



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:14 AM UTC

PDB ID : 4C91 / pdb_00004c91
Title : Evidence that GH115 alpha-glucuronidase activity is dependent on conformational flexibility
Authors : Rogowski, A.; Basle, A.; Farinas, C.S.; Solovyova, A.; Mortimer, J.C.; Dupree, P.; Gilbert, H.J.; Bolam, D.N.
Deposited on : 2013-10-02
Resolution : 2.14 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

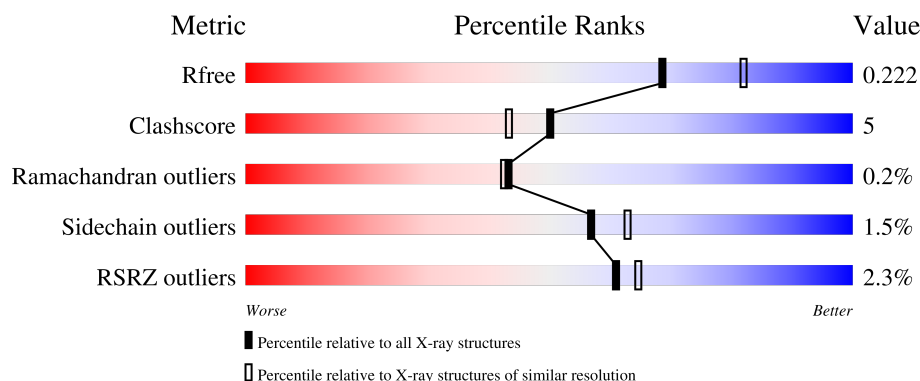
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

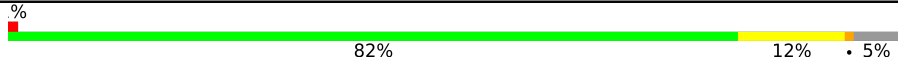
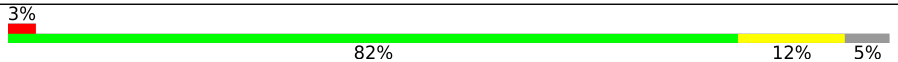
The reported resolution of this entry is 2.14 Å.

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}	180053	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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 $\leq 5\%$. 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	856	
1	B	856	

2 Entry composition [i](#)

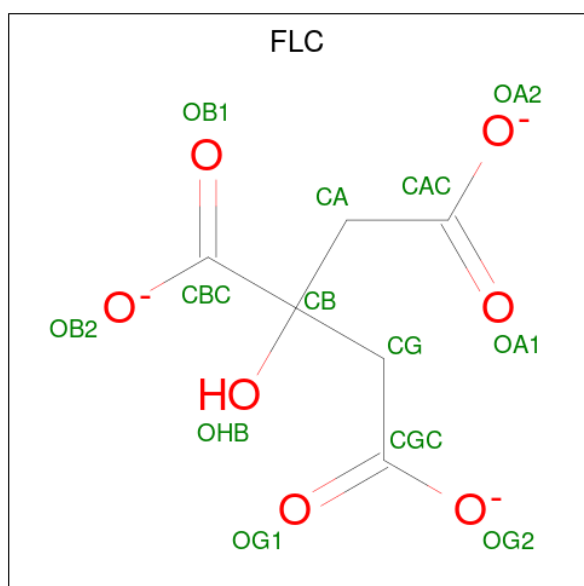
There are 4 unique types of molecules in this entry. The entry contains 13323 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ALPHA-GLUCURONIDASE GH115.

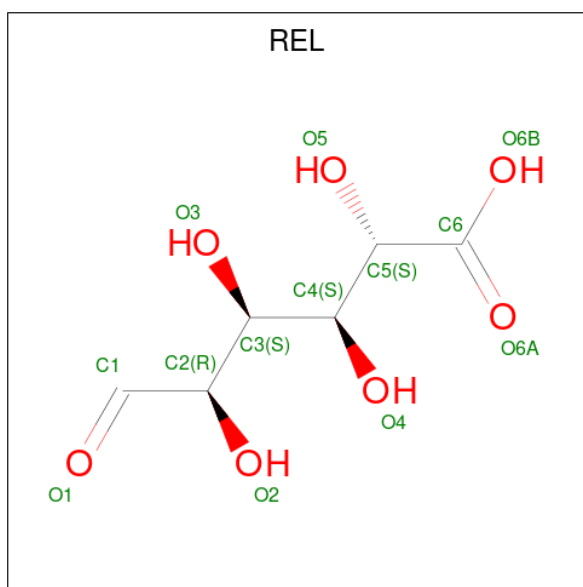
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	811	Total	C	N	O	S	0	1	0
			6373	4097	1053	1185	38			
1	B	809	Total	C	N	O	S	0	0	0
			6322	4065	1034	1185	38			

- Molecule 2 is CITRATE ANION (CCD ID: FLC) (formula: $C_6H_5O_7^-$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is D-glucuronic acid (CCD ID: REL) (formula: $C_6H_{10}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	339	Total	O	0	0
			339	339		
4	B	263	Total	O	0	0
			263	263		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.04Å 130.29Å 190.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.74 – 2.14 44.74 – 2.14	Depositor EDS
% Data completeness (in resolution range)	93.8 (44.74-2.14) 93.7 (44.74-2.14)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.174 , 0.219 0.179 , 0.222	Depositor DCC
R_{free} test set	4649 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	22.4	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 40.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13323	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.19% 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, 0.333 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: REL, FLC

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	1.10	5/6549 (0.1%)	0.97	6/8927 (0.1%)
1	B	1.07	5/6493 (0.1%)	0.96	1/8856 (0.0%)
All	All	1.08	10/13042 (0.1%)	0.96	7/17783 (0.0%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	494	HIS	N-CA	-8.15	1.41	1.46
1	A	575	ILE	CA-C	-5.52	1.45	1.52
1	B	573	GLN	C-O	-5.52	1.17	1.24
1	A	656	ALA	C-O	-5.35	1.17	1.23
1	B	315	ARG	C-O	-5.21	1.17	1.24
1	B	144	VAL	N-CA	-5.18	1.40	1.46
1	B	704	VAL	C-O	-5.16	1.18	1.24
1	A	482	ASN	N-CA	-5.09	1.41	1.46
1	A	535	TYR	CA-C	-5.04	1.46	1.52
1	A	547	ASP	C-O	-5.03	1.18	1.24

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	293	TYR	N-CA-C	7.43	120.47	111.40
1	A	386	VAL	CA-C-N	-6.36	113.74	120.03
1	A	386	VAL	C-N-CA	-6.36	113.74	120.03
1	A	808	VAL	CB-CA-C	-5.88	104.42	110.71
1	A	188	GLY	N-CA-C	-5.31	106.72	112.08
1	B	704	VAL	CB-CA-C	-5.31	104.87	111.08
1	A	471	TYR	CA-CB-CG	-5.05	104.81	113.90

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	6373	0	5971	66	0
1	B	6322	0	5872	68	0
2	A	13	0	5	0	0
3	A	13	0	9	3	0
4	A	339	0	0	3	0
4	B	263	0	0	3	0
All	All	13323	0	11857	131	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 5.

All (131) 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:66:MET:HE3	1:A:66:MET:HA	1.50	0.92
1:A:205:ASN:OD1	3:A:1856:REL:H1	1.71	0.89
1:B:326:GLY:HA3	1:B:370:TRP:CZ3	2.08	0.88
1:A:386:VAL:HG11	1:A:392:MET:SD	2.22	0.80
1:B:112:ALA:O	1:B:132:ILE:HG21	1.82	0.79
1:A:276:HIS:NE2	1:A:373:TYR:OH	2.16	0.78
1:B:797:ARG:HB2	4:B:2241:HOH:O	1.85	0.77
1:A:369:VAL:HG12	1:A:391:ILE:HB	1.70	0.72
1:A:493:ASP:OD1	1:A:496[B]:ARG:NH1	2.23	0.72
1:B:178:MET:HE1	1:B:566:GLU:HG3	1.71	0.72
1:A:205:ASN:OD1	3:A:1856:REL:C1	2.38	0.70
1:B:493:ASP:OD1	1:B:496:ARG:NH1	2.25	0.70
1:B:344:LEU:HD21	1:B:370:TRP:HZ2	1.57	0.69
1:B:75:ASP:OD2	1:B:161:SER:OG	2.13	0.65
1:A:370:TRP:CZ3	1:A:386:VAL:HG22	2.34	0.63
1:A:293:TYR:O	1:A:304:VAL:HG11	2.00	0.62
1:A:160:LEU:O	1:A:164:MET:HG3	2.00	0.61
1:B:344:LEU:HD21	1:B:370:TRP:CZ2	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:675:TYR:CZ	1:B:853:ARG:HD2	2.37	0.59
1:A:76:ILE:CG1	1:A:164:MET:HE1	2.33	0.58
1:A:675:TYR:CZ	1:A:853:ARG:HD2	2.39	0.58
1:B:115:ILE:HG23	1:B:119:GLU:OE1	2.03	0.58
1:B:90:THR:HG23	1:B:136:CYS:SG	2.44	0.58
1:B:79:VAL:HG21	1:B:164:MET:HG2	1.86	0.58
1:B:112:ALA:N	1:B:113:GLY:HA2	2.18	0.57
1:A:76:ILE:HG13	1:A:164:MET:HE1	1.87	0.57
1:B:205:ASN:O	1:B:464:GLY:HA2	2.04	0.57
1:A:205:ASN:O	1:A:464:GLY:HA2	2.04	0.56
1:B:90:THR:CG2	1:B:136:CYS:SG	2.94	0.56
1:B:610:ALA:HB1	1:B:662:ILE:HD12	1.88	0.56
1:A:206:ASP:OD1	3:A:1856:REL:H2	2.06	0.56
1:B:275:HIS:H	1:B:275:HIS:CD2	2.25	0.55
1:A:66:MET:HE3	1:A:66:MET:CA	2.28	0.54
1:A:66:MET:HA	1:A:66:MET:CE	2.32	0.54
1:A:109:LEU:HD21	1:A:144:VAL:HG11	1.88	0.54
1:A:445:GLU:OE1	1:B:749:LYS:HE3	2.08	0.53
1:A:787:VAL:HG13	1:A:788:TYR:CD2	2.44	0.53
1:A:675:TYR:CE2	1:A:853:ARG:HD2	2.44	0.53
1:A:110:MET:C	1:A:112:ALA:H	2.17	0.53
1:A:435:LEU:HD12	1:A:582:MET:HE2	1.91	0.53
1:A:554:ALA:HB2	1:B:554:ALA:HB2	1.90	0.53
1:B:435:LEU:HD12	1:B:582:MET:HE2	1.90	0.53
1:B:518:TYR:CD1	1:B:518:TYR:C	2.87	0.53
1:B:675:TYR:CE2	1:B:853:ARG:HD2	2.44	0.53
1:B:243:PHE:CE1	1:B:322:ILE:HD12	2.45	0.52
1:A:610:ALA:HB1	1:A:662:ILE:HD12	1.91	0.52
1:A:290:ARG:O	1:A:294:GLY:HA2	2.10	0.51
1:B:127:TYR:OH	1:B:159:GLU:HG2	2.10	0.51
1:B:120:LEU:HD21	1:B:128:ILE:HG13	1.92	0.51
1:A:459:TRP:HB3	1:A:476:PHE:CZ	2.45	0.51
1:B:404:ARG:NH2	1:B:410:GLU:OE2	2.43	0.51
1:A:127:TYR:OH	1:A:159:GLU:HG2	2.10	0.51
1:B:206:ASP:HA	1:B:249:TRP:CH2	2.46	0.51
1:B:459:TRP:HB3	1:B:476:PHE:CZ	2.47	0.50
1:A:75:ASP:HB3	1:A:166:VAL:HG21	1.93	0.50
1:A:518:TYR:C	1:A:518:TYR:CD1	2.89	0.50
1:B:75:ASP:HB3	1:B:166:VAL:HG21	1.93	0.49
1:B:750:SER:HA	1:B:800:VAL:HG23	1.94	0.49
1:B:206:ASP:HA	1:B:249:TRP:CZ2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:CYS:SG	1:A:139:ILE:HD12	2.53	0.48
1:B:90:THR:HG22	1:B:90:THR:O	2.12	0.48
1:B:679:GLY:HA2	1:B:684:ILE:HG12	1.95	0.48
1:B:136:CYS:O	1:B:137:GLU:C	2.56	0.47
1:B:322:ILE:CG2	1:B:369:VAL:HG23	2.45	0.47
1:B:94:ARG:HA	1:B:141:GLU:O	2.14	0.47
1:A:206:ASP:HA	1:A:249:TRP:CZ2	2.50	0.47
1:A:76:ILE:HG12	1:A:164:MET:HE1	1.97	0.46
1:A:276:HIS:CD2	1:A:373:TYR:HH	2.26	0.46
1:B:393:LEU:HD12	1:B:418:GLY:C	2.40	0.46
1:B:763:SER:HA	1:B:772:GLN:O	2.15	0.45
1:B:572:LYS:HA	1:B:576:LEU:HB3	1.99	0.45
1:A:750:SER:HA	1:A:800:VAL:HG23	1.97	0.45
1:A:243:PHE:CE1	1:A:322:ILE:HD12	2.51	0.45
1:B:58:ASP:OD2	1:B:60:SER:OG	2.22	0.45
1:A:275:HIS:HB2	1:A:371:ALA:CB	2.47	0.45
1:A:94:ARG:HA	1:A:141:GLU:O	2.17	0.45
1:A:547:ASP:HB3	1:B:547:ASP:HB3	1.99	0.45
1:A:679:GLY:HA2	1:A:684:ILE:HG12	1.99	0.45
1:B:466:LEU:C	1:B:466:LEU:HD23	2.42	0.45
1:A:572:LYS:HA	1:A:576:LEU:HB3	1.98	0.44
1:B:106:ILE:O	1:B:110:MET:HG3	2.17	0.44
1:B:398:ASN:HB3	1:B:425:TYR:CD1	2.53	0.44
1:B:305:ILE:HD13	1:B:327:MET:HE1	1.98	0.44
1:B:322:ILE:HG21	1:B:369:VAL:HG23	1.99	0.44
1:A:206:ASP:HA	1:A:249:TRP:CH2	2.53	0.44
1:B:99:GLY:O	1:B:146:ILE:HA	2.18	0.43
1:A:322:ILE:HG21	1:A:369:VAL:HG13	2.00	0.43
1:B:404:ARG:HD3	4:B:2096:HOH:O	2.18	0.43
1:A:774:ILE:HD11	1:A:804:ALA:HB2	2.00	0.43
1:A:216:LYS:HA	1:A:221:THR:O	2.19	0.43
1:A:99:GLY:O	1:A:146:ILE:HA	2.18	0.42
1:A:348:VAL:HG21	1:A:370:TRP:CH2	2.54	0.42
1:B:90:THR:HG23	1:B:139:ILE:HD12	2.02	0.42
1:A:129:LEU:HD23	1:A:129:LEU:C	2.44	0.42
1:B:451:TYR:CG	1:B:483:PRO:HG2	2.54	0.42
1:A:487:ASN:HB2	4:A:2162:HOH:O	2.19	0.42
1:A:496[A]:ARG:NH1	1:A:505:GLU:OE2	2.49	0.42
1:B:686:ILE:O	1:B:831:LYS:HG3	2.19	0.42
1:B:850:LYS:HA	4:B:2176:HOH:O	2.20	0.42
1:B:691:TYR:HA	1:B:731:TYR:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:369:VAL:HG21	4:A:2078:HOH:O	2.19	0.42
1:A:451:TYR:CG	1:A:483:PRO:HG2	2.55	0.42
1:B:391:ILE:HG12	1:B:457:LYS:HG2	2.02	0.42
1:A:708:MET:HE2	1:A:749:LYS:HD2	2.01	0.42
1:A:769:GLY:HA3	4:A:2312:HOH:O	2.20	0.42
1:B:273:THR:HB	1:B:277:GLU:HB2	2.01	0.42
1:B:681:ASP:O	1:B:838:GLY:HA3	2.20	0.42
1:B:136:CYS:SG	1:B:139:ILE:HD12	2.60	0.41
1:A:637:LYS:O	1:A:638:ASN:HB2	2.19	0.41
1:B:92:SER:O	1:B:139:ILE:HA	2.20	0.41
1:A:393:LEU:HD12	1:A:418:GLY:C	2.46	0.41
1:A:763:SER:HA	1:A:772:GLN:O	2.19	0.41
1:A:437:VAL:HA	1:A:522:ASN:HB3	2.02	0.41
1:B:195:PRO:HB3	1:B:481:TRP:CE3	2.56	0.41
1:B:512:MET:C	1:B:512:MET:SD	3.03	0.41
1:A:407:ASN:OD1	1:A:407:ASN:C	2.64	0.41
1:B:398:ASN:HB3	1:B:425:TYR:CG	2.56	0.41
1:B:298:TYR:CZ	1:B:302:GLN:HG3	2.56	0.41
1:A:391:ILE:HG12	1:A:457:LYS:HG2	2.03	0.40
1:A:512:MET:C	1:A:512:MET:SD	3.05	0.40
1:A:682:GLY:HA2	1:A:836:TYR:CE2	2.56	0.40
1:B:323:VAL:O	1:B:368:GLN:HA	2.21	0.40
1:A:197:VAL:HA	1:A:456:GLU:O	2.21	0.40
1:A:54:PRO:HB2	1:A:87:LEU:HG	2.02	0.40
1:A:276:HIS:CD2	1:A:373:TYR:OH	2.72	0.40
1:B:90:THR:HG21	1:B:136:CYS:SG	2.62	0.40
1:B:492:LEU:HD23	1:B:492:LEU:HA	1.83	0.40
1:A:92:SER:O	1:A:139:ILE:HA	2.22	0.40
1:B:103:THR:HG23	1:B:104:PRO:HD2	2.03	0.40
1:B:503:PHE:HA	1:B:567:TYR:CD1	2.57	0.40
1:B:510:GLU:HA	1:B:510:GLU:OE1	2.21	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	808/856 (94%)	775 (96%)	32 (4%)	1 (0%)	48	49
1	B	803/856 (94%)	770 (96%)	31 (4%)	2 (0%)	43	42
All	All	1611/1712 (94%)	1545 (96%)	63 (4%)	3 (0%)	43	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	137	GLU
1	A	113	GLY
1	B	374	LYS

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	638/740 (86%)	628 (98%)	10 (2%)	55	61
1	B	628/740 (85%)	619 (99%)	9 (1%)	59	65
All	All	1266/1480 (86%)	1247 (98%)	19 (2%)	57	63

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	ARG
1	A	109	LEU
1	A	262	LYS
1	A	340	ASN
1	A	502	GLN
1	A	517	LEU
1	A	518	TYR
1	A	538	GLU
1	A	542	TRP
1	A	549	TYR

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Mol	Chain	Res	Type
1	B	109	LEU
1	B	128	ILE
1	B	370	TRP
1	B	460	ILE
1	B	489	SER
1	B	502	GLN
1	B	518	TYR
1	B	542	TRP
1	B	812	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	GLN
1	A	180	GLN
1	A	284	GLN
1	B	284	GLN
1	B	605	GLN
1	B	807	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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
3	REL	A	1856	-	11,12,12	1.20	1 (9%)	14,16,16	2.67	6 (42%)
2	FLC	A	1855	-	12,12,12	1.14	0	17,17,17	5.69	9 (52%)

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
3	REL	A	1856	-	-	11/17/18/18	-
2	FLC	A	1855	-	-	4/16/16/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1856	REL	C3-C2	2.20	1.56	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1855	FLC	OHB-CB-CBC	-13.77	89.43	108.96
2	A	1855	FLC	OHB-CB-CG	-12.55	80.75	109.38
2	A	1855	FLC	CG-CB-CBC	8.24	128.27	110.03
2	A	1855	FLC	OHB-CB-CA	-7.27	92.80	109.38
2	A	1855	FLC	CB-CG-CGC	-6.13	97.15	113.92
3	A	1856	REL	O4-C4-C3	-5.51	96.59	109.46
3	A	1856	REL	O3-C3-C2	5.32	119.02	109.13
2	A	1855	FLC	OG1-CGC-CG	-4.21	111.02	122.95
3	A	1856	REL	O3-C3-C4	-3.47	101.35	109.46
3	A	1856	REL	O2-C2-C3	-3.17	102.03	109.46
3	A	1856	REL	O4-C4-C5	2.78	114.28	109.29
2	A	1855	FLC	CA-CB-CBC	2.56	115.71	110.03
2	A	1855	FLC	CG-CB-CA	2.38	115.42	109.31
2	A	1855	FLC	OG2-CGC-CG	2.29	121.59	114.35
3	A	1856	REL	O6B-C6-C5	2.16	119.31	113.31

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1856	REL	O4-C4-C5-C6
3	A	1856	REL	C3-C4-C5-C6
3	A	1856	REL	O4-C4-C5-O5
3	A	1856	REL	C3-C4-C5-O5
3	A	1856	REL	O2-C2-C3-C4
3	A	1856	REL	C1-C2-C3-C4
3	A	1856	REL	O2-C2-C3-O3
3	A	1856	REL	C1-C2-C3-O3
2	A	1855	FLC	CAC-CA-CB-CG
2	A	1855	FLC	CA-CB-CG-CGC
2	A	1855	FLC	CBC-CB-CG-CGC
3	A	1856	REL	O3-C3-C4-C5
2	A	1855	FLC	OHB-CB-CG-CGC
3	A	1856	REL	C2-C3-C4-C5
3	A	1856	REL	O3-C3-C4-O4

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1856	REL	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	811/856 (94%)	-0.21	11 (1%) 73 77	11, 23, 45, 78	1 (0%)
1	B	809/856 (94%)	-0.06	27 (3%) 49 53	15, 25, 50, 79	0
All	All	1620/1712 (94%)	-0.13	38 (2%) 61 65	11, 25, 47, 79	1 (0%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	113	GLY	5.4
1	B	112	ALA	4.7
1	B	370	TRP	4.5
1	B	373	TYR	4.3
1	B	376	VAL	3.9
1	A	112	ALA	3.4
1	A	373	TYR	3.2
1	A	813	ASP	3.2
1	B	86	LEU	3.2
1	B	111	SER	3.2
1	B	378	ASP	3.1
1	B	139	ILE	3.1
1	A	111	SER	2.7
1	B	379	TYR	2.7
1	A	114	LYS	2.6
1	B	377	LEU	2.6
1	B	113	GLY	2.5
1	B	454	GLY	2.5
1	B	206	ASP	2.4
1	B	374	LYS	2.4
1	A	790	ILE	2.4
1	B	115	ILE	2.3
1	B	650	TRP	2.3
1	B	652	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	649	SER	2.2
1	B	88	THR	2.2
1	B	249	TRP	2.2
1	B	138	GLY	2.2
1	A	42	ASN	2.2
1	B	116	ASP	2.2
1	B	375	GLU	2.1
1	B	104	PRO	2.1
1	B	341	VAL	2.1
1	A	108	LYS	2.1
1	B	329	GLY	2.1
1	B	109	LEU	2.1
1	A	115	ILE	2.0
1	A	40	ALA	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	REL	A	1856	13/13	0.86	0.11	28,35,43,44	0
2	FLC	A	1855	13/13	0.92	0.09	27,33,45,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.