



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:38 PM GMT

PDB ID : 1L9N
Title : Three-dimensional structure of the human transglutaminase 3 enzyme: binding of calcium ions change structure for activation
Authors : Ahvazi, B.
Deposited on : 2002-03-26
Resolution : 2.10 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

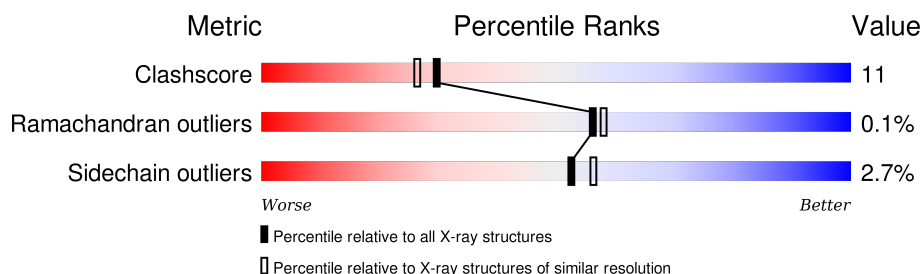
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	692	 73% 23% ..
1	B	692	 77% 19% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11561 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.

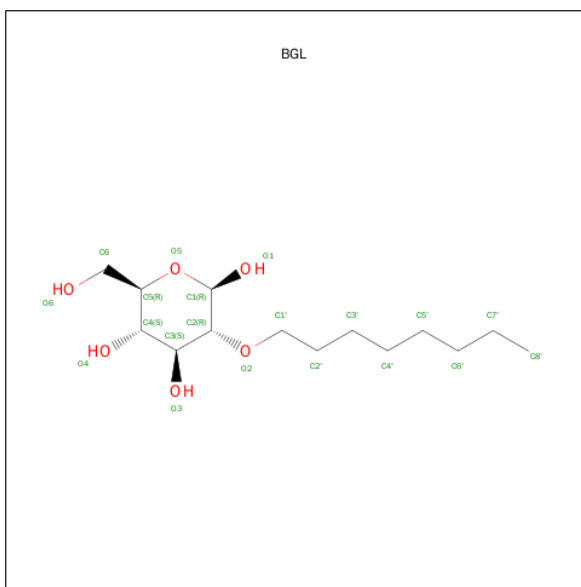
- Molecule 1 is a protein called Protein-glutamine glutamyltransferase E3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	673	Total	C	N	O	S	0	0	0
			5250	3313	913	1001	23			
1	B	673	Total	C	N	O	S	0	0	0
			5250	3313	913	1001	23			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	250	ASP	ASN	SEE REMARK 999	UNP Q08188
A	264	LEU	PHE	ENGINEERED	UNP Q08188
A	561	ARG	LYS	SEE REMARK 999	UNP Q08188
A	653	ARG	GLY	SEE REMARK 999	UNP Q08188
B	250	ASP	ASN	SEE REMARK 999	UNP Q08188
B	264	LEU	PHE	ENGINEERED	UNP Q08188
B	561	ARG	LYS	SEE REMARK 999	UNP Q08188
B	653	ARG	GLY	SEE REMARK 999	UNP Q08188

- Molecule 2 is SUGAR (B-2-OCTYLGLUCOSIDE) (three-letter code: BGL) (formula: C₁₄H₂₈O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			20	14	6		
2	B	1	Total	C	O	0	0
			20	14	6		

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

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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	511	Total	O	0	0
			511	511		

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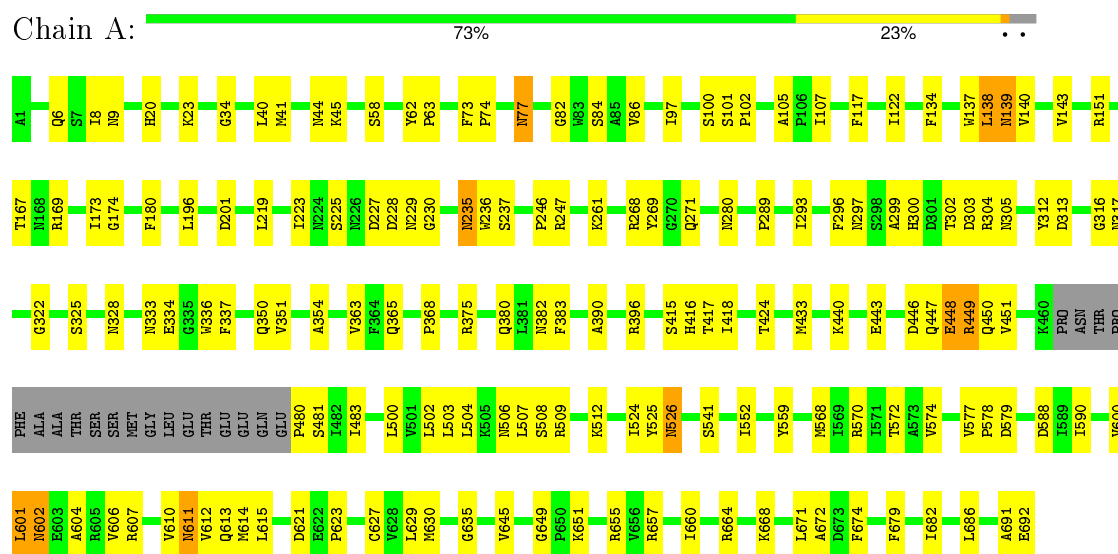
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	502	Total	O	0	0
			502	502		

3 Residue-property plots

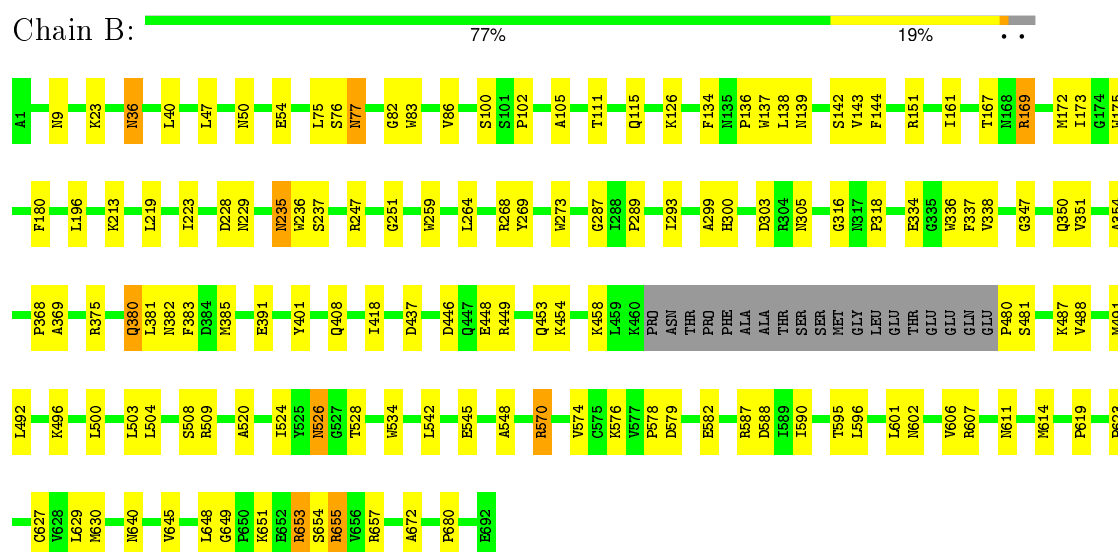
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

• Molecule 1: Protein-glutamine glutamyltransferase E3



• Molecule 1: Protein-glutamine glutamyltransferase E3



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.49Å 116.54Å 60.77Å 93.23° 92.99° 89.51°	Depositor
Resolution (Å)	20.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.189 , 0.233	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11561	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.32	0/5360	0.60	0/7270
1	B	0.32	0/5360	0.60	0/7270
All	All	0.32	0/10720	0.60	0/14540

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	5250	0	5194	132	0
1	B	5250	0	5194	105	0
2	A	20	0	28	1	0
2	B	20	0	28	4	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	511	0	0	18	0
5	B	502	0	0	16	0
All	All	11561	0	10444	234	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 11.

All (234) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:606:VAL:HG12	1:B:607:ARG:HG3	1.46	0.97
1:A:691:ALA:O	1:A:692:GLU:HB2	1.75	0.85
1:A:299:ALA:HB2	1:A:418:ILE:HD13	1.64	0.80
1:A:502:LEU:HG	1:A:504:LEU:CD2	2.12	0.79
1:B:653:ARG:HG3	1:B:653:ARG:HH11	1.47	0.78
1:B:82:GLY:HA2	1:B:102:PRO:HB3	1.65	0.77
1:A:502:LEU:HG	1:A:504:LEU:HD21	1.67	0.76
1:A:169:ARG:HD2	2:A:1015:BGL:H5	1.67	0.76
1:A:600:VAL:HG23	1:A:686:LEU:HD21	1.69	0.75
1:A:570:ARG:HD3	1:A:588:ASP:OD1	1.85	0.74
1:A:303:ASP:HB3	1:A:305:ASN:ND2	2.02	0.74
1:A:657:ARG:HD3	5:A:1509:HOH:O	1.89	0.73
1:B:570:ARG:HD3	1:B:588:ASP:OD1	1.88	0.72
1:A:173:ILE:HD13	5:A:1344:HOH:O	1.88	0.72
1:A:449:ARG:HA	1:A:449:ARG:HE	1.52	0.72
1:A:82:GLY:HA2	1:A:102:PRO:HB3	1.70	0.72
1:A:325:SER:HB2	5:A:1455:HOH:O	1.89	0.71
1:B:526:ASN:HD22	1:B:526:ASN:H	1.38	0.71
1:A:167:THR:HG22	1:A:296:PHE:HB3	1.73	0.71
1:A:526:ASN:H	1:A:526:ASN:HD22	1.38	0.69
1:B:492:LEU:HD12	2:B:1016:BGL:H4	1.74	0.69
1:B:437:ASP:HB3	5:B:1124:HOH:O	1.92	0.69
1:A:122:ILE:HG13	1:B:619:PRO:HB3	1.75	0.68
1:B:509:ARG:HG2	5:B:1410:HOH:O	1.94	0.68
1:A:77:ASN:HA	1:A:86:VAL:HG13	1.75	0.67
1:B:235:ASN:ND2	1:B:237:SER:H	1.93	0.67
1:A:6:GLN:NE2	1:A:44:ASN:HA	2.11	0.66
1:B:449:ARG:O	1:B:453:GLN:HG2	1.96	0.65
1:A:139:ASN:HD22	1:A:140:VAL:H	1.44	0.65
1:B:418:ILE:HB	5:B:1128:HOH:O	1.97	0.65
1:B:576:LYS:HD3	1:B:582:GLU:HG3	1.80	0.64
1:A:606:VAL:HG22	1:A:607:ARG:HG3	1.80	0.64
1:A:382:ASN:HB3	1:A:383:PHE:CD1	2.33	0.63
1:A:635:GLY:HA3	5:A:1443:HOH:O	1.98	0.63
1:A:235:ASN:ND2	1:A:237:SER:H	1.97	0.63
1:B:102:PRO:HG2	1:B:105:ALA:HB2	1.79	0.63
1:A:526:ASN:N	1:A:526:ASN:HD22	1.93	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:337:PHE:CE1	1:A:350:GLN:HG3	2.34	0.63
1:A:9:ASN:HB3	1:A:40:LEU:HB2	1.80	0.62
1:B:526:ASN:HD22	1:B:526:ASN:N	1.96	0.62
1:B:111:THR:HG23	1:B:126:LYS:HE3	1.80	0.61
1:A:316:GLY:HA2	1:A:574:VAL:HG23	1.82	0.61
1:A:541:SER:HA	5:A:1170:HOH:O	2.00	0.61
1:A:668:LYS:HE2	5:A:1443:HOH:O	2.00	0.60
1:B:235:ASN:C	1:B:235:ASN:HD22	2.05	0.60
1:B:77:ASN:OD1	1:B:86:VAL:HG13	2.02	0.60
1:B:488:VAL:HA	1:B:500:LEU:HD23	1.82	0.60
1:B:337:PHE:CE1	1:B:350:GLN:HG3	2.36	0.60
1:B:380:GLN:HG3	1:B:458:LYS:HD3	1.84	0.60
1:A:449:ARG:NE	1:A:449:ARG:HA	2.17	0.59
1:B:542:LEU:HD21	1:B:548:ALA:HB2	1.85	0.59
1:B:611:ASN:OD1	1:B:657:ARG:HD2	2.02	0.59
1:B:235:ASN:HD22	1:B:236:TRP:N	2.00	0.59
1:B:219:LEU:O	1:B:223:ILE:HG12	2.03	0.58
1:A:235:ASN:HD22	1:A:235:ASN:C	2.07	0.57
1:A:289:PRO:HB2	1:A:336:TRP:HB3	1.87	0.57
1:A:23:LYS:HE3	1:A:180:PHE:CE2	2.40	0.57
1:B:134:PHE:HB3	1:B:143:VAL:HG21	1.86	0.57
1:B:54:GLU:HB2	1:B:115:GLN:HB3	1.84	0.57
1:B:169:ARG:O	1:B:169:ARG:HG3	2.03	0.56
1:A:396:ARG:HD3	1:A:417:THR:HG21	1.87	0.56
1:A:293:ILE:HG13	1:A:334:GLU:HG3	1.87	0.56
1:A:322:GLY:HA3	5:A:1456:HOH:O	2.03	0.56
1:B:653:ARG:HG3	1:B:653:ARG:NH1	2.19	0.56
1:B:259:TRP:CZ2	1:B:264:LEU:HD22	2.41	0.56
1:A:446:ASP:O	1:A:450:GLN:HG3	2.07	0.55
1:A:382:ASN:HB3	1:A:383:PHE:CG	2.41	0.55
1:B:23:LYS:HE3	1:B:180:PHE:CE2	2.42	0.54
1:B:382:ASN:HB3	1:B:383:PHE:CG	2.42	0.54
1:A:137:TRP:CE2	1:A:151:ARG:HD3	2.42	0.54
1:A:627:CYS:HB3	1:A:674:PHE:CZ	2.43	0.54
1:A:602:ASN:N	1:A:602:ASN:HD22	2.04	0.54
1:A:138:LEU:HD22	1:A:140:VAL:HG22	1.89	0.54
1:A:102:PRO:HG2	1:A:105:ALA:HB2	1.90	0.53
1:A:167:THR:HG23	5:A:1077:HOH:O	2.07	0.53
1:A:117:PHE:CD1	1:B:651:LYS:HD2	2.44	0.53
1:B:623:PRO:HB3	1:B:649:GLY:HA2	1.90	0.53
1:B:648:LEU:HD22	1:B:654:SER:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:ILE:HB	1:A:354:ALA:HB1	1.90	0.53
1:A:235:ASN:HD22	1:A:236:TRP:N	2.07	0.52
1:A:610:VAL:HG23	1:A:660:ILE:CG1	2.39	0.52
1:A:502:LEU:CG	1:A:504:LEU:HD21	2.38	0.52
1:B:228:ASP:O	1:B:229:ASN:HB2	2.10	0.52
1:B:587:ARG:HD3	5:B:1126:HOH:O	2.10	0.52
1:B:289:PRO:HB2	1:B:336:TRP:HB3	1.91	0.51
1:A:139:ASN:HD22	1:A:140:VAL:N	2.07	0.51
1:B:196:LEU:HG	1:B:228:ASP:HB3	1.93	0.51
1:B:247:ARG:HG2	1:B:273:TRP:CZ2	2.46	0.51
1:A:219:LEU:O	1:A:223:ILE:HG12	2.11	0.51
1:A:623:PRO:HB3	1:A:649:GLY:HA2	1.93	0.51
1:B:526:ASN:H	1:B:526:ASN:ND2	2.08	0.51
1:A:447:GLN:O	1:A:451:VAL:HG23	2.10	0.51
1:B:142:SER:HB2	1:B:338:VAL:HG22	1.92	0.50
1:B:47:LEU:HD23	1:B:47:LEU:C	2.31	0.50
1:B:169:ARG:HD2	2:B:1016:BGL:H62	1.93	0.50
1:B:382:ASN:HB3	1:B:383:PHE:CD1	2.46	0.50
1:B:161:ILE:HD12	1:B:172:MET:CE	2.41	0.50
1:B:655:ARG:HB2	5:B:1448:HOH:O	2.10	0.50
1:A:691:ALA:O	1:A:692:GLU:CB	2.54	0.50
1:B:167:THR:HG23	5:B:1285:HOH:O	2.12	0.49
1:A:235:ASN:HD22	1:A:237:SER:H	1.59	0.49
1:A:390:ALA:HB3	5:A:1101:HOH:O	2.12	0.49
1:A:316:GLY:HA2	1:A:574:VAL:CG2	2.43	0.49
1:A:524:ILE:HB	1:A:526:ASN:HD21	1.78	0.49
1:A:512:LYS:HD2	1:A:577:VAL:HG11	1.95	0.48
1:A:679:PHE:HB3	1:A:682:ILE:HD11	1.95	0.48
1:A:611:ASN:OD1	1:A:657:ARG:HD2	2.13	0.48
1:B:524:ILE:HB	1:B:526:ASN:ND2	2.27	0.48
1:A:139:ASN:ND2	1:A:140:VAL:H	2.10	0.48
1:A:664:ARG:NH1	5:A:1073:HOH:O	2.45	0.48
1:B:137:TRP:CE2	1:B:151:ARG:HD3	2.48	0.48
1:A:167:THR:HG22	1:A:296:PHE:CB	2.43	0.48
1:B:235:ASN:HD22	1:B:237:SER:H	1.58	0.48
1:A:201:ASP:HB3	5:A:1129:HOH:O	2.13	0.48
1:A:139:ASN:N	1:A:139:ASN:HD22	2.12	0.48
1:B:36:ASN:HD22	1:B:36:ASN:C	2.16	0.48
1:A:524:ILE:HB	1:A:526:ASN:ND2	2.29	0.48
1:A:351:VAL:O	1:A:368:PRO:HA	2.13	0.48
1:A:173:ILE:HG21	5:A:1344:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:351:VAL:HB	1:B:369:ALA:HB3	1.96	0.47
1:A:44:ASN:OD1	1:A:45:LYS:HG2	2.15	0.47
1:A:375:ARG:HG3	1:A:440:LYS:HA	1.96	0.47
1:B:640:ASN:ND2	5:B:1150:HOH:O	2.47	0.47
1:B:300:HIS:HB2	5:B:1068:HOH:O	2.14	0.47
1:B:503:LEU:HD23	1:B:504:LEU:N	2.29	0.47
1:A:174:GLY:HA3	1:A:671:LEU:HD21	1.96	0.47
1:A:293:ILE:HD13	1:A:424:THR:HB	1.95	0.47
1:B:520:ALA:HB3	1:B:534:TRP:HB3	1.96	0.47
1:B:351:VAL:O	1:B:368:PRO:HA	2.14	0.47
1:B:491:MET:CG	1:B:496:LYS:HE2	2.45	0.47
1:B:316:GLY:HA2	1:B:574:VAL:HG23	1.97	0.47
1:B:655:ARG:HD3	5:B:1175:HOH:O	2.15	0.47
1:A:134:PHE:HB3	1:A:143:VAL:HG21	1.97	0.47
1:B:524:ILE:HB	1:B:526:ASN:HD21	1.80	0.47
1:B:401:TYR:HD2	1:B:408:GLN:HB2	1.80	0.46
1:A:228:ASP:O	1:A:229:ASN:HB2	2.16	0.46
1:B:293:ILE:CG1	1:B:334:GLU:HG3	2.45	0.46
1:A:502:LEU:HG	1:A:504:LEU:HD22	1.97	0.46
1:A:41:MET:HE3	1:A:97:ILE:HD12	1.96	0.46
1:B:680:PRO:HB3	5:B:1488:HOH:O	2.14	0.46
1:B:595:THR:HG22	1:B:596:LEU:N	2.31	0.46
1:A:610:VAL:HG23	1:A:660:ILE:HG12	1.98	0.46
1:A:621:ASP:OD1	1:A:651:LYS:NZ	2.48	0.46
1:A:630:MET:O	1:A:672:ALA:HA	2.16	0.46
1:B:380:GLN:H	1:B:380:GLN:CD	2.19	0.46
1:A:107:ILE:HD13	1:A:134:PHE:CE2	2.51	0.45
1:B:578:PRO:O	1:B:579:ASP:HB2	2.15	0.45
1:B:375:ARG:HD3	5:B:1482:HOH:O	2.15	0.45
1:B:9:ASN:HB3	1:B:40:LEU:HB2	1.97	0.45
1:A:139:ASN:ND2	1:A:140:VAL:N	2.65	0.45
1:A:424:THR:O	1:A:433:MET:HB3	2.16	0.45
1:A:58:SER:HB2	1:A:63:PRO:HB3	1.98	0.45
1:B:75:LEU:O	1:B:75:LEU:HD13	2.17	0.45
1:A:602:ASN:N	1:A:602:ASN:ND2	2.65	0.45
1:A:416:HIS:CD2	1:A:443:GLU:OE1	2.69	0.45
1:A:606:VAL:HG12	1:A:692:GLU:CB	2.46	0.45
1:B:382:ASN:HA	1:B:383:PHE:HA	1.74	0.45
1:B:293:ILE:HG13	1:B:334:GLU:HG3	1.97	0.45
1:A:415:SER:O	1:A:416:HIS:HD2	1.99	0.45
1:A:247:ARG:HD2	5:A:1033:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:480:PRO:HD3	5:B:1487:HOH:O	2.17	0.45
1:A:481:SER:OG	1:A:508:SER:HB3	2.17	0.45
1:A:225:SER:HA	1:A:230:GLY:N	2.32	0.45
1:A:246:PRO:CB	1:A:271:GLN:HG3	2.47	0.45
1:A:303:ASP:O	1:A:304:ARG:HB2	2.16	0.44
1:A:196:LEU:HG	1:A:228:ASP:HB3	2.00	0.44
1:A:578:PRO:O	1:A:579:ASP:HB2	2.17	0.44
1:B:82:GLY:CA	1:B:102:PRO:HB3	2.43	0.44
1:B:481:SER:HB3	1:B:508:SER:HB2	1.99	0.44
1:A:483:ILE:HD13	1:A:507:LEU:HD11	1.98	0.44
1:A:568:MET:SD	1:A:590:ILE:HB	2.57	0.44
1:A:606:VAL:HG13	1:A:607:ARG:NH1	2.33	0.44
1:A:448:GLU:OE2	1:A:449:ARG:NE	2.51	0.44
1:A:328:ASN:ND2	1:A:525:TYR:HA	2.32	0.44
1:B:347:GLY:HA3	5:B:1096:HOH:O	2.18	0.44
1:B:173:ILE:HA	5:B:1342:HOH:O	2.18	0.44
1:A:541:SER:HB3	5:A:1283:HOH:O	2.18	0.44
1:B:161:ILE:HD12	1:B:172:MET:HE3	2.00	0.44
1:A:312:TYR:CD2	1:A:572:THR:HG21	2.53	0.43
1:B:303:ASP:HB2	1:B:305:ASN:ND2	2.33	0.43
1:A:500:LEU:HB2	1:A:552:ILE:HB	2.00	0.43
1:A:62:TYR:N	1:A:63:PRO:HD3	2.33	0.43
1:A:300:HIS:NE2	1:A:302:THR:HG22	2.33	0.43
1:A:611:ASN:HD22	1:A:612:VAL:H	1.66	0.43
1:A:261:LYS:NZ	5:A:1518:HOH:O	2.51	0.43
1:B:268:ARG:HA	1:B:269:TYR:HA	1.67	0.43
1:A:526:ASN:N	1:A:526:ASN:ND2	2.65	0.43
1:A:526:ASN:H	1:A:526:ASN:ND2	2.10	0.43
1:A:679:PHE:CB	1:A:682:ILE:HD11	2.49	0.43
1:B:213:LYS:NZ	1:B:213:LYS:HB2	2.34	0.43
1:A:313:ASP:OD2	1:A:317:ASN:HB2	2.18	0.43
1:A:480:PRO:HG2	5:A:1457:HOH:O	2.17	0.43
1:B:601:LEU:O	1:B:602:ASN:HB2	2.19	0.43
1:A:328:ASN:HD22	1:A:525:TYR:HA	1.83	0.42
1:B:136:PRO:HG3	1:B:287:GLY:O	2.19	0.42
1:B:381:LEU:O	1:B:385:MET:HG3	2.19	0.42
1:A:73:PHE:HA	1:A:74:PRO:HD3	1.84	0.42
1:A:615:LEU:HD23	1:A:655:ARG:HG2	2.01	0.42
1:B:630:MET:O	1:B:672:ALA:HA	2.19	0.42
1:A:363:VAL:HG22	1:A:365:GLN:NE2	2.34	0.42
1:B:454:LYS:O	1:B:458:LYS:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:PHE:HB3	1:B:651:LYS:HD2	2.00	0.42
1:B:83:TRP:HA	1:B:100:SER:O	2.18	0.42
1:B:82:GLY:HA3	5:B:1269:HOH:O	2.20	0.42
1:B:380:GLN:CG	1:B:458:LYS:HD3	2.48	0.42
1:A:297:ASN:O	1:A:418:ILE:HG23	2.20	0.42
1:A:334:GLU:HA	1:A:350:GLN:O	2.20	0.42
1:B:259:TRP:CE2	1:B:264:LEU:HD22	2.54	0.42
1:A:268:ARG:HA	1:A:269:TYR:HA	1.66	0.42
1:B:653:ARG:CG	1:B:653:ARG:NH1	2.79	0.42
1:B:526:ASN:ND2	1:B:528:THR:H	2.18	0.41
1:B:139:ASN:HA	1:B:144:PHE:CD1	2.55	0.41
1:A:601:LEU:HD11	1:A:613:GLN:NE2	2.35	0.41
1:A:280:ASN:HD22	1:A:333:ASN:HD22	1.68	0.41
1:A:612:VAL:HG12	1:A:613:GLN:N	2.36	0.41
1:A:627:CYS:HB2	1:A:645:VAL:HB	2.01	0.41
1:A:604:ALA:HA	1:A:610:VAL:HG11	2.03	0.41
1:B:487:LYS:HG2	2:B:1016:BGL:H8'1	2.02	0.41
1:B:318:PRO:HG2	1:B:570:ARG:HG2	2.02	0.41
1:B:76:SER:O	1:B:77:ASN:O	2.39	0.41
1:B:223:ILE:HB	1:B:354:ALA:HB1	2.03	0.41
1:A:268:ARG:HB3	1:A:269:TYR:CD1	2.55	0.41
1:A:34:GLY:HA2	1:A:101:SER:O	2.21	0.41
1:A:559:TYR:C	1:A:559:TYR:CD1	2.94	0.41
1:A:20:HIS:HD2	5:A:1092:HOH:O	2.02	0.41
1:A:606:VAL:CG1	1:A:692:GLU:HG2	2.51	0.40
1:B:590:ILE:H	2:B:1016:BGL:C6	2.33	0.40
1:B:299:ALA:O	1:B:391:GLU:HA	2.21	0.40
1:A:229:ASN:HA	5:A:1097:HOH:O	2.20	0.40
1:B:50:ASN:HB3	5:B:1041:HOH:O	2.20	0.40
1:A:84:SER:OG	1:A:100:SER:HB3	2.20	0.40
1:B:23:LYS:HE3	1:B:180:PHE:CZ	2.56	0.40
1:B:627:CYS:HB2	1:B:645:VAL:HB	2.04	0.40
1:B:175:TRP:CE2	1:B:251:GLY:HA2	2.56	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	669/692 (97%)	643 (96%)	25 (4%)	1 (0%)	56	58
1	B	669/692 (97%)	638 (95%)	30 (4%)	1 (0%)	56	58
All	All	1338/1384 (97%)	1281 (96%)	55 (4%)	2 (0%)	56	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	77	ASN
1	A	77	ASN

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	579/595 (97%)	562 (97%)	17 (3%)	50	53
1	B	579/595 (97%)	565 (98%)	14 (2%)	57	61
All	All	1158/1190 (97%)	1127 (97%)	31 (3%)	52	56

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ILE
1	A	138	LEU
1	A	139	ASN
1	A	227	ASP

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Mol	Chain	Res	Type
1	A	235	ASN
1	A	380	GLN
1	A	448	GLU
1	A	449	ARG
1	A	503	LEU
1	A	506	ASN
1	A	509	ARG
1	A	526	ASN
1	A	601	LEU
1	A	602	ASN
1	A	611	ASN
1	A	614	MET
1	A	629	LEU
1	B	36	ASN
1	B	138	LEU
1	B	169	ARG
1	B	235	ASN
1	B	380	GLN
1	B	446	ASP
1	B	448	GLU
1	B	526	ASN
1	B	545	GLU
1	B	570	ARG
1	B	614	MET
1	B	629	LEU
1	B	653	ARG
1	B	655	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	20	HIS
1	A	115	GLN
1	A	139	ASN
1	A	168	ASN
1	A	235	ASN
1	A	280	ASN
1	A	328	ASN
1	A	408	GLN
1	A	411	ASN
1	A	416	HIS

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Mol	Chain	Res	Type
1	A	450	GLN
1	A	506	ASN
1	A	517	ASN
1	A	526	ASN
1	A	602	ASN
1	A	640	ASN
1	B	20	HIS
1	B	36	ASN
1	B	91	ASN
1	B	168	ASN
1	B	226	ASN
1	B	229	ASN
1	B	235	ASN
1	B	280	ASN
1	B	357	GLN
1	B	408	GLN
1	B	526	ASN
1	B	640	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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	BGL	A	1015	-	19,20,20	1.21	1 (5%)	23,25,25	1.68	7 (30%)
2	BGL	B	1016	-	19,20,20	1.20	1 (5%)	23,25,25	1.77	7 (30%)

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	BGL	A	1015	-	-	0/11/31/31	0/1/1/1
2	BGL	B	1016	-	-	0/11/31/31	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1016	BGL	O2-C1'	3.83	1.53	1.42
2	A	1015	BGL	O2-C1'	3.96	1.54	1.42

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1015	BGL	C1-C2-C3	-2.95	105.24	110.45
2	B	1016	BGL	C1-C2-C3	-2.78	105.53	110.45
2	A	1015	BGL	O2-C2-C3	2.14	114.35	110.04
2	A	1015	BGL	O3-C3-C2	2.23	115.15	109.87
2	B	1016	BGL	O2-C2-C3	2.38	114.83	110.04
2	B	1016	BGL	O3-C3-C2	2.50	115.80	109.87
2	A	1015	BGL	C1'-O2-C2	2.51	121.28	114.40
2	B	1016	BGL	C1'-O2-C2	2.53	121.34	114.40
2	A	1015	BGL	O4-C4-C3	2.73	116.49	110.34
2	B	1016	BGL	O4-C4-C3	2.85	116.76	110.34
2	A	1015	BGL	O6-C6-C5	3.18	121.85	111.33
2	B	1016	BGL	O6-C6-C5	3.29	122.19	111.33
2	A	1015	BGL	C6-C5-C4	3.36	121.31	113.02
2	B	1016	BGL	C6-C5-C4	3.51	121.66	113.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1015	BGL	1	0
2	B	1016	BGL	4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.