0.397	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 36.8	EDS
Estimated twinning fraction	0.008 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 76732 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10196	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, GLC

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	0.35	0/4906	0.62	3/6641 (0.0%)
1	B	0.35	0/4906	0.60	1/6641 (0.0%)
All	All	0.35	0/9812	0.61	4/13282 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	277	LYS	N-CA-C	-7.84	89.83	111.00
1	A	276	SER	N-CA-C	5.99	127.18	111.00
1	A	279	SER	N-CA-C	-5.39	96.45	111.00
1	B	323	ARG	N-CA-C	-5.08	97.29	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4776	0	4609	143	0
1	B	4776	0	4609	129	0
2	A	67	0	57	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	67	0	57	4	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	249	0	0	6	0
4	B	259	0	0	14	0
All	All	10196	0	9332	269	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 14.

All (269) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:342:VAL:HG11	1:A:351:ILE:HD11	1.46	0.97
1:B:293:MET:HE1	2:B:702:GLC:H62	1.45	0.97
1:A:293:MET:HE1	2:A:702:GLC:H62	1.48	0.94
1:A:585:ARG:HH11	1:A:585:ARG:HB3	1.35	0.89
1:B:198:SER:HB3	1:B:203:LYS:HG3	1.57	0.87
1:B:293:MET:CE	2:B:702:GLC:H62	2.05	0.86
1:A:140:ARG:HG2	1:A:469:ARG:O	1.77	0.84
1:A:290:VAL:HG11	1:A:293:MET:CE	2.06	0.84
1:A:293:MET:CE	2:A:702:GLC:H62	2.07	0.84
1:A:280:ARG:HA	1:A:289:GLN:OE1	1.79	0.81
1:B:290:VAL:HG11	1:B:293:MET:HE3	1.64	0.80
1:B:46:ALA:HB1	1:B:50:GLU:HG3	1.63	0.80
1:B:523:VAL:HG22	1:B:524:GLN:NE2	1.97	0.79
1:A:290:VAL:HG11	1:A:293:MET:HE2	1.65	0.78
1:A:243:ASN:HD22	1:A:244:HIS:HD2	1.32	0.76
1:A:447:LEU:HB2	1:A:505:VAL:HG21	1.66	0.76
1:A:484:PHE:CE1	1:A:488:LYS:HD2	2.21	0.76
1:B:470:ARG:HG3	4:B:741:HOH:O	1.85	0.75
1:A:504:ASN:C	1:A:504:ASN:HD22	1.91	0.73
1:B:505:VAL:HG12	1:B:521:ARG:CD	2.18	0.73
1:A:191:TYR:CZ	1:A:323:ARG:HD3	2.22	0.73
1:B:275:VAL:O	1:B:282:ASN:ND2	2.23	0.72
1:B:290:VAL:HG11	1:B:293:MET:CE	2.20	0.72
1:B:139:GLU:HB3	1:B:140:ARG:HH11	1.56	0.71
1:A:341:LEU:O	1:A:345:LEU:HD13	1.90	0.71
1:A:569:LEU:HG	1:A:571:LEU:HD13	1.72	0.71
1:A:390:HIS:HD2	1:A:393:ARG:H	1.39	0.71
1:A:277:LYS:HG3	1:A:277:LYS:O	1.91	0.70
1:B:328:ASN:HD22	1:B:328:ASN:N	1.89	0.70
1:A:194:PRO:HB2	1:A:203:LYS:HB2	1.74	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:487:TYR:O	1:B:491:ILE:HG12	1.93	0.69
1:A:516:LEU:HD13	1:A:541:VAL:HG11	1.74	0.69
1:A:330:VAL:HG22	1:A:335:TRP:NE1	2.08	0.69
1:A:447:LEU:HB2	1:A:505:VAL:CG2	2.23	0.68
1:A:271:GLU:HG3	1:A:272:ASP:H	1.58	0.68
1:A:400:ARG:HH21	1:A:400:ARG:CB	2.07	0.68
1:B:547:GLU:HG2	1:B:551:LYS:HE2	1.76	0.67
1:B:139:GLU:HB3	1:B:140:ARG:NH1	2.09	0.66
1:A:290:VAL:HG11	1:A:293:MET:HE3	1.76	0.66
1:A:224:ARG:HA	1:A:224:ARG:HE	1.59	0.66
1:A:477:LYS:HD2	1:A:477:LYS:N	2.11	0.65
1:B:492:ARG:O	1:B:496:ARG:HG3	1.98	0.64
1:A:275:VAL:O	1:A:275:VAL:HG12	1.97	0.64
1:B:400:ARG:O	1:B:404:LEU:HD13	1.98	0.63
1:B:255:VAL:HG11	1:B:270:ILE:HD11	1.78	0.63
1:B:504:ASN:HD22	1:B:504:ASN:C	2.02	0.62
1:B:523:VAL:HG22	1:B:524:GLN:HE22	1.64	0.62
1:A:386:THR:OG1	1:A:388:GLU:HG3	2.00	0.62
1:B:183:GLU:OE2	1:B:232:ARG:HD2	2.00	0.62
1:B:328:ASN:HD22	1:B:328:ASN:H	1.47	0.61
1:A:118:ARG:HG2	4:B:727:HOH:O	1.99	0.61
1:A:271:GLU:HG3	1:A:272:ASP:N	2.14	0.61
1:A:129:LYS:HD2	1:A:502:ARG:HH12	1.66	0.60
1:A:390:HIS:CD2	1:A:393:ARG:H	2.19	0.60
1:B:64:GLU:HB2	4:B:816:HOH:O	2.00	0.60
1:A:224:ARG:NE	1:A:224:ARG:HA	2.17	0.60
1:B:484:PHE:CE1	1:B:488:LYS:HD2	2.36	0.60
1:A:129:LYS:HB3	1:A:411:GLN:OE1	2.02	0.59
1:B:260:GLU:HB2	1:B:273:PHE:CD2	2.38	0.59
1:B:133:ILE:HB	1:B:451:LEU:HD23	1.85	0.59
1:A:129:LYS:HD2	1:A:502:ARG:NH1	2.17	0.59
1:A:409:ALA:O	1:A:413:LEU:HD13	2.04	0.58
1:A:295:LYS:HE2	1:B:115:TYR:CZ	2.39	0.58
1:B:390:HIS:NE2	1:B:512:LYS:HE2	2.19	0.57
1:B:447:LEU:HB2	1:B:505:VAL:CG1	2.34	0.57
1:A:382:ARG:HG2	1:A:389:ILE:HG23	1.86	0.57
1:B:505:VAL:HG12	1:B:521:ARG:HD2	1.86	0.56
1:B:312:ARG:O	1:B:316:GLU:HG3	2.04	0.56
1:B:448:GLY:O	1:B:494:ARG:NH2	2.38	0.56
1:B:328:ASN:H	1:B:328:ASN:ND2	2.03	0.56
1:B:28:ARG:HD2	4:B:819:HOH:O	2.04	0.56
1:A:505:VAL:HG22	1:A:521:ARG:NE	2.21	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:416:LEU:H	1:B:416:LEU:HD23	1.70	0.55
1:B:190:LEU:HD13	1:B:234:ILE:CG2	2.36	0.55
1:A:26:ARG:HD3	1:A:70:GLU:OE2	2.05	0.55
1:A:254:ASP:OD2	1:A:262:SER:HB2	2.06	0.55
1:A:201:HIS:HE1	1:A:469:ARG:HH11	1.53	0.55
1:A:411:GLN:HG2	4:A:909:HOH:O	2.06	0.55
1:B:382:ARG:NH1	1:B:397:GLU:OE1	2.39	0.55
1:A:57:ALA:HB2	1:A:71:ALA:HB2	1.88	0.55
1:B:129:LYS:HG2	1:B:411:GLN:NE2	2.22	0.54
1:A:115:TYR:CZ	1:B:295:LYS:HE2	2.43	0.54
1:B:277:LYS:O	1:B:278:THR:OG1	2.23	0.54
1:A:139:GLU:OE2	1:A:140:ARG:NH1	2.41	0.54
1:A:504:ASN:ND2	1:A:504:ASN:C	2.59	0.54
1:A:514:ALA:O	1:A:535:ARG:HG3	2.08	0.54
1:B:572:THR:C	1:B:573:LEU:HD23	2.27	0.53
1:B:522:THR:OG1	1:B:527:HIS:HD2	1.90	0.53
1:B:139:GLU:OE2	1:B:140:ARG:NH1	2.42	0.53
1:A:275:VAL:O	1:A:276:SER:CB	2.56	0.53
1:B:328:ASN:ND2	1:B:328:ASN:N	2.56	0.53
1:B:255:VAL:HG11	1:B:270:ILE:CD1	2.38	0.52
1:B:541:VAL:HG22	1:B:543:LEU:HD12	1.91	0.52
1:B:190:LEU:HD13	1:B:234:ILE:HG21	1.91	0.52
1:A:162:PRO:HB3	1:A:168:TYR:HE2	1.75	0.52
1:B:193:THR:HB	1:B:194:PRO:HD2	1.91	0.52
1:A:281:THR:HG23	1:A:283:TYR:CE2	2.44	0.52
1:A:416:LEU:HD23	1:A:416:LEU:H	1.73	0.52
1:A:8:HIS:HD2	1:A:26:ARG:O	1.93	0.52
1:B:393:ARG:HH21	1:B:393:ARG:HG3	1.75	0.52
1:B:280:ARG:NH2	1:B:289:GLN:NE2	2.58	0.51
1:A:400:ARG:HH21	1:A:400:ARG:HB3	1.75	0.51
1:A:65:ARG:HB2	1:B:4:GLU:HG3	1.92	0.51
1:B:325:ASN:HD21	2:B:703:GLC:C1	2.24	0.51
1:B:447:LEU:HB2	1:B:505:VAL:HG11	1.92	0.51
1:A:275:VAL:O	1:A:276:SER:HB2	2.10	0.51
1:A:129:LYS:HG2	1:A:411:GLN:NE2	2.26	0.51
1:A:201:HIS:CE1	1:A:469:ARG:HH11	2.29	0.51
1:B:107:LYS:HE3	4:B:845:HOH:O	2.10	0.51
1:B:200:SER:O	1:B:203:LYS:HD2	2.11	0.50
1:B:504:ASN:HB2	4:B:751:HOH:O	2.11	0.50
1:B:332:HIS:HD2	1:B:367:GLN:OE1	1.94	0.50
1:B:228:GLU:O	1:B:232:ARG:HG2	2.12	0.50
1:B:219:LEU:HB3	1:B:220:PRO:HD3	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:47:SER:HB3	1:B:50:GLU:HG2	1.93	0.50
1:A:574:ARG:HB2	1:A:574:ARG:NH1	2.27	0.50
1:B:357:HIS:HD2	4:B:719:HOH:O	1.94	0.50
1:A:458:ILE:CD1	1:A:460:MET:HG3	2.42	0.50
1:A:522:THR:OG1	1:A:527:HIS:HD2	1.95	0.50
1:B:12:GLY:O	1:B:364:MET:HE1	2.12	0.50
1:A:213:ASP:OD1	1:A:215:GLN:HG2	2.12	0.49
1:A:346:ASN:ND2	1:A:348:ASP:H	2.10	0.49
1:A:488:LYS:O	1:A:492:ARG:HG3	2.12	0.49
1:A:140:ARG:HH12	1:A:201:HIS:HB2	1.78	0.49
1:A:346:ASN:HD22	1:A:346:ASN:C	2.15	0.49
1:A:47:SER:HB3	1:A:50:GLU:HG3	1.95	0.49
1:A:382:ARG:HG3	1:A:388:GLU:HB2	1.95	0.49
1:B:232:ARG:HG3	1:B:232:ARG:HH11	1.78	0.49
1:B:275:VAL:O	1:B:282:ASN:CG	2.51	0.48
1:B:504:ASN:ND2	1:B:504:ASN:C	2.66	0.48
1:A:281:THR:HG22	1:A:283:TYR:H	1.77	0.48
1:A:82:TYR:N	1:A:110:VAL:CG2	2.76	0.48
1:A:323:ARG:HD2	1:A:372:MET:SD	2.54	0.48
1:A:162:PRO:HB3	1:A:168:TYR:CE2	2.48	0.48
1:B:248:GLN:HB2	4:B:783:HOH:O	2.12	0.48
1:A:448:GLY:O	1:A:494:ARG:NH2	2.47	0.48
1:A:255:VAL:HG12	1:A:275:VAL:HG21	1.95	0.48
1:A:68:TYR:CD2	1:A:403:MET:HG3	2.49	0.48
1:B:535:ARG:HD3	1:B:539:GLN:CD	2.34	0.48
1:A:585:ARG:NH1	1:A:585:ARG:HB3	2.17	0.48
1:B:158:LYS:HG2	1:B:478:GLU:OE2	2.14	0.47
1:B:82:TYR:N	1:B:110:VAL:HG22	2.29	0.47
1:A:505:VAL:HG22	1:A:521:ARG:CD	2.44	0.47
1:A:193:THR:HB	1:A:194:PRO:CD	2.45	0.47
1:B:277:LYS:O	1:B:277:LYS:HD3	2.14	0.47
1:A:179:LEU:N	1:A:180:PRO:CD	2.78	0.47
1:A:326:VAL:HG12	1:A:329:GLU:HB2	1.97	0.47
1:A:293:MET:HE2	2:A:702:GLC:H62	1.95	0.47
1:B:547:GLU:CG	1:B:551:LYS:HE2	2.45	0.47
1:B:393:ARG:HG3	1:B:393:ARG:NH2	2.29	0.47
1:B:477:LYS:NZ	1:B:477:LYS:HB3	2.30	0.47
1:A:275:VAL:O	1:A:275:VAL:CG1	2.63	0.47
1:B:223:ARG:HH21	1:B:223:ARG:HG3	1.80	0.47
1:A:275:VAL:C	1:A:282:ASN:OD1	2.54	0.46
1:A:140:ARG:NH2	4:A:751:HOH:O	2.48	0.46
1:B:276:SER:HB2	1:B:283:TYR:HE2	1.80	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2:LEU:HD12	1:A:30:LYS:CD	2.45	0.46
1:A:77:THR:O	1:A:78:LYS:HB2	2.16	0.46
1:B:127:TRP:CG	1:B:235:LYS:HE3	2.51	0.46
1:A:217:GLY:HA2	4:A:745:HOH:O	2.16	0.46
1:B:504:ASN:HD21	1:B:522:THR:HB	1.80	0.46
1:A:197:ALA:HB3	1:A:208:ASP:HB3	1.97	0.46
1:B:277:LYS:O	1:B:278:THR:HG23	2.16	0.46
1:B:381:ILE:O	1:B:385:ALA:HB3	2.16	0.46
1:A:40:LEU:HD22	1:A:40:LEU:N	2.31	0.46
1:A:488:LYS:HB3	1:A:488:LYS:NZ	2.30	0.45
1:A:330:VAL:HG22	1:A:335:TRP:CE2	2.51	0.45
1:A:475:GLU:O	1:A:479:GLN:HG3	2.16	0.45
1:B:377:ARG:O	1:B:380:VAL:HG22	2.17	0.45
1:A:232:ARG:NE	4:A:896:HOH:O	2.41	0.45
1:B:293:MET:HE2	2:B:702:GLC:H62	1.96	0.45
1:A:244:HIS:CD2	1:A:286:PHE:HB2	2.51	0.45
1:A:416:LEU:H	1:A:416:LEU:CD2	2.29	0.45
1:B:118:ARG:NH1	4:B:786:HOH:O	2.49	0.45
1:A:136:ILE:O	1:A:138:PRO:HD3	2.16	0.45
1:A:569:LEU:HG	1:A:571:LEU:CD1	2.42	0.45
1:A:271:GLU:HG2	1:A:282:ASN:O	2.17	0.45
1:A:444:MET:O	1:A:494:ARG:NH1	2.45	0.45
1:B:191:TYR:CE1	1:B:323:ARG:HG3	2.52	0.45
1:B:132:VAL:HG11	1:B:491:ILE:HD12	1.99	0.45
1:A:223:ARG:HD3	1:A:317:GLN:OE1	2.17	0.45
1:A:585:ARG:CB	1:A:585:ARG:HH11	2.18	0.45
1:B:133:ILE:HD13	1:B:189:ALA:HB3	1.99	0.45
1:B:223:ARG:HB3	1:B:223:ARG:CZ	2.46	0.45
1:B:535:ARG:HD3	1:B:539:GLN:NE2	2.32	0.45
1:A:129:LYS:CB	1:A:411:GLN:OE1	2.65	0.44
1:B:133:ILE:CD1	1:B:189:ALA:HB3	2.47	0.44
1:B:416:LEU:CD2	1:B:416:LEU:H	2.31	0.44
1:B:447:LEU:HB2	1:B:505:VAL:HG13	2.00	0.44
1:B:138:PRO:HD2	1:B:193:THR:OG1	2.18	0.44
1:B:251:ALA:O	1:B:255:VAL:HG23	2.17	0.44
1:B:298:THR:HB	1:B:334:PHE:CD2	2.52	0.44
1:A:323:ARG:HH12	1:A:325:ASN:HD22	1.65	0.44
1:B:232:ARG:HG3	1:B:232:ARG:NH1	2.32	0.44
1:B:272:ASP:OD2	1:B:282:ASN:ND2	2.50	0.44
1:B:280:ARG:HA	1:B:280:ARG:HD2	1.87	0.44
1:A:280:ARG:HG3	1:A:280:ARG:O	2.18	0.43
1:B:491:ILE:O	1:B:495:HIS:ND1	2.51	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:504:ASN:HD21	1:A:522:THR:HB	1.83	0.43
1:A:524:GLN:HB3	1:A:525:ASP:H	1.58	0.43
1:B:582:TRP:CZ2	1:B:584:GLY:HA2	2.53	0.43
1:B:382:ARG:HA	1:B:386:THR:OG1	2.19	0.43
1:A:81:LYS:HB2	1:A:110:VAL:HG21	1.99	0.43
1:B:438:LEU:CD2	1:B:532:LEU:HD22	2.48	0.43
1:A:223:ARG:NE	1:A:223:ARG:HA	2.33	0.43
1:A:381:ILE:HD13	1:A:425:PHE:CE1	2.53	0.43
1:A:105:ARG:HH21	1:A:105:ARG:HG2	1.83	0.43
1:A:332:HIS:HE1	4:B:906:HOH:O	2.02	0.43
1:A:477:LYS:CD	1:A:477:LYS:N	2.81	0.43
1:B:227:ASP:O	1:B:231:ARG:HG2	2.18	0.43
1:B:275:VAL:HG12	1:B:276:SER:N	2.34	0.43
1:B:277:LYS:C	1:B:277:LYS:HD3	2.39	0.43
1:A:107:LYS:HD3	4:A:947:HOH:O	2.18	0.43
1:A:110:VAL:HG22	1:A:111:PHE:O	2.19	0.42
1:A:478:GLU:HA	1:A:478:GLU:OE2	2.20	0.42
1:B:269:PHE:HB2	1:B:284:GLU:HB3	2.01	0.42
1:B:565:LYS:HE3	4:B:831:HOH:O	2.19	0.42
1:A:518:ALA:HA	1:A:530:VAL:O	2.19	0.42
1:A:330:VAL:CG2	1:A:335:TRP:CE2	3.03	0.42
1:A:82:TYR:C	1:A:110:VAL:HG23	2.40	0.42
1:B:8:HIS:CE1	1:B:25:VAL:HG13	2.55	0.42
1:B:178:ARG:HG3	1:B:474:TRP:CZ2	2.55	0.42
1:A:82:TYR:O	1:A:110:VAL:HG23	2.19	0.42
1:A:499:SER:OG	1:A:526:GLN:HG2	2.20	0.42
1:B:458:ILE:HD12	1:B:479:GLN:HG2	2.01	0.42
1:B:523:VAL:HG13	1:B:523:VAL:O	2.19	0.42
1:A:325:ASN:HD21	2:A:703:GLC:C1	2.33	0.42
1:B:217:GLY:HA2	4:B:867:HOH:O	2.20	0.42
1:A:308:PHE:O	1:A:312:ARG:HG3	2.20	0.42
1:B:24:ARG:HG3	1:B:407:GLU:OE1	2.19	0.42
1:A:464:THR:O	1:A:465:ASP:C	2.59	0.42
1:B:477:LYS:HZ3	1:B:477:LYS:HB3	1.85	0.42
1:A:107:LYS:HE2	1:A:107:LYS:HB3	1.86	0.42
1:A:240:ALA:HB2	1:A:322:TRP:CE3	2.55	0.42
1:A:12:GLY:HA2	1:A:364:MET:SD	2.60	0.41
1:A:335:TRP:CE3	1:A:335:TRP:HA	2.56	0.41
1:A:275:VAL:O	1:A:282:ASN:OD1	2.38	0.41
1:A:278:THR:HG23	1:A:291:PRO:CG	2.50	0.41
1:A:426:LEU:HD22	1:A:431:GLY:HA2	2.01	0.41
1:A:164:HIS:CE1	1:A:466:PRO:HD3	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:541:VAL:HG22	1:B:542:LEU:N	2.36	0.41
1:A:117:HIS:HB2	1:A:120:GLU:HG3	2.02	0.41
1:A:88:GLY:HA3	1:A:92:GLU:OE1	2.21	0.41
1:A:330:VAL:HG22	1:A:335:TRP:HE1	1.83	0.41
1:B:543:LEU:N	1:B:543:LEU:HD12	2.35	0.41
1:B:163:ARG:HH11	1:B:163:ARG:HG3	1.86	0.41
1:B:179:LEU:N	1:B:180:PRO:CD	2.83	0.41
1:B:280:ARG:HG3	1:B:280:ARG:O	2.21	0.41
1:B:27:LEU:C	1:B:27:LEU:HD23	2.41	0.41
1:B:192:PHE:O	1:B:239:ASP:HB2	2.21	0.41
1:A:574:ARG:HH11	1:A:574:ARG:CB	2.34	0.41
1:B:477:LYS:NZ	1:B:477:LYS:CB	2.84	0.41
1:A:332:HIS:HD2	1:A:367:GLN:OE1	2.04	0.41
1:B:277:LYS:O	1:B:278:THR:CB	2.69	0.41
1:A:1:MET:HB3	4:A:846:HOH:O	2.20	0.41
1:A:150:PRO:HG2	1:A:167:PHE:CD2	2.56	0.41
1:B:244:HIS:CD2	1:B:286:PHE:HB2	2.56	0.41
1:B:146:PRO:HA	1:B:149:ASP:OD1	2.21	0.40
1:A:27:LEU:C	1:A:27:LEU:HD23	2.41	0.40
1:B:400:ARG:NH2	1:B:400:ARG:HG3	2.37	0.40
1:B:250:PHE:CG	1:B:251:ALA:N	2.89	0.40
1:B:325:ASN:HB3	4:B:728:HOH:O	2.20	0.40
1:A:130:GLU:HG2	1:A:130:GLU:H	1.81	0.40
1:B:335:TRP:HA	1:B:335:TRP:CE3	2.56	0.40
1:A:376:PHE:CE1	1:A:415:ASN:HB3	2.56	0.40
1:B:282:ASN:O	1:B:282:ASN:OD1	2.39	0.40
1:A:30:LYS:O	1:A:33:ASP:HB2	2.22	0.40
1:A:573:LEU:CD1	1:A:579:MET:HG3	2.51	0.40
1:B:475:GLU:HG2	4:B:846:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	583/585 (100%)	556 (95%)	24 (4%)	3 (0%)	38	38
1	B	583/585 (100%)	556 (95%)	22 (4%)	5 (1%)	25	21
All	All	1166/1170 (100%)	1112 (95%)	46 (4%)	8 (1%)	30	28

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	279	SER
1	B	275	VAL
1	B	278	THR
1	A	275	VAL
1	B	281	THR
1	B	547	GLU
1	B	280	ARG
1	A	276	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	493/493 (100%)	468 (95%)	25 (5%)	33	38
1	B	493/493 (100%)	474 (96%)	19 (4%)	43	52
All	All	986/986 (100%)	942 (96%)	44 (4%)	38	44

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	GLU
1	A	85	LEU
1	A	122	PHE
1	A	191	TYR
1	A	219	LEU
1	A	263	ARG
1	A	276	SER
1	A	277	LYS
1	A	279	SER

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Mol	Chain	Res	Type
1	A	330	VAL
1	A	346	ASN
1	A	398	LEU
1	A	400	ARG
1	A	404	LEU
1	A	411	GLN
1	A	413	LEU
1	A	426	LEU
1	A	444	MET
1	A	466	PRO
1	A	483	LEU
1	A	504	ASN
1	A	535	ARG
1	A	573	LEU
1	A	581	LEU
1	A	585	ARG
1	B	24	ARG
1	B	122	PHE
1	B	158	LYS
1	B	191	TYR
1	B	248	GLN
1	B	281	THR
1	B	328	ASN
1	B	398	LEU
1	B	400	ARG
1	B	411	GLN
1	B	438	LEU
1	B	451	LEU
1	B	466	PRO
1	B	504	ASN
1	B	524	GLN
1	B	542	LEU
1	B	552	THR
1	B	565	LYS
1	B	569	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	90	GLN
1	A	135	GLN

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Mol	Chain	Res	Type
1	A	164	HIS
1	A	201	HIS
1	A	244	HIS
1	A	261	GLN
1	A	325	ASN
1	A	332	HIS
1	A	346	ASN
1	A	367	GLN
1	A	390	HIS
1	A	504	ASN
1	A	527	HIS
1	A	563	HIS
1	B	135	GLN
1	B	243	ASN
1	B	244	HIS
1	B	257	GLN
1	B	261	GLN
1	B	289	GLN
1	B	328	ASN
1	B	332	HIS
1	B	357	HIS
1	B	367	GLN
1	B	411	GLN
1	B	504	ASN
1	B	509	HIS
1	B	524	GLN
1	B	527	HIS
1	B	568	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

12 carbohydrates 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	GLC	A	701	2	10,11,12	0.40	0	11,15,17	0.22	0
2	GLC	A	702	2	10,11,12	0.43	0	11,15,17	0.42	0
2	GLC	A	703	2	10,11,12	0.62	0	11,15,17	1.30	1 (9%)
2	GLC	A	704	2	10,11,12	0.56	0	11,15,17	0.35	0
2	GLC	A	705	2	12,12,12	0.42	0	17,17,17	0.38	0
2	GLC	A	706	2	10,11,12	0.38	0	11,15,17	0.30	0
2	GLC	B	701	2	10,11,12	0.40	0	11,15,17	0.24	0
2	GLC	B	702	2	10,11,12	0.44	0	11,15,17	0.37	0
2	GLC	B	703	2	10,11,12	0.41	0	11,15,17	0.72	0
2	GLC	B	704	2	10,11,12	0.49	0	11,15,17	0.52	0
2	GLC	B	705	2	12,12,12	0.36	0	17,17,17	0.34	0
2	GLC	B	706	2	10,11,12	0.39	0	11,15,17	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	GLC	A	701	2	-	0/2/19/22	0/1/1/1
2	GLC	A	702	2	-	0/2/19/22	0/1/1/1
2	GLC	A	703	2	-	0/2/19/22	0/1/1/1
2	GLC	A	704	2	-	0/2/19/22	0/1/1/1
2	GLC	A	705	2	-	0/2/22/22	0/1/1/1
2	GLC	A	706	2	-	0/2/19/22	0/1/1/1
2	GLC	B	701	2	-	0/2/19/22	0/1/1/1
2	GLC	B	702	2	-	0/2/19/22	0/1/1/1
2	GLC	B	703	2	-	0/2/19/22	0/1/1/1
2	GLC	B	704	2	-	0/2/19/22	0/1/1/1
2	GLC	B	705	2	-	0/2/22/22	0/1/1/1
2	GLC	B	706	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	703	GLC	O5-C5-C4	2.42	113.72	110.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	585/585 (100%)	-0.08	22 (3%)	38 39	18, 28, 48, 96	0
1	B	585/585 (100%)	-0.07	24 (4%)	35 36	19, 29, 51, 106	0
All	All	1170/1170 (100%)	-0.07	46 (3%)	37 38	18, 28, 49, 106	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	279	SER	15.5
1	B	279	SER	13.8
1	B	273	PHE	10.7
1	B	274	PRO	9.3
1	B	272	ASP	8.4
1	B	275	VAL	8.1
1	B	278	THR	8.0
1	B	277	LYS	7.8
1	B	280	ARG	7.2
1	B	276	SER	7.0
1	A	278	THR	6.6
1	A	274	PRO	6.5
1	A	280	ARG	6.1
1	A	272	ASP	6.1
1	A	275	VAL	5.3
1	A	273	PHE	4.8
1	B	513	GLN	4.3
1	A	277	LYS	4.0
1	B	51	GLU	3.7
1	A	49	GLU	3.5
1	B	477	LYS	3.4
1	A	281	THR	3.0
1	B	48	PRO	2.9
1	A	276	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	164	HIS	2.6
1	B	271	GLU	2.6
1	B	281	THR	2.5
1	A	566	GLN	2.4
1	B	158	LYS	2.4
1	A	548	SER	2.3
1	B	49	GLU	2.3
1	A	451	LEU	2.3
1	A	190	LEU	2.2
1	B	282	ASN	2.2
1	A	191	TYR	2.2
1	A	107	LYS	2.1
1	A	192	PHE	2.1
1	A	375	LEU	2.1
1	B	159	ASP	2.1
1	A	327	ALA	2.1
1	A	237	ILE	2.1
1	B	155	GLN	2.1
1	A	90	GLN	2.0
1	B	548	SER	2.0
1	B	566	GLN	2.0
1	B	260	GLU	2.0

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

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

6.3 Carbohydrates ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	GLC	B	706	11/12	0.25	10.44	56,59,60,61	0
2	GLC	A	706	11/12	0.21	7.00	48,52,54,55	0
2	GLC	A	705	12/12	0.17	5.34	36,42,45,47	0
2	GLC	B	705	12/12	0.19	5.22	46,51,54,54	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	GLC	A	701	11/12	0.14	3.88	30,35,40,46	0
2	GLC	B	704	11/12	0.15	0.76	37,43,47,52	0
2	GLC	B	703	11/12	0.17	0.68	28,32,36,46	0
2	GLC	A	703	11/12	0.18	0.51	24,28,31,42	0
2	GLC	B	701	11/12	0.12	-0.17	37,39,42,43	0
2	GLC	A	702	11/12	0.08	-0.85	26,28,30,31	0
2	GLC	A	704	11/12	0.11	-1.08	31,34,37,43	0
2	GLC	B	702	11/12	0.09	-1.23	30,30,32,36	0

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. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	CA	A	601	1/1	0.05	-2.12	26,26,26,26	0
3	CA	B	602	1/1	0.03	-3.59	34,34,34,34	0

6.5 Other polymers

There are no such residues in this entry.