



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:02 PM GMT

PDB ID : 3VU2
Title : Structure of the Starch Branching Enzyme I (BEI) complexed with maltopentaose from *Oryza sativa* L
Authors : Chaen, K.; Kakuta, Y.; Kimura, M.
Deposited on : 2012-06-14
Resolution : 2.23 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

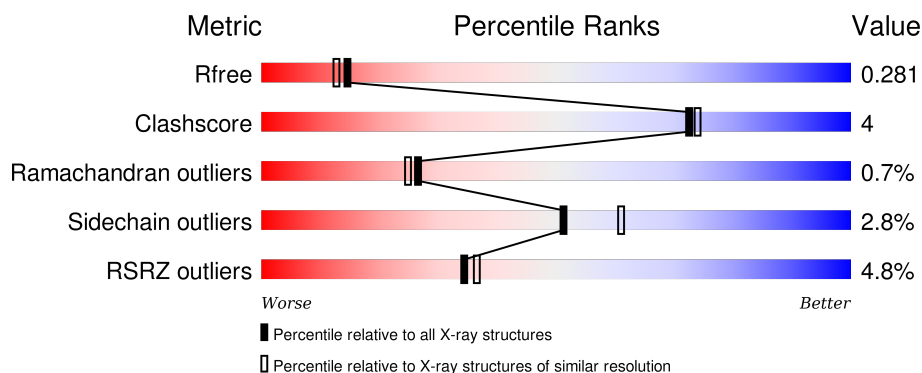
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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}	91344	1611 (2.26-2.22)
Clashscore	102246	1764 (2.26-2.22)
Ramachandran outliers	100387	1724 (2.26-2.22)
Sidechain outliers	100360	1724 (2.26-2.22)
RSRZ outliers	91569	1616 (2.26-2.22)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	702	<div> <div>5%</div> <div>88%</div> <div>10% ..</div> </div>
1	B	702	<div> <div>5%</div> <div>88%</div> <div>10% ..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	B	804	-	-	-	X
4	GOL	B	806	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 12313 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.

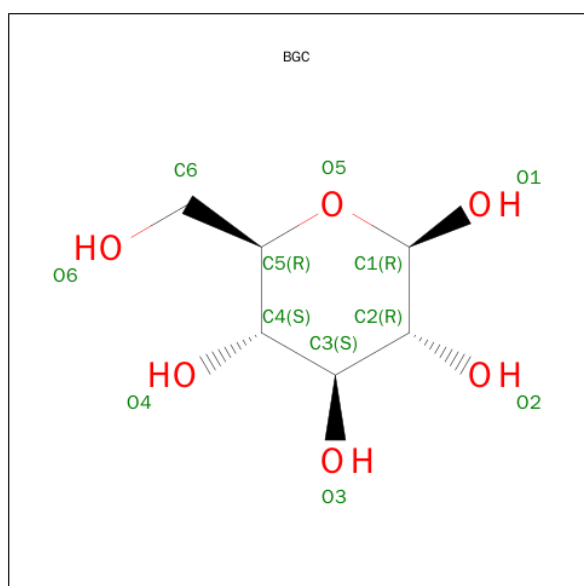
- Molecule 1 is a protein called 1,4-alpha-glucan-branching enzyme, chloroplastic/amyloplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	692	Total	C	N	O	S	0	5	0
			5673	3627	978	1037	31			
1	B	691	Total	C	N	O	S	0	4	0
			5663	3620	978	1034	31			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	399	GLN	GLU	ENGINEERED MUTATION	UNP Q01401
B	399	GLN	GLU	ENGINEERED MUTATION	UNP Q01401

- Molecule 2 is SUGAR (BETA-D-GLUCOSE) (three-letter code: BGC) (formula: C₆H₁₂O₆).



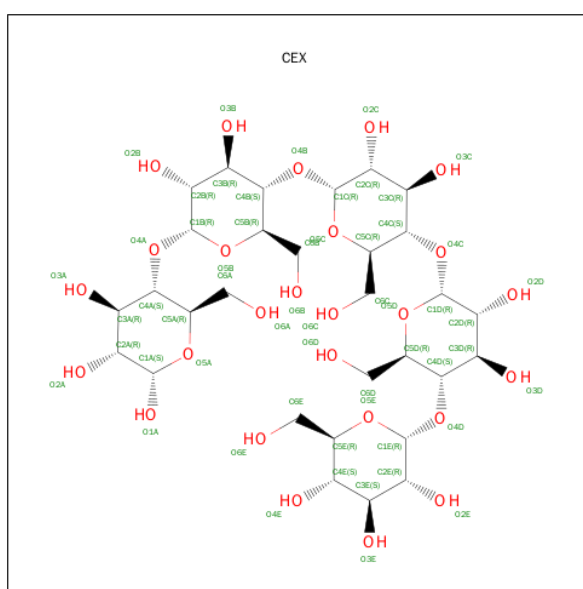
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	6	6		

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

- Molecule 3 is ALPHA-D-GLUCOPYRANOSYL-(1->4)-ALPHA-D-GLUCOPYRANOSYL-(1->4)-ALPHA-D-GLUCOPYRANOSYL-(1->4)-ALPHA-D-GLUCOPYRANOSYL-(1->4)-ALPHA-D-GLUCOPYRANOSE (three-letter code: CEX) (formula: $C_{30}H_{52}O_{26}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			56	30	26		
3	B	1	Total	C	O	0	0
			56	30	26		

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



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

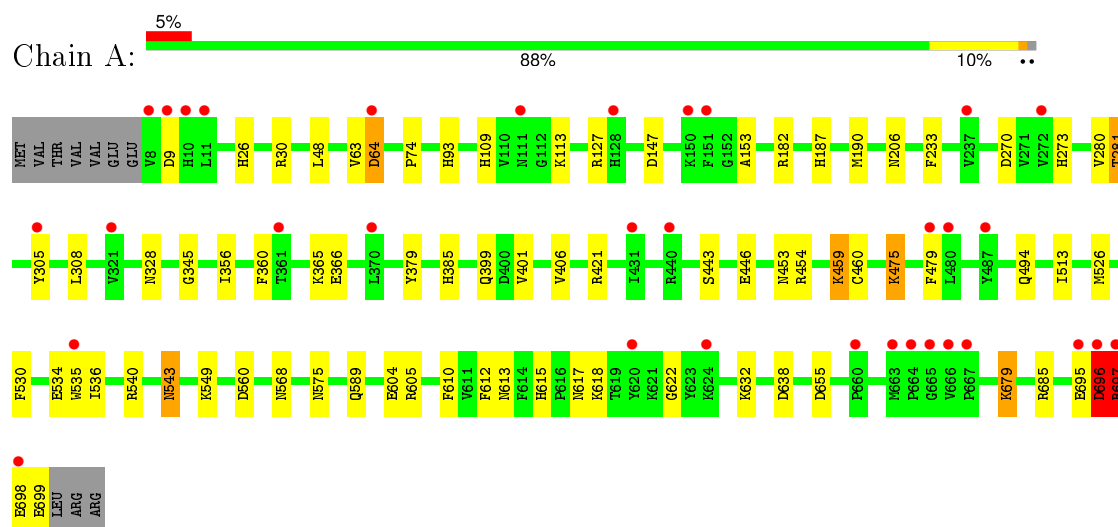
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	401	Total	O	0	0
			401	401		
5	B	386	Total	O	0	0
			386	386		

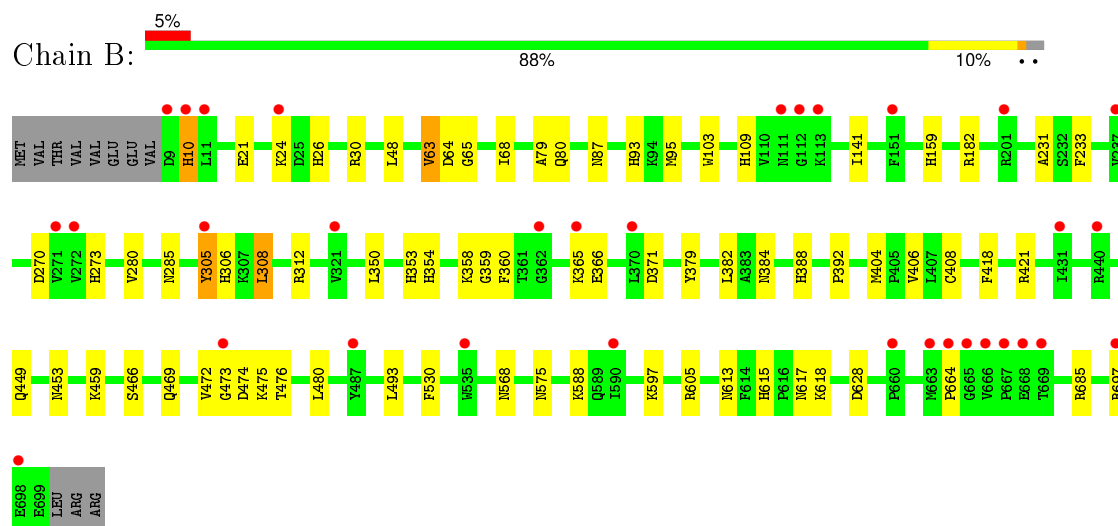
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: 1,4-alpha-glucan-branching enzyme, chloroplastic/amyloplastic



- Molecule 1: 1,4-alpha-glucan-branching enzyme, chloroplastic/amyloplastic



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.81Å 66.56Å 169.62Å 90.00° 89.97° 90.00°	Depositor
Resolution (Å)	37.22 – 2.23 37.22 – 2.23	Depositor EDS
% Data completeness (in resolution range)	88.0 (37.22-2.23) 87.9 (37.22-2.23)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	17.40 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.226 , 0.286 0.222 , 0.281	Depositor DCC
R_{free} test set	4075 reflections (6.09%)	DCC
Wilson B-factor (Å ²)	31.7	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 32.4	EDS
Estimated twinning fraction	0.460 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 70524 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12313	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, BGC, CEX

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	0.36	1/5860 (0.0%)	0.51	3/7934 (0.0%)
1	B	0.34	0/5847	0.50	0/7914
All	All	0.35	1/11707 (0.0%)	0.50	3/15848 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	696	ASP	C-O	5.04	1.32	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	696	ASP	O-C-N	-7.14	111.27	122.70
1	A	696	ASP	C-N-CA	6.53	138.01	121.70
1	A	697	ARG	N-CA-C	-5.43	96.34	111.00

There are no chirality outliers.

There are no planarity outliers.

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	5673	0	5398	50	0
1	B	5663	0	5388	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	24	0	24	0	0
2	B	24	0	24	0	0
3	A	56	0	52	1	0
3	B	56	0	52	0	0
4	A	6	0	8	0	0
4	B	24	0	32	5	0
5	A	401	0	0	6	0
5	B	386	0	0	5	0
All	All	12313	0	10978	94	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 (94) 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:695:GLU:HA	1:A:696:ASP:O	1.60	1.01
1:A:475:LYS:HD3	1:A:479:PHE:HD1	1.26	1.01
1:B:159:HIS:HA	4:B:804:GOL:H32	1.52	0.89
1:A:610:PHE:HD2	5:A:1288:HOH:O	1.55	0.89
1:A:615:HIS:HD2	1:A:617:ASN:H	1.29	0.81
1:B:63:VAL:HG23	1:B:64:ASP:H	1.46	0.79
1:A:475:LYS:HD3	1:A:479:PHE:CD1	2.16	0.79
1:A:604:GLU:HA	5:A:1288:HOH:O	1.86	0.75
1:B:231:ALA:HB2	4:B:806:GOL:H2	1.66	0.75
1:B:285:ASN:OD1	1:B:312:ARG:HG3	1.89	0.73
1:B:273:HIS:HD2	1:B:379:TYR:OH	1.72	0.73
1:B:26:HIS:HE1	1:B:30:ARG:HH21	1.35	0.72
1:B:466:SER:H	1:B:469:GLN:HE21	1.38	0.71
1:A:345:GLY:H	1:A:399:GLN:HE21	1.38	0.71
1:A:459:LYS:HE3	5:A:923:HOH:O	1.91	0.70
1:B:449:GLN:O	1:B:453:ASN:HB2	1.91	0.70
1:A:26:HIS:HE1	1:A:30:ARG:HH21	1.38	0.70
1:A:182:ARG:HD2	1:A:575:ASN:HD22	1.54	0.70
1:A:622:GLY:HA2	1:A:679:LYS:HD2	1.73	0.69
1:B:182:ARG:HD2	1:B:575:ASN:HD22	1.59	0.68
1:A:540:ARG:H	1:A:543:ASN:HD21	1.42	0.66
1:A:494[A]:GLN:HE21	1:A:494[A]:GLN:HA	1.60	0.66
1:B:615:HIS:HD2	1:B:617:ASN:H	1.44	0.66
1:A:494[A]:GLN:NE2	1:A:494[A]:GLN:HA	2.12	0.64
1:A:308:LEU:HD21	1:A:356:ILE:HD11	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:HIS:HD2	5:B:929:HOH:O	1.80	0.64
1:A:206[A]:ASN:ND2	5:A:1251:HOH:O	2.30	0.63
1:A:610:PHE:CD2	5:A:1288:HOH:O	2.39	0.63
1:A:695:GLU:HA	1:A:696:ASP:C	2.17	0.62
1:A:345:GLY:H	1:A:399:GLN:NE2	1.98	0.62
1:B:472:VAL:HG12	1:B:473:GLY:H	1.66	0.60
1:A:360:PHE:HA	1:A:366:GLU:OE2	2.02	0.59
1:A:273:HIS:HD2	1:A:379:TYR:OH	1.86	0.59
1:B:273:HIS:CD2	1:B:379:TYR:OH	2.54	0.58
1:B:615:HIS:CE1	1:B:618:LYS:HD3	2.40	0.56
1:B:305[B]:TYR:CZ	1:B:312:ARG:HD3	2.40	0.56
1:A:534:GLU:HG2	1:A:549:LYS:HE3	1.88	0.55
1:B:353:HIS:CD2	1:B:371[B]:ASP:OD2	2.60	0.54
1:A:613:ASN:O	1:A:685:ARG:HA	2.08	0.54
1:B:384:ASN:O	1:B:388:HIS:HD2	1.90	0.54
1:B:613:ASN:O	1:B:685:ARG:HA	2.08	0.53
1:A:190:MET:CE	1:A:536:ILE:HD12	2.37	0.53
1:A:26:HIS:HE1	1:A:30:ARG:NH2	2.05	0.53
1:A:615:HIS:CD2	1:A:618:LYS:H	2.26	0.52
1:A:190:MET:HE1	1:A:536:ILE:HD12	1.90	0.52
1:A:589:GLN:HE21	1:A:605:ARG:HD3	1.74	0.52
1:B:141:ILE:CD1	4:B:804:GOL:H31	2.40	0.51
1:B:63:VAL:HG23	1:B:64:ASP:N	2.20	0.51
1:B:65:GLY:O	5:B:1036:HOH:O	2.19	0.51
1:A:147[B]:ASP:OD1	1:A:153:ALA:HB1	2.10	0.51
1:A:454:ARG:HH22	1:A:589:GLN:HE22	1.57	0.51
1:B:615:HIS:CD2	1:B:618:LYS:H	2.29	0.50
1:B:360:PHE:HA	1:B:366:GLU:OE1	2.11	0.49
1:B:141:ILE:HD12	4:B:804:GOL:H31	1.93	0.49
1:B:10:HIS:CD2	1:B:10:HIS:C	2.86	0.49
1:A:540:ARG:H	1:A:543:ASN:ND2	2.09	0.49
1:A:543:ASN:C	1:A:543:ASN:HD22	2.15	0.49
1:A:187:HIS:ND1	1:A:190:MET:HG2	2.28	0.49
1:A:63:VAL:O	1:A:64:ASP:C	2.52	0.48
1:A:615:HIS:CD2	1:A:617:ASN:H	2.20	0.47
1:B:63:VAL:HG11	1:B:68:ILE:HD12	1.95	0.47
1:B:469:GLN:O	1:B:474:ASP:HB2	2.14	0.47
1:B:358:LYS:HA	1:B:359:GLY:HA3	1.75	0.47
1:B:421:ARG:HD2	5:B:1262:HOH:O	2.15	0.47
1:B:231:ALA:CB	4:B:806:GOL:H2	2.42	0.46
1:B:26:HIS:HE1	1:B:30:ARG:NH2	2.09	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:472:VAL:HG12	1:B:473:GLY:N	2.30	0.45
1:A:698:GLU:HA	1:A:699:GLU:HA	1.45	0.45
1:A:443:SER:HB3	1:A:446:GLU:HB2	1.98	0.45
1:A:93:HIS:HD2	5:A:902:HOH:O	2.00	0.45
1:B:530:PHE:HB3	1:B:568:ASN:HB2	1.98	0.45
1:B:306:HIS:ND1	1:B:354:HIS:NE2	2.61	0.45
1:A:281:THR:HG22	5:B:1078:HOH:O	2.18	0.44
1:A:74:PRO:HB3	3:A:803:CEX:H6AA	2.00	0.44
1:B:476:THR:O	1:B:480:LEU:HG	2.18	0.44
1:A:530:PHE:HB3	1:A:568:ASN:HB2	2.00	0.43
1:A:534:GLU:HB3	1:A:535:TRP:H	1.58	0.43
1:A:513:ILE:HB	1:A:612:PHE:CE1	2.54	0.43
1:A:421:ARG:O	1:A:460:CYS:HA	2.18	0.42
1:B:48:LEU:HD21	1:B:382:LEU:HD22	1.99	0.42
1:A:534:GLU:HG2	1:A:549:LYS:CE	2.48	0.42
1:A:273:HIS:CD2	1:A:379:TYR:OH	2.69	0.42
1:B:459:LYS:HE3	5:B:933:HOH:O	2.19	0.42
1:B:79:ALA:HB3	1:B:103:TRP:CE3	2.54	0.42
1:A:273:HIS:CE1	1:A:328:ASN:HD22	2.37	0.42
1:B:408:CYS:HA	1:B:418:PHE:O	2.20	0.42
1:B:388:HIS:O	1:B:392:PRO:HA	2.20	0.41
1:A:632:LYS:HD3	1:A:655:ASP:OD1	2.21	0.41
1:B:350:LEU:HD13	1:B:404:MET:HE2	2.03	0.41
1:A:48:LEU:HD12	1:A:385:HIS:HD2	1.86	0.41
1:A:697:ARG:HA	1:A:697:ARG:HD2	1.84	0.41
1:B:588:LYS:O	1:B:605:ARG:HA	2.21	0.40
1:B:80:GLN:C	1:B:95:MET:HE2	2.42	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	695/702 (99%)	672 (97%)	18 (3%)	5 (1%)	26	25
1	B	693/702 (99%)	670 (97%)	19 (3%)	4 (1%)	30	29
All	All	1388/1404 (99%)	1342 (97%)	37 (3%)	9 (1%)	26	29

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	64	ASP
1	A	696	ASP
1	A	697	ARG
1	B	664	PRO
1	B	628	ASP
1	A	526	MET
1	B	63	VAL
1	A	406	VAL
1	B	406	VAL

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	604/609 (99%)	585 (97%)	19 (3%)	47	57
1	B	602/609 (99%)	586 (97%)	16 (3%)	52	63
All	All	1206/1218 (99%)	1171 (97%)	35 (3%)	51	59

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ASP
1	A	109	HIS
1	A	113	LYS
1	A	127	ARG
1	A	233	PHE
1	A	270	ASP
1	A	280	VAL

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Mol	Chain	Res	Type
1	A	281	THR
1	A	305[A]	TYR
1	A	305[B]	TYR
1	A	365	LYS
1	A	401	VAL
1	A	453	ASN
1	A	459	LYS
1	A	475	LYS
1	A	543	ASN
1	A	560	ASP
1	A	638	ASP
1	A	679	LYS
1	B	10	HIS
1	B	21	GLU
1	B	24	LYS
1	B	87	ASN
1	B	109	HIS
1	B	233	PHE
1	B	270	ASP
1	B	280	VAL
1	B	305[A]	TYR
1	B	305[B]	TYR
1	B	308	LEU
1	B	365	LYS
1	B	475	LYS
1	B	493	LEU
1	B	597	LYS
1	B	697	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	HIS
1	A	93	HIS
1	A	214	ASN
1	A	215	ASN
1	A	220	GLN
1	A	239	ASN
1	A	273	HIS
1	A	328	ASN
1	A	384	ASN
1	A	385	HIS

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Mol	Chain	Res	Type
1	A	388	HIS
1	A	399	GLN
1	A	453	ASN
1	A	524	ASN
1	A	543	ASN
1	A	575	ASN
1	A	589	GLN
1	A	615	HIS
1	A	676	ASN
1	B	10	HIS
1	B	26	HIS
1	B	93	HIS
1	B	214	ASN
1	B	273	HIS
1	B	328	ASN
1	B	384	ASN
1	B	388	HIS
1	B	469	GLN
1	B	524	ASN
1	B	575	ASN
1	B	589	GLN
1	B	615	HIS
1	B	672	ASN
1	B	676	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

11 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	BGC	A	801	-	12,12,12	0.51	0	17,17,17	0.49	0
2	BGC	A	802	-	12,12,12	0.56	0	17,17,17	1.37	2 (11%)
3	CEX	A	803	-	60,60,60	0.48	0	89,89,89	0.84	3 (3%)
4	GOL	A	804	-	5,5,5	0.34	0	5,5,5	0.19	0
2	BGC	B	801	-	12,12,12	0.43	0	17,17,17	0.63	0
2	BGC	B	802	-	12,12,12	0.52	0	17,17,17	0.96	1 (5%)
3	CEX	B	803	-	60,60,60	0.46	0	89,89,89	0.85	3 (3%)
4	GOL	B	804	-	5,5,5	0.38	0	5,5,5	0.33	0
4	GOL	B	805	-	5,5,5	0.33	0	5,5,5	0.32	0
4	GOL	B	806	-	5,5,5	0.33	0	5,5,5	0.20	0
4	GOL	B	807	-	5,5,5	0.35	0	5,5,5	0.21	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	BGC	A	801	-	-	0/2/22/22	0/1/1/1
2	BGC	A	802	-	-	0/2/22/22	0/1/1/1
3	CEX	A	803	-	-	0/26/126/126	0/5/5/5
4	GOL	A	804	-	-	0/4/4/4	0/0/0/0
2	BGC	B	801	-	-	0/2/22/22	0/1/1/1
2	BGC	B	802	-	-	0/2/22/22	0/1/1/1
3	CEX	B	803	-	-	0/26/126/126	0/5/5/5
4	GOL	B	804	-	-	0/4/4/4	0/0/0/0
4	GOL	B	805	-	-	0/4/4/4	0/0/0/0
4	GOL	B	806	-	-	0/4/4/4	0/0/0/0
4	GOL	B	807	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	803	CEX	O5A-C1A-C2A	2.12	113.17	109.80
2	B	802	BGC	C3-C4-C5	2.19	114.02	110.20
3	B	803	CEX	O5A-C1A-C2A	2.48	113.75	109.80
3	B	803	CEX	O4A-C4A-C3A	2.57	113.80	107.17
3	A	803	CEX	O4A-C4A-C3A	2.68	114.09	107.17
3	B	803	CEX	C1A-C2A-C3A	2.87	114.70	110.43
3	A	803	CEX	C1A-C2A-C3A	2.91	114.75	110.43
2	A	802	BGC	C4-C3-C2	2.93	116.26	110.79
2	A	802	BGC	C1-C2-C3	3.62	115.81	110.43

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
3	A	803	CEX	1	0
4	B	804	GOL	3	0
4	B	806	GOL	2	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	692/702 (98%)	0.19	33 (4%) 34 36	29, 42, 63, 83	0
1	B	691/702 (98%)	0.19	33 (4%) 34 36	26, 42, 63, 82	1 (0%)
All	All	1383/1404 (98%)	0.19	66 (4%) 34 36	26, 42, 63, 83	1 (0%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	8	VAL	5.5
1	B	665	GLY	5.1
1	B	664	PRO	5.1
1	B	663	MET	4.9
1	A	665	GLY	4.7
1	B	667	PRO	4.6
1	B	487	TYR	4.3
1	B	11	LEU	4.3
1	B	666	VAL	4.1
1	B	305[A]	TYR	4.1
1	A	9	ASP	4.0
1	A	664	PRO	3.7
1	B	473	GLY	3.4
1	A	305[A]	TYR	3.4
1	B	9	ASP	3.3
1	A	535	TRP	3.3
1	A	667	PRO	3.2
1	B	669	THR	3.2
1	B	10	HIS	3.2
1	B	698	GLU	3.2
1	A	487	TYR	3.1
1	A	111	ASN	3.0
1	A	150	LYS	3.0
1	B	111	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	271	VAL	2.9
1	B	535	TRP	2.8
1	A	272	VAL	2.8
1	A	10	HIS	2.7
1	B	321	VAL	2.7
1	A	370	LEU	2.7
1	A	11	LEU	2.7
1	A	663	MET	2.6
1	A	321	VAL	2.6
1	B	370	LEU	2.6
1	A	128	HIS	2.6
1	A	620	TYR	2.5
1	A	624	LYS	2.5
1	A	660	PRO	2.5
1	A	697	ARG	2.4
1	B	660	PRO	2.4
1	A	666	VAL	2.4
1	B	272	VAL	2.4
1	A	151	PHE	2.4
1	B	151	PHE	2.3
1	B	112	GLY	2.3
1	A	237	VAL	2.3
1	A	695	GLU	2.3
1	A	698	GLU	2.3
1	A	479	PHE	2.3
1	B	365	LYS	2.3
1	B	590	ILE	2.2
1	B	431	ILE	2.2
1	B	201	ARG	2.2
1	B	440	ARG	2.2
1	B	697	ARG	2.2
1	B	237	VAL	2.1
1	B	668	GLU	2.1
1	B	24	LYS	2.1
1	A	361	THR	2.1
1	B	362	GLY	2.1
1	A	64	ASP	2.1
1	A	440	ARG	2.0
1	A	696	ASP	2.0
1	B	113	LYS	2.0
1	A	431	ILE	2.0
1	A	480	LEU	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	GOL	B	804	6/6	0.91	0.23	4.75	40,41,41,42	0
4	GOL	B	806	6/6	0.87	0.17	3.84	43,43,44,44	0
2	BGC	A	802	12/12	0.82	0.17	1.27	94,94,95,95	0
2	BGC	B	802	12/12	0.79	0.13	0.68	95,95,95,95	0
3	CEX	A	803	56/56	0.88	0.12	-0.29	47,55,65,66	0
4	GOL	B	807	6/6	0.49	0.18	-0.44	98,98,98,98	0
3	CEX	B	803	56/56	0.89	0.12	-0.73	47,55,66,67	0
2	BGC	A	801	12/12	0.85	0.11	-1.10	65,65,65,65	0
2	BGC	B	801	12/12	0.84	0.09	-1.56	63,64,64,64	0
4	GOL	A	804	6/6	0.80	0.27	-	75,75,75,75	0
4	GOL	B	805	6/6	0.65	0.27	-	74,74,75,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.