



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:27 PM GMT

PDB ID : 3ZJ7
Title : Crystal structure of strictosidine glucosidase in complex with inhibitor-1
Authors : Xia, L.; Lin, H.; Panjikar, S.; Ruppert, M.; Castiglia, A.; Rajendran, C.;
Wang, M.; Schuebel, H.; Warzecha, H.; Jaeger, V.; Stoeckigt, J.
Deposited on : 2013-01-17
Resolution : 2.50 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

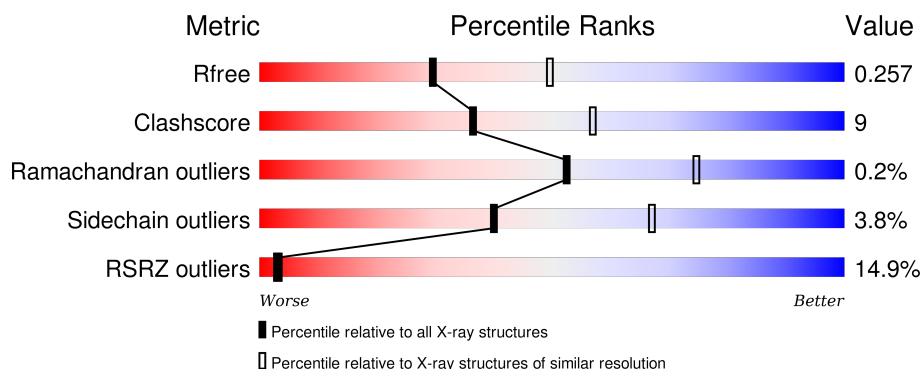
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	532	<div> <div>12%</div> <div>67%</div> <div>18%</div> <div>•</div> <div>12%</div> </div>
1	B	532	<div> <div>14%</div> <div>69%</div> <div>17%</div> <div>•</div> <div>12%</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
2	C1K	B	1509	-	-	-	X

2 Entry composition [i](#)

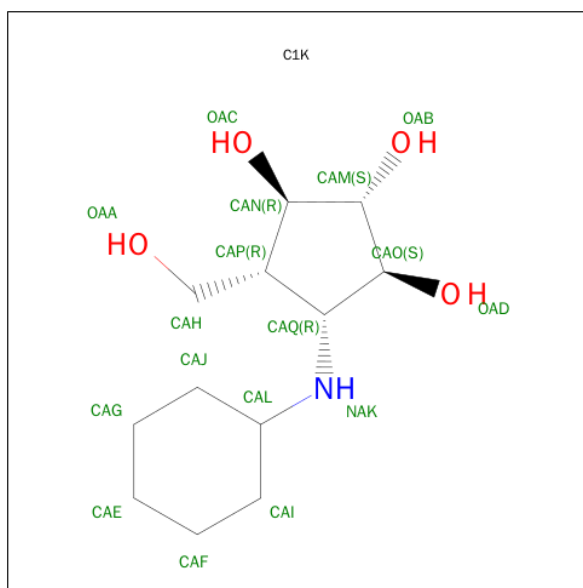
There are 3 unique types of molecules in this entry. The entry contains 7735 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 STRICTOSIDINE-O-BETA-D-GLUCOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	S	0	0	0
			3796	2444	632	705	15			
1	B	467	Total	C	N	O	S	0	0	0
			3796	2444	632	705	15			

- Molecule 2 is (1R,2S,3S,4R,5R)-4-(CYCLOHEXYLAMINO)-5-(HYDROXYMETHYL)CYCLOPENTANE-1,2,3-TRIOL (three-letter code: C1K) (formula: $C_{12}H_{23}NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			17	12	1	4		
2	B	1	Total	C	N	O	0	0
			17	12	1	4		

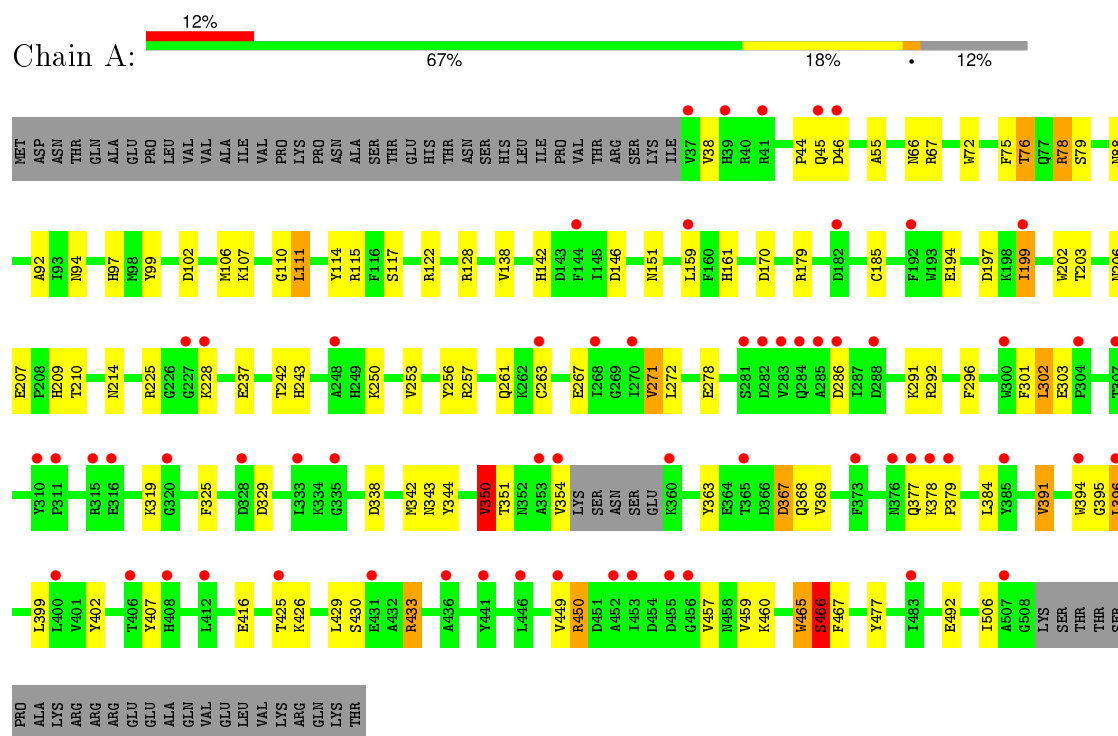
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	56	Total 56	O 56	0	0
3	B	53	Total 53	O 53	0	0

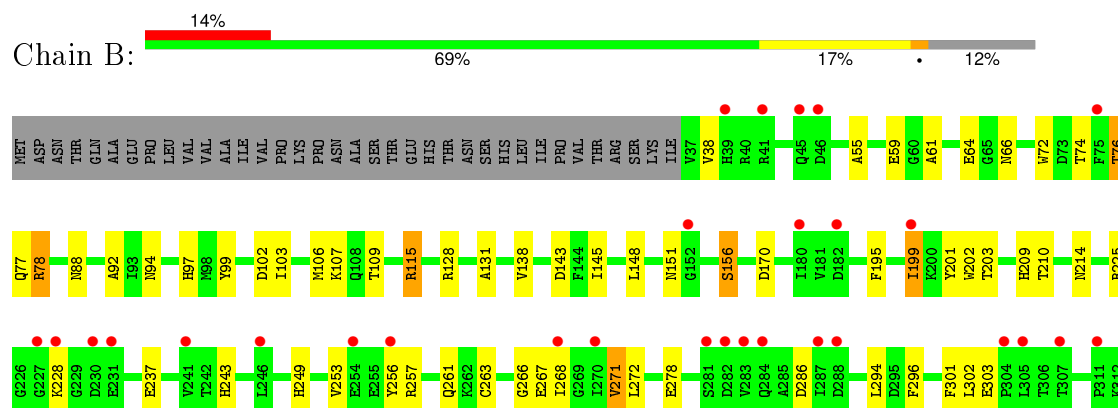
3 Residue-property plots

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: STRICTOSIDINE-O-BETA-D-GLUCOSIDASE



• Molecule 1: STRICTOSIDINE-O-BETA-D-GLUCOSIDASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	159.22Å 159.22Å 110.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.73 – 2.50 19.75 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.7 (19.73-2.50) 97.6 (19.75-2.50)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.17 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.258 , 0.276 0.265 , 0.257	Depositor DCC
R_{free} test set	599 reflections (1.25%)	DCC
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	3 of 48449 reflections (0.006%)	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	7735	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: C1K

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	1.07	6/3908 (0.2%)	0.99	7/5292 (0.1%)
1	B	1.09	2/3908 (0.1%)	0.99	11/5292 (0.2%)
All	All	1.08	8/7816 (0.1%)	0.99	18/10584 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	350	VAL	CB-CG2	-6.78	1.38	1.52
1	A	350	VAL	CB-CG1	-6.70	1.38	1.52
1	B	350	VAL	CB-CG1	-6.18	1.39	1.52
1	A	114	TYR	CD1-CE1	5.52	1.47	1.39
1	A	99	TYR	CE1-CZ	5.35	1.45	1.38
1	B	78	ARG	CZ-NH1	-5.21	1.26	1.33
1	A	492	GLU	CD-OE1	5.15	1.31	1.25
1	A	185	CYS	CB-SG	-5.13	1.73	1.81

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	78	ARG	NE-CZ-NH1	8.57	124.58	120.30
1	B	78	ARG	NE-CZ-NH1	7.97	124.28	120.30
1	A	367	ASP	C-N-CA	-6.56	105.30	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	315	ARG	NE-CZ-NH2	-6.53	117.03	120.30
1	A	115	ARG	NE-CZ-NH1	-6.33	117.13	120.30
1	B	433	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	A	433	ARG	CB-CA-C	-5.69	99.01	110.40
1	B	451	ASP	CB-CG-OD2	5.66	123.39	118.30
1	B	412	LEU	CA-CB-CG	5.61	128.20	115.30
1	A	450	ARG	NE-CZ-NH1	-5.56	117.52	120.30
1	B	450	ARG	NE-CZ-NH1	-5.45	117.57	120.30
1	A	146	ASP	CB-CG-OD1	5.42	123.18	118.30
1	B	433	ARG	CB-CA-C	-5.42	99.57	110.40
1	A	111	LEU	CB-CG-CD1	5.38	120.14	111.00
1	B	367	ASP	C-N-CA	-5.30	108.46	121.70
1	B	115	ARG	NE-CZ-NH1	-5.14	117.73	120.30
1	B	286	ASP	CB-CG-OD1	5.13	122.92	118.30
1	B	367	ASP	N-CA-C	-5.04	97.39	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	45	GLN	Peptide
1	A	465	TRP	Peptide

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	3796	0	3604	73	0
1	B	3796	0	3604	69	0
2	A	17	0	23	5	0
2	B	17	0	23	3	0
3	A	56	0	0	4	0
3	B	53	0	0	6	0
All	All	7735	0	7254	141	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 9.

All (141) 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)
2:A:1509:C1K:HAH1	2:A:1509:C1K:HAJ2	1.36	1.02
1:B:429:LEU:O	1:B:433:ARG:HG3	1.65	0.96
2:A:1509:C1K:HAH1	2:A:1509:C1K:CAJ	1.99	0.91
1:A:76:THR:HG21	1:A:88:ASN:HB2	1.54	0.87
2:B:1509:C1K:HAJ2	2:B:1509:C1K:HAH1	1.56	0.87
1:B:145:ILE:HD12	3:B:2035:HOH:O	1.75	0.85
1:B:195:PHE:HD1	3:B:2035:HOH:O	1.59	0.85
1:B:195:PHE:CD1	3:B:2035:HOH:O	2.33	0.82
1:B:76:THR:HG23	1:B:88:ASN:HB3	1.61	0.81
1:B:94:ASN:HD21	1:B:97:HIS:HD2	1.28	0.79
1:B:256:TYR:CE2	1:B:261:GLN:HB2	2.18	0.79
1:B:481:TYR:OH	3:B:2053:HOH:O	1.89	0.78
1:A:76:THR:CG2	1:A:88:ASN:HB2	2.15	0.77
1:A:76:THR:HG23	1:A:88:ASN:HB3	1.68	0.75
1:A:225:ARG:NH1	1:A:237:GLU:OE2	2.22	0.73
1:A:344:TYR:OH	1:A:395:GLY:HA3	1.88	0.73
1:A:94:ASN:HD21	1:A:97:HIS:HD2	1.36	0.72
1:A:203:THR:HG21	1:A:271:VAL:HG13	1.73	0.70
1:A:429:LEU:O	1:A:433:ARG:HG3	1.91	0.70
1:B:76:THR:HG21	1:B:88:ASN:HB2	1.72	0.69
1:B:61:ALA:HB1	1:B:64:GLU:HB2	1.74	0.69
1:A:203:THR:HG21	1:A:271:VAL:CG1	2.23	0.69
1:A:256:TYR:CE2	1:A:261:GLN:HB2	2.28	0.69
2:A:1509:C1K:HAJ2	2:A:1509:C1K:CAH	2.19	0.69
1:A:78:ARG:HD2	1:B:128:ARG:NH1	2.08	0.68
1:A:425:THR:O	1:A:426:LYS:HB2	1.94	0.68
1:A:76:THR:CG2	1:A:88:ASN:CB	2.71	0.67
1:B:266:GLY:O	1:B:267:GLU:HG2	1.95	0.67
1:B:203:THR:HG21	1:B:271:VAL:CG1	2.26	0.66
1:B:203:THR:HG21	1:B:271:VAL:HG13	1.76	0.66
1:A:72:TRP:O	1:A:76:THR:HB	1.96	0.64
1:B:94:ASN:HD21	1:B:97:HIS:CD2	2.13	0.64
1:A:76:THR:HG23	1:A:88:ASN:CB	2.27	0.63
1:B:427:ILE:HD11	1:B:432:ALA:HB2	1.80	0.63
2:B:1509:C1K:HAH1	2:B:1509:C1K:CAJ	2.27	0.63
1:B:72:TRP:O	1:B:76:THR:HB	1.99	0.62
1:B:76:THR:CG2	1:B:88:ASN:CB	2.77	0.62
1:A:465:TRP:CG	1:A:466:SER:N	2.64	0.62
1:B:76:THR:HG23	1:B:88:ASN:CB	2.29	0.61
1:A:46:ASP:OD2	1:A:460:LYS:NZ	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:VAL:O	1:A:257:ARG:HG3	2.01	0.60
1:B:243:HIS:CE1	1:B:325:PHE:CE1	2.90	0.60
1:A:384:LEU:HD11	1:A:391:VAL:HG12	1.83	0.60
1:B:76:THR:CG2	1:B:88:ASN:HB2	2.32	0.60
1:B:103:ILE:HG12	1:B:148:LEU:HD23	1.84	0.59
1:A:107:LYS:HD2	1:A:151:ASN:HD22	1.68	0.58
1:B:115:ARG:HG2	1:B:156:SER:OG	2.05	0.57
1:A:350:VAL:HG22	1:A:369:VAL:CG1	2.34	0.57
1:B:107:LYS:HD2	1:B:151:ASN:HD22	1.70	0.57
1:A:425:THR:O	1:A:426:LYS:CB	2.53	0.56
1:A:396:LEU:HD22	1:A:449:VAL:CG2	2.35	0.56
1:B:210:THR:O	1:B:214:ASN:HB2	2.05	0.56
1:A:399:LEU:HG	1:A:399:LEU:O	2.05	0.56
1:B:278:GLU:HG3	1:B:394:TRP:HH2	1.71	0.55
1:B:296:PHE:CG	1:B:367:ASP:HB3	2.41	0.55
1:A:207:GLU:OE1	2:A:1509:C1K:HAI1	2.07	0.55
1:A:44:PRO:C	1:A:46:ASP:H	2.10	0.55
1:A:75:PHE:O	1:A:79:SER:HB2	2.07	0.55
1:B:396:LEU:HD23	1:B:449:VAL:HG23	1.89	0.55
1:B:131:ALA:HB1	3:B:2033:HOH:O	2.07	0.54
1:A:303:GLU:OE1	1:A:407:TYR:HE1	1.90	0.54
1:A:350:VAL:HG22	1:A:369:VAL:HG11	1.89	0.54
1:B:425:THR:O	1:B:426:LYS:HB2	2.08	0.54
1:A:296:PHE:CG	1:A:367:ASP:HB3	2.44	0.53
1:A:242:THR:HG23	1:A:301:PHE:CE2	2.44	0.53
1:A:243:HIS:CE1	1:A:325:PHE:CE1	2.96	0.52
1:A:111:LEU:HD11	1:A:467:PHE:CE1	2.44	0.52
2:A:1509:C1K:HAH1	2:A:1509:C1K:CAL	2.29	0.51
1:A:278:GLU:HG3	1:A:394:TRP:HH2	1.73	0.51
1:B:74:THR:HG23	1:B:78:ARG:HD2	1.93	0.51
1:B:272:LEU:N	1:B:341:GLY:O	2.38	0.51
1:A:66:ASN:ND2	1:B:66:ASN:H	2.09	0.51
1:A:210:THR:O	1:A:214:ASN:HB2	2.12	0.50
1:B:249:HIS:O	1:B:253:VAL:HG23	2.12	0.49
1:A:66:ASN:HD21	1:B:66:ASN:H	1.61	0.49
1:B:366:ASP:C	1:B:367:ASP:O	2.50	0.48
1:B:92:ALA:HA	1:B:477:TYR:OH	2.13	0.48
1:B:38:VAL:HG12	3:B:2001:HOH:O	2.13	0.48
1:A:102:ASP:O	1:A:106:MET:HG3	2.14	0.48
1:B:399:LEU:O	1:B:399:LEU:HG	2.11	0.48
1:A:291:LYS:NZ	1:A:402:TYR:OH	2.37	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:LEU:O	1:A:342:MET:HA	2.13	0.48
1:A:225:ARG:HH11	1:A:237:GLU:CD	2.17	0.48
1:B:303:GLU:OE1	1:B:407:TYR:HE1	1.97	0.48
1:B:384:LEU:HD11	1:B:391:VAL:HG12	1.96	0.48
1:A:237:GLU:HB2	3:A:2043:HOH:O	2.13	0.47
1:B:225:ARG:NH1	1:B:237:GLU:OE2	2.48	0.47
1:A:250:LYS:NZ	1:A:329:ASP:OD1	2.44	0.47
2:B:1509:C1K:CAL	2:B:1509:C1K:HAH1	2.46	0.46
1:A:170:ASP:CG	1:B:170:ASP:HB3	2.35	0.46
1:A:286:ASP:OD1	1:A:351:THR:OG1	2.06	0.45
1:B:396:LEU:CD2	1:B:449:VAL:HG23	2.46	0.45
1:A:396:LEU:HD22	1:A:449:VAL:HG23	1.98	0.45
1:A:199:ILE:HD11	1:A:202:TRP:CE2	2.52	0.45
1:A:292:ARG:HE	1:A:368:GLN:H	1.63	0.45
1:B:475:LEU:O	1:B:478:ILE:HG12	2.17	0.45
1:B:156:SER:HB2	1:B:201:TYR:HB2	1.99	0.45
1:A:396:LEU:HD22	1:A:449:VAL:HG22	1.99	0.45
1:A:319:LYS:HG2	1:A:319:LYS:HZ2	1.67	0.45
1:B:102:ASP:O	1:B:106:MET:HG3	2.17	0.45
1:A:457:VAL:HG12	1:A:459:VAL:HG23	1.99	0.45
1:A:225:ARG:HD3	1:A:237:GLU:OE1	2.17	0.44
1:B:243:HIS:CE1	1:B:325:PHE:CD1	3.06	0.44
1:A:197:ASP:CG	3:A:2039:HOH:O	2.56	0.44
1:A:92:ALA:HA	1:A:477:TYR:OH	2.17	0.44
1:B:202:TRP:O	1:B:268:ILE:HA	2.18	0.44
1:B:55:ALA:O	1:B:59:GLU:HB2	2.17	0.44
1:B:199:ILE:HD11	1:B:202:TRP:CD1	2.54	0.43
1:B:209:HIS:HB2	1:B:301:PHE:HE1	1.83	0.43
1:B:256:TYR:CD2	1:B:261:GLN:HB2	2.54	0.43
1:A:67:ARG:HB2	1:A:122:ARG:HG3	1.99	0.43
1:B:76:THR:HG22	1:B:77:GLN:HG3	2.00	0.43
1:A:128:ARG:HD3	3:A:2029:HOH:O	2.19	0.42
1:B:349:TYR:CE2	1:B:380:ILE:HB	2.55	0.42
1:A:450:ARG:HH11	1:A:450:ARG:HD3	1.68	0.42
1:A:66:ASN:H	1:B:66:ASN:ND2	2.17	0.42
1:A:363:TYR:C	1:A:363:TYR:CD1	2.93	0.42
1:A:110:GLY:O	1:A:506:ILE:HG21	2.19	0.42
1:B:253:VAL:O	1:B:257:ARG:HG3	2.20	0.42
1:A:267:GLU:OE1	1:A:338:ASP:HB3	2.19	0.42
1:B:344:TYR:OH	1:B:395:GLY:HA3	2.19	0.42
1:A:199:ILE:HD11	1:A:202:TRP:CD1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:ASP:N	3:A:2039:HOH:O	2.47	0.42
1:A:161:HIS:CE1	1:A:206:ASN:ND2	2.88	0.42
1:A:209:HIS:HB2	1:A:301:PHE:HE1	1.85	0.41
1:B:397:TYR:O	1:B:398:LYS:C	2.59	0.41
1:B:296:PHE:CD1	1:B:367:ASP:HB3	2.55	0.41
1:A:66:ASN:H	1:B:66:ASN:HD21	1.67	0.41
1:A:302:LEU:HD12	1:A:302:LEU:HA	1.79	0.41
1:B:302:LEU:HA	1:B:302:LEU:HD12	1.55	0.41
1:B:396:LEU:HD21	1:B:449:VAL:CG2	2.51	0.41
1:A:343:ASN:CG	1:A:416:GLU:HB2	2.41	0.41
1:B:109:THR:O	1:B:503:LYS:HA	2.21	0.41
1:A:142:HIS:CE1	1:A:194:GLU:O	2.74	0.41
1:A:170:ASP:HB3	1:B:170:ASP:CG	2.41	0.40
1:B:440:ASP:OD2	1:B:444:LYS:HE2	2.21	0.40
1:B:425:THR:O	1:B:426:LYS:CB	2.67	0.40
1:A:170:ASP:HB3	1:B:170:ASP:HB3	2.02	0.40
1:B:99:TYR:OH	1:B:143:ASP:HB3	2.21	0.40
1:A:378:LYS:HA	1:A:379:PRO:HD3	1.99	0.40
1:A:55:ALA:HB2	1:A:117:SER:O	2.22	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	463/532 (87%)	436 (94%)	26 (6%)	1 (0%)	52	75
1	B	463/532 (87%)	433 (94%)	29 (6%)	1 (0%)	52	75
All	All	926/1064 (87%)	869 (94%)	55 (6%)	2 (0%)	52	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	466	SER
1	B	385	TYR

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	396/456 (87%)	379 (96%)	17 (4%)	35	61
1	B	396/456 (87%)	383 (97%)	13 (3%)	45	73
All	All	792/912 (87%)	762 (96%)	30 (4%)	40	67

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	VAL
1	A	76	THR
1	A	138	VAL
1	A	159	LEU
1	A	179	ARG
1	A	199	ILE
1	A	228	LYS
1	A	263	CYS
1	A	271	VAL
1	A	302	LEU
1	A	350	VAL
1	A	354	VAL
1	A	377	GLN
1	A	391	VAL
1	A	396	LEU
1	A	430	SER
1	A	466	SER
1	B	76	THR
1	B	138	VAL
1	B	156	SER
1	B	199	ILE
1	B	228	LYS

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Mol	Chain	Res	Type
1	B	263	CYS
1	B	271	VAL
1	B	294	LEU
1	B	342	MET
1	B	377	GLN
1	B	406	THR
1	B	412	LEU
1	B	430	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	GLN
1	A	57	GLN
1	A	66	ASN
1	A	77	GLN
1	A	94	ASN
1	A	97	HIS
1	A	108	GLN
1	A	151	ASN
1	A	161	HIS
1	A	206	ASN
1	A	214	ASN
1	A	264	GLN
1	A	504	ASN
1	B	66	ASN
1	B	77	GLN
1	B	94	ASN
1	B	97	HIS
1	B	108	GLN
1	B	151	ASN
1	B	214	ASN
1	B	264	GLN
1	B	504	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 ⓘ

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$
2	C1K	A	1509	-	18,18,18	1.63	5 (27%)	17,25,25	0.87	1 (5%)
2	C1K	B	1509	-	18,18,18	1.56	4 (22%)	17,25,25	1.37	2 (11%)

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	C1K	A	1509	-	-	0/6/34/34	0/2/2/2
2	C1K	B	1509	-	-	0/6/34/34	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1509	C1K	CAP-CAN	-2.12	1.50	1.53
2	A	1509	C1K	CAL-NAK	2.01	1.51	1.48
2	A	1509	C1K	OAD-CAO	2.15	1.48	1.43
2	A	1509	C1K	CAE-CAF	2.17	1.60	1.51
2	B	1509	C1K	OAD-CAO	2.24	1.48	1.43
2	A	1509	C1K	CAO-CAQ	2.82	1.59	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1509	C1K	CAO-CAQ	2.96	1.59	1.53
2	A	1509	C1K	CAG-CAJ	2.98	1.61	1.53
2	B	1509	C1K	CAG-CAJ	3.31	1.62	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1509	C1K	CAJ-CAL-CAI	-3.57	104.74	110.82
2	B	1509	C1K	OAA-CAH-CAP	-2.82	104.41	111.26
2	A	1509	C1K	CAF-CAI-CAL	2.12	114.42	111.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1509	C1K	5	0
2	B	1509	C1K	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	467/532 (87%)	0.99	62 (13%) 4 4	35, 39, 45, 57	0
1	B	467/532 (87%)	1.08	77 (16%) 2 2	35, 39, 45, 55	0
All	All	934/1064 (87%)	1.03	139 (14%) 3 3	35, 39, 45, 57	0

All (139) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	354	VAL	6.8
1	A	283	VAL	5.8
1	A	408	HIS	5.3
1	B	408	HIS	5.2
1	B	376	ASN	5.1
1	B	377	GLN	4.9
1	A	45	GLN	4.9
1	B	328	ASP	4.8
1	B	406	THR	4.7
1	A	456	GLY	4.5
1	B	456	GLY	4.5
1	A	39	HIS	4.4
1	B	39	HIS	4.4
1	A	455	ASP	4.3
1	B	326	SER	4.1
1	B	283	VAL	4.1
1	B	304	PRO	4.0
1	A	354	VAL	4.0
1	B	228	LYS	3.9
1	A	353	ALA	3.9
1	A	379	PRO	3.8
1	A	406	THR	3.7
1	B	387	GLY	3.7
1	B	455	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	376	ASN	3.5
1	A	360	LYS	3.5
1	A	227	GLY	3.4
1	B	385	TYR	3.4
1	B	281	SER	3.4
1	B	333	LEU	3.4
1	A	284	GLN	3.4
1	B	311	PRO	3.4
1	B	287	ILE	3.3
1	B	199	ILE	3.3
1	A	436	ALA	3.3
1	A	453	ILE	3.3
1	B	316	GLU	3.2
1	B	180	ILE	3.2
1	B	327	ALA	3.1
1	B	284	GLN	3.1
1	B	254	GLU	3.1
1	B	330	SER	3.1
1	B	313	SER	3.1
1	A	228	LYS	3.1
1	A	311	PRO	3.1
1	A	263	CYS	3.1
1	A	365	THR	3.1
1	A	378	LYS	3.0
1	B	45	GLN	3.0
1	A	377	GLN	3.0
1	B	396	LEU	3.0
1	B	383	ALA	3.0
1	A	316	GLU	3.0
1	B	400	LEU	2.9
1	B	374	GLU	2.9
1	A	449	VAL	2.9
1	B	46	ASP	2.9
1	A	333	LEU	2.8
1	A	46	ASP	2.8
1	B	379	PRO	2.8
1	B	246	LEU	2.8
1	B	449	VAL	2.8
1	B	325	PHE	2.8
1	B	394	TRP	2.8
1	A	315	ARG	2.8
1	B	378	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	307	THR	2.8
1	A	385	TYR	2.7
1	A	400	LEU	2.7
1	B	502	TYR	2.7
1	B	231	GLU	2.7
1	B	270	ILE	2.7
1	A	394	TRP	2.7
1	A	431	GLU	2.6
1	B	434	ARG	2.6
1	B	403	THR	2.6
1	B	305	LEU	2.6
1	B	414	VAL	2.6
1	B	402	TYR	2.6
1	A	288	ASP	2.6
1	A	304	PRO	2.6
1	B	227	GLY	2.5
1	A	268	ILE	2.5
1	B	41	ARG	2.5
1	A	441	TYR	2.5
1	B	282	ASP	2.5
1	B	152	GLY	2.5
1	B	353	ALA	2.5
1	B	329	ASP	2.5
1	A	452	ALA	2.4
1	A	320	GLY	2.4
1	B	431	GLU	2.4
1	B	441	TYR	2.4
1	A	41	ARG	2.4
1	B	182	ASP	2.4
1	A	483	ILE	2.4
1	A	396	LEU	2.3
1	A	425	THR	2.3
1	B	331	GLU	2.3
1	B	392	VAL	2.3
1	B	368	GLN	2.3
1	B	334	LYS	2.3
1	A	182	ASP	2.3
1	B	484	ILE	2.2
1	A	192	PHE	2.2
1	A	507	ALA	2.2
1	A	335	GLY	2.2
1	A	248	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	436	ALA	2.2
1	A	412	LEU	2.2
1	A	328	ASP	2.2
1	B	288	ASP	2.2
1	A	37	VAL	2.2
1	A	282	ASP	2.2
1	A	285	ALA	2.2
1	B	256	TYR	2.2
1	A	270	ILE	2.2
1	A	286	ASP	2.2
1	B	230	ASP	2.1
1	B	307	THR	2.1
1	B	453	ILE	2.1
1	A	446	LEU	2.1
1	B	241	VAL	2.1
1	B	382	HIS	2.1
1	B	360	LYS	2.1
1	B	454	ASP	2.1
1	A	199	ILE	2.0
1	B	268	ILE	2.0
1	A	281	SER	2.0
1	B	320	GLY	2.0
1	B	500	ILE	2.0
1	A	159	LEU	2.0
1	A	310	TYR	2.0
1	A	144	PHE	2.0
1	B	425	THR	2.0
1	B	319	LYS	2.0
1	A	300	TRP	2.0
1	A	373	PHE	2.0
1	B	75	PHE	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 ⓘ

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
2	C1K	B	1509	17/17	0.83	0.25	3.00	45,56,71,73	0
2	C1K	A	1509	17/17	0.83	0.23	1.35	50,57,67,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.