



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:35 AM UTC

PDB ID : 1PX8 / pdb_00001px8
Title : Crystal structure of beta-D-xylosidase from Thermoanaerobacterium saccharolyticum, a family 39 glycoside hydrolase
Authors : Yang, J.K.; Yoon, H.J.; Ahn, H.J.; Il Lee, B.; Pedelacq, J.D.; Liong, E.C.; Berendzen, J.; Laivenieks, M.; Vieille, C.; Zeikus, G.J.; Vocadlo, D.J.; Withers, S.G.; Suh, S.W.
Deposited on : 2003-07-03
Resolution : 2.40 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

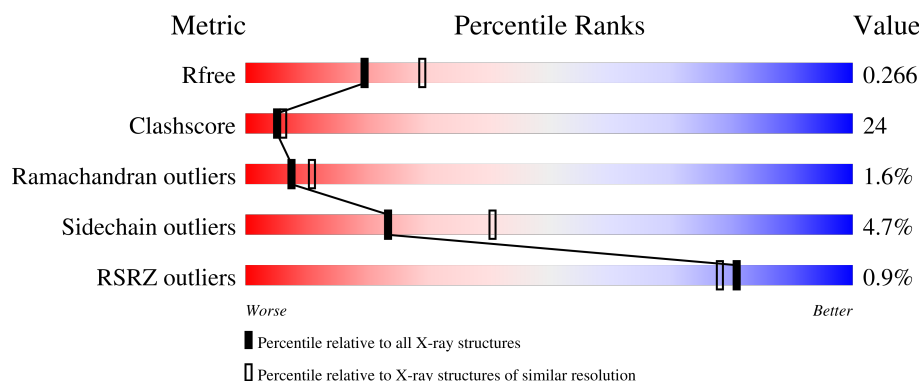
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	500	% 57% 39% .
1	B	500	% 56% 40% .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8655 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.

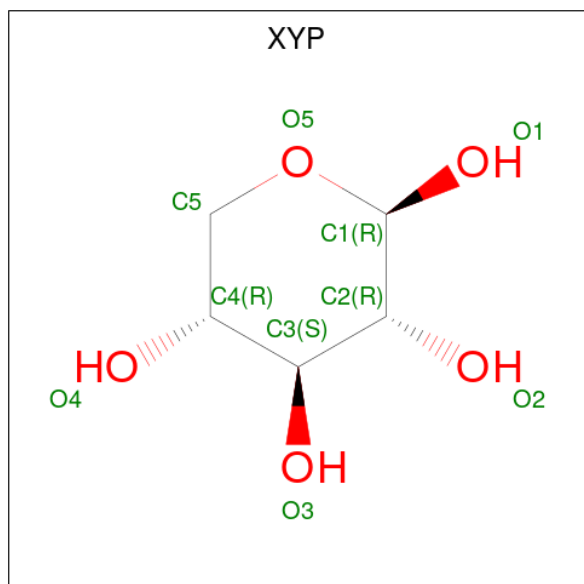
- Molecule 1 is a protein called Beta-xylosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	500	Total	C	N	O	S	0	0	0
			4154	2691	676	772	15			
1	B	500	Total	C	N	O	S	0	0	0
			4154	2691	676	772	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	230	TYR	THR	SEE REMARK 999	UNP P36906
B	230	TYR	THR	SEE REMARK 999	UNP P36906

- Molecule 2 is beta-D-xylopyranose (CCD ID: XYP) (formula: C₅H₁₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	5	5		

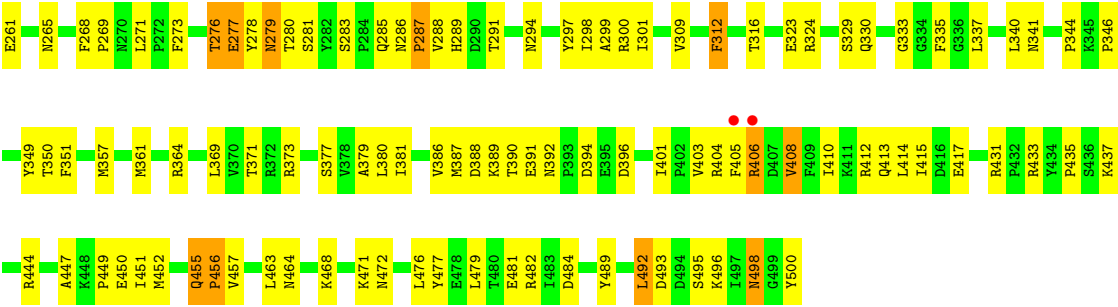
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			10	5	5		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	150	Total	O	0	0
			150	150		
3	B	177	Total	O	0	0
			177	177		



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.72Å 92.72Å 241.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.91 – 2.40 19.91 – 2.40	Depositor EDS
% Data completeness (in resolution range)	84.7 (19.91-2.40) 88.8 (19.91-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.41Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.224 , 0.271 0.222 , 0.266	Depositor DCC
R_{free} test set	3747 reflections (10.01%)	wwPDB-VP
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 33.7	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	0.93	EDS
Total number of atoms	8655	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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: XYP

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	0.42	0/4278	0.92	15/5799 (0.3%)
1	B	0.43	0/4278	0.92	15/5799 (0.3%)
All	All	0.43	0/8556	0.92	30/11598 (0.3%)

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	408	VAL	N-CA-C	6.89	117.82	108.17
1	B	350	THR	N-CA-C	-6.83	103.76	111.14
1	B	97	PHE	N-CA-C	-6.78	100.15	109.71
1	A	238	THR	CA-C-N	-6.75	112.63	120.12
1	A	238	THR	C-N-CA	-6.75	112.63	120.12
1	A	118	GLU	N-CA-C	6.68	119.37	111.02
1	A	350	THR	N-CA-C	-6.57	104.05	111.14
1	B	59	ASP	N-CA-C	6.49	120.46	112.54
1	B	238	THR	CA-C-N	-6.47	112.94	120.12
1	B	238	THR	C-N-CA	-6.47	112.94	120.12
1	A	408	VAL	N-CA-C	6.46	117.22	108.17
1	A	59	ASP	N-CA-C	6.42	120.37	112.54
1	B	238	THR	N-CA-C	-6.41	100.76	110.50
1	B	337	LEU	N-CA-C	-6.38	104.97	112.89
1	A	238	THR	N-CA-C	-6.33	100.88	110.50
1	A	337	LEU	N-CA-C	-6.20	105.20	112.89
1	B	118	GLU	N-CA-C	6.07	118.61	111.02
1	A	55	GLY	N-CA-C	5.74	123.27	115.30
1	B	64	TYR	N-CA-C	5.67	117.54	108.41
1	A	64	TYR	N-CA-C	5.66	117.53	108.41
1	B	55	GLY	N-CA-C	5.66	122.88	115.36
1	B	241	LEU	N-CA-C	5.24	115.45	108.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	LYS	N-CA-C	-5.20	106.91	113.20
1	B	81	TYR	N-CA-C	5.19	117.73	111.40
1	A	98	VAL	N-CA-C	5.17	116.91	109.51
1	A	241	LEU	N-CA-C	5.15	115.33	108.38
1	B	125	LYS	N-CA-C	-5.11	107.02	113.20
1	A	10	SER	N-CA-C	5.08	117.00	108.73
1	B	71	ASP	N-CA-C	-5.06	107.16	113.38
1	A	81	TYR	N-CA-C	5.06	117.57	111.40

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	4154	0	3993	206	0
1	B	4154	0	3993	198	0
2	A	10	0	0	1	0
2	B	10	0	0	1	0
3	A	150	0	0	12	0
3	B	177	0	0	14	0
All	All	8655	0	7986	399	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 24.

All (399) 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:279:ASN:HD22	1:A:280:THR:H	1.11	0.99
1:B:279:ASN:HD22	1:B:280:THR:H	1.10	0.92
1:A:403:VAL:HG12	1:A:405:PHE:H	1.39	0.86
1:B:268:PHE:HA	3:B:1195:HOH:O	1.73	0.86
1:A:202:GLY:HA2	1:A:227:ARG:HH21	1.40	0.86
1:B:403:VAL:HG12	1:B:405:PHE:H	1.38	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:468:LYS:HD2	1:B:468:LYS:N	1.93	0.84
1:A:250:GLU:HG2	1:A:300:ARG:HH12	1.42	0.84
1:B:202:GLY:HA2	1:B:227:ARG:HH21	1.41	0.83
1:B:250:GLU:HG2	1:B:300:ARG:HH12	1.44	0.83
1:A:238:THR:HG22	1:A:240:HIS:H	1.43	0.82
1:A:237:TYR:HA	1:A:242:ILE:HG23	1.62	0.82
1:B:238:THR:HG22	1:B:240:HIS:H	1.42	0.81
1:A:279:ASN:ND2	1:A:280:THR:H	1.77	0.81
1:B:286:ASN:OD1	1:B:288:VAL:HG23	1.81	0.81
1:A:286:ASN:OD1	1:A:288:VAL:HG23	1.81	0.81
1:B:279:ASN:ND2	1:B:280:THR:H	1.79	0.81
1:A:468:LYS:HD2	1:A:468:LYS:N	1.95	0.80
1:A:413:GLN:HG2	1:A:451:ILE:HG22	1.63	0.79
1:B:413:GLN:HG2	1:B:451:ILE:HG22	1.64	0.79
1:B:237:TYR:HA	1:B:242:ILE:HG23	1.65	0.78
1:A:279:ASN:HD22	1:A:280:THR:N	1.81	0.78
1:A:328:ARG:HD2	3:A:1114:HOH:O	1.84	0.77
1:A:292:PRO:HB3	3:A:1278:HOH:O	1.83	0.77
1:B:498:ASN:HD22	1:B:498:ASN:H	1.31	0.77
1:B:451:ILE:HD12	1:B:451:ILE:O	1.84	0.76
1:A:455:GLN:HG3	1:A:482:ARG:NE	2.00	0.76
1:B:279:ASN:HD22	1:B:280:THR:N	1.83	0.76
1:A:498:ASN:H	1:A:498:ASN:HD22	1.31	0.75
1:A:435:PRO:O	1:B:144:ARG:NH2	2.20	0.75
1:B:455:GLN:HG3	1:B:482:ARG:NE	2.02	0.75
1:B:12:LYS:HE2	1:B:361:MET:HE2	1.68	0.75
1:B:103:MET:HE1	1:B:107:LEU:HB3	1.69	0.74
1:A:455:GLN:HG3	1:A:482:ARG:CD	2.18	0.74
1:A:69:VAL:HG23	1:A:72:GLU:HB3	1.69	0.73
1:A:19:ARG:HD2	3:A:1035:HOH:O	1.89	0.73
1:B:69:VAL:HG23	1:B:72:GLU:HB3	1.69	0.73
1:A:451:ILE:HD12	1:A:451:ILE:O	1.87	0.72
1:B:103:MET:HG3	1:B:122:THR:O	1.89	0.72
1:B:412:ARG:NH1	1:B:452:MET:HE2	2.05	0.72
1:B:455:GLN:HG3	1:B:482:ARG:CD	2.19	0.71
1:A:103:MET:HG3	1:A:122:THR:O	1.90	0.71
1:A:252:MET:SD	1:A:301:ILE:HD13	2.31	0.71
1:B:412:ARG:HH11	1:B:452:MET:HE2	1.56	0.71
1:A:103:MET:HE1	1:A:107:LEU:HB3	1.70	0.71
1:A:12:LYS:HE2	1:A:361:MET:HE2	1.73	0.70
1:A:388:ASP:CG	1:A:389:LYS:H	1.99	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:ARG:NH1	1:A:452:MET:HE2	2.07	0.70
1:A:390:THR:HG22	1:A:392:ASN:H	1.57	0.69
1:B:390:THR:HG22	1:B:392:ASN:H	1.56	0.69
1:B:138:LEU:O	1:B:142:ILE:HG12	1.93	0.68
1:B:388:ASP:CG	1:B:389:LYS:H	2.02	0.68
1:B:277:GLU:OE1	2:B:701:XYP:C1	2.41	0.68
1:A:277:GLU:OE1	2:A:601:XYP:C1	2.42	0.68
1:A:412:ARG:HH11	1:A:452:MET:HE2	1.59	0.68
1:A:227:ARG:HG2	1:A:228:HIS:N	2.09	0.67
1:B:330:GLN:HE22	1:B:341:ASN:HD22	1.42	0.67
1:B:498:ASN:HD22	1:B:498:ASN:N	1.92	0.67
1:A:13:LYS:HE2	3:A:1300:HOH:O	1.95	0.67
1:A:498:ASN:HD22	1:A:498:ASN:N	1.91	0.67
1:B:227:ARG:HG2	1:B:228:HIS:N	2.10	0.66
1:B:431:ARG:NH1	3:B:1045:HOH:O	2.27	0.66
1:B:252:MET:SD	1:B:301:ILE:HD13	2.35	0.66
1:B:202:GLY:CA	1:B:227:ARG:HH21	2.07	0.66
1:A:121:VAL:HG13	1:A:166:PHE:C	2.21	0.66
1:A:138:LEU:HD11	1:A:186:ILE:HG12	1.78	0.65
1:A:238:THR:HG23	1:A:239:PRO:HD2	1.77	0.65
1:B:238:THR:HG23	1:B:239:PRO:HD2	1.77	0.65
1:A:202:GLY:CA	1:A:227:ARG:HH21	2.07	0.65
1:A:330:GLN:HE22	1:A:341:ASN:HD22	1.43	0.65
1:B:109:SER:HA	1:B:125:LYS:HE2	1.77	0.65
1:A:109:SER:HA	1:A:125:LYS:HE2	1.79	0.65
1:A:202:GLY:HA2	1:A:227:ARG:NH2	2.12	0.64
1:A:493:ASP:OD2	1:A:496:LYS:HG3	1.97	0.64
1:B:121:VAL:HG13	1:B:166:PHE:C	2.21	0.64
1:B:138:LEU:HD11	1:B:186:ILE:HG12	1.79	0.64
1:A:227:ARG:HH11	1:A:259:VAL:HG21	1.61	0.64
1:B:471:LYS:HG2	1:B:472:ASN:ND2	2.13	0.63
1:A:158:TRP:CD1	1:A:159:ASN:H	2.16	0.63
1:B:227:ARG:HH11	1:B:259:VAL:HG21	1.62	0.63
1:B:198:PRO:HG2	1:B:200:ILE:HG23	1.81	0.63
1:A:330:GLN:NE2	3:A:1190:HOH:O	2.32	0.62
1:B:22:VAL:HG22	1:B:48:PHE:CG	2.34	0.62
1:B:172:GLU:HA	1:B:207:TRP:CH2	2.34	0.62
1:A:404:ARG:HG3	1:A:404:ARG:HH11	1.65	0.62
1:B:433:ARG:HD2	3:B:1147:HOH:O	2.00	0.62
1:A:138:LEU:O	1:A:142:ILE:HG12	1.99	0.62
1:A:22:VAL:HG22	1:A:48:PHE:CG	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:471:LYS:HG2	1:A:472:ASN:ND2	2.14	0.62
1:B:386:VAL:HG21	1:B:471:LYS:HG3	1.82	0.61
1:B:495:SER:HA	1:B:500:TYR:OXT	2.00	0.61
1:B:404:ARG:HG3	1:B:404:ARG:HH11	1.64	0.61
1:B:406:ARG:O	1:B:457:VAL:HG13	1.99	0.61
1:A:386:VAL:HG21	1:A:471:LYS:HG3	1.83	0.61
1:B:493:ASP:OD2	1:B:496:LYS:HG3	2.00	0.61
1:A:406:ARG:O	1:A:457:VAL:HG13	2.00	0.61
1:B:202:GLY:HA2	1:B:227:ARG:NH2	2.13	0.61
1:A:121:VAL:O	1:A:121:VAL:CG1	2.49	0.61
1:B:158:TRP:CD1	1:B:159:ASN:H	2.19	0.61
1:B:121:VAL:HG12	1:B:121:VAL:O	2.01	0.60
1:A:121:VAL:O	1:A:121:VAL:HG12	2.00	0.60
1:A:388:ASP:CG	1:A:389:LYS:N	2.60	0.60
1:A:172:GLU:HA	1:A:207:TRP:CH2	2.37	0.60
1:B:79:PHE:HA	1:B:82:ILE:HD11	1.83	0.60
1:A:198:PRO:HG2	1:A:200:ILE:HG23	1.83	0.60
1:B:103:MET:HE1	1:B:107:LEU:CB	2.32	0.60
1:B:121:VAL:O	1:B:121:VAL:CG1	2.50	0.60
1:A:240:HIS:CE1	1:B:67:ASP:OD1	2.55	0.59
1:A:495:SER:HA	1:A:500:TYR:OXT	2.01	0.59
1:A:79:PHE:HA	1:A:82:ILE:HD11	1.85	0.59
1:A:214:PHE:CE1	1:A:218:GLU:HG3	2.38	0.59
1:B:214:PHE:CE1	1:B:218:GLU:HG3	2.38	0.59
1:A:103:MET:HE1	1:A:107:LEU:CB	2.32	0.58
1:B:380:LEU:HD23	1:B:380:LEU:C	2.28	0.58
1:A:238:THR:HG22	1:A:240:HIS:N	2.17	0.58
1:A:380:LEU:C	1:A:380:LEU:HD23	2.29	0.57
1:A:414:LEU:HD22	1:A:415:ILE:H	1.69	0.57
1:B:414:LEU:HD22	1:B:415:ILE:H	1.68	0.57
1:B:121:VAL:HG13	1:B:166:PHE:O	2.05	0.57
1:A:158:TRP:HZ3	3:A:1017:HOH:O	1.88	0.57
1:A:455:GLN:HG3	1:A:482:ARG:HD2	1.84	0.56
1:B:388:ASP:CG	1:B:389:LYS:N	2.62	0.56
1:B:455:GLN:HG3	1:B:482:ARG:HD2	1.86	0.56
1:B:126:ASP:OD1	1:B:128:GLU:HB2	2.04	0.56
1:B:269:PRO:HD2	3:B:1195:HOH:O	2.05	0.56
1:B:106:LYS:HD3	3:B:1268:HOH:O	2.06	0.56
1:A:126:ASP:OD1	1:A:128:GLU:HB2	2.05	0.56
1:A:396:ASP:OD1	1:A:468:LYS:HG3	2.06	0.56
1:A:110:GLY:HA3	1:A:122:THR:HG21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:238:THR:HG22	1:B:240:HIS:N	2.17	0.55
1:A:121:VAL:HG13	1:A:166:PHE:O	2.06	0.55
1:B:103:MET:O	1:B:120:ASN:HB3	2.07	0.55
1:A:403:VAL:HA	3:A:1217:HOH:O	2.06	0.55
1:B:387:MET:HE1	3:B:1108:HOH:O	2.07	0.55
1:A:139:HIS:CE1	1:A:189:VAL:HG13	2.43	0.54
1:A:234:GLN:HE21	1:A:234:GLN:HA	1.72	0.54
1:A:227:ARG:HH11	1:A:259:VAL:CG2	2.20	0.54
1:B:156:GLU:OE1	1:B:226:SER:OG	2.24	0.54
1:B:406:ARG:HD3	3:B:1203:HOH:O	2.08	0.54
1:B:396:ASP:OD1	1:B:468:LYS:HG3	2.06	0.54
1:A:103:MET:O	1:A:120:ASN:HB3	2.08	0.54
1:A:285:GLN:OE1	1:A:324:ARG:HD3	2.08	0.54
1:B:50:TYR:HA	1:B:95:ARG:O	2.08	0.54
1:A:373:ARG:HD3	1:A:377:SER:OG	2.08	0.53
1:A:242:ILE:HD11	1:A:283:SER:OG	2.09	0.53
1:B:110:GLY:HA3	1:B:122:THR:HG21	1.89	0.53
1:B:234:GLN:HA	1:B:234:GLN:HE21	1.73	0.53
1:A:87:ASP:OD2	1:A:144:ARG:NH1	2.41	0.53
1:B:482:ARG:NH1	1:B:484:ASP:HB2	2.24	0.53
1:B:414:LEU:HD22	1:B:415:ILE:N	2.23	0.53
1:A:144:ARG:NH2	1:B:435:PRO:O	2.42	0.53
1:B:227:ARG:HH11	1:B:259:VAL:CG2	2.22	0.53
1:A:227:ARG:HG2	1:A:228:HIS:H	1.74	0.52
1:A:482:ARG:NH1	1:A:484:ASP:HB2	2.24	0.52
1:A:238:THR:C	1:A:240:HIS:H	2.17	0.52
1:A:410:ILE:HG12	1:A:479:LEU:HD22	1.91	0.52
1:B:242:ILE:HD11	1:B:283:SER:OG	2.09	0.52
1:B:346:PRO:HB3	3:B:1078:HOH:O	2.09	0.52
1:B:410:ILE:HG12	1:B:479:LEU:HD22	1.90	0.52
1:A:161:PRO:HA	1:A:167:TRP:HB2	1.92	0.52
1:A:165:GLU:OE1	1:A:165:GLU:N	2.42	0.52
1:B:403:VAL:HG13	1:B:405:PHE:CD2	2.45	0.51
1:B:19:ARG:O	1:B:48:PHE:HA	2.10	0.51
1:B:68:VAL:HG23	1:B:68:VAL:O	2.09	0.51
1:B:87:ASP:OD2	1:B:144:ARG:NH1	2.44	0.51
1:A:414:LEU:HD22	1:A:415:ILE:N	2.25	0.51
1:A:386:VAL:HB	3:A:1160:HOH:O	2.11	0.51
1:A:403:VAL:HG13	1:A:405:PHE:CD2	2.46	0.51
1:B:361:MET:HE3	1:B:364:ARG:HB3	1.93	0.51
1:B:238:THR:C	1:B:240:HIS:H	2.19	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:161:PRO:HA	1:B:167:TRP:HB2	1.93	0.50
1:A:245:GLU:C	1:A:246:ILE:HD12	2.36	0.50
1:A:361:MET:HE3	1:A:364:ARG:HB3	1.93	0.50
1:B:285:GLN:OE1	1:B:324:ARG:HD3	2.11	0.50
1:A:50:TYR:HA	1:A:95:ARG:O	2.12	0.50
1:B:11:ASP:OD2	1:B:12:LYS:HG3	2.12	0.49
1:A:241:LEU:HD13	1:A:243:TYR:CE1	2.47	0.49
1:A:268:PHE:HB3	1:A:271:LEU:HG	1.93	0.49
1:B:241:LEU:HD13	1:B:243:TYR:CE1	2.47	0.49
1:B:168:LYS:HE3	3:B:1189:HOH:O	2.11	0.49
1:B:386:VAL:HG12	1:B:388:ASP:O	2.13	0.49
1:A:68:VAL:O	1:A:68:VAL:HG23	2.10	0.49
1:B:40:LYS:O	1:B:44:GLU:HG3	2.13	0.49
1:B:227:ARG:HG2	1:B:228:HIS:H	1.76	0.49
1:A:278:TYR:O	1:A:279:ASN:HB2	2.11	0.49
1:A:361:MET:HE3	1:A:364:ARG:CB	2.42	0.49
1:B:373:ARG:HD3	1:B:377:SER:OG	2.12	0.49
1:A:433:ARG:HD2	3:B:1257:HOH:O	2.12	0.49
1:A:463:LEU:HD23	1:A:464:ASN:N	2.28	0.49
1:B:50:TYR:CD2	1:B:95:ARG:HB2	2.47	0.49
1:B:357:MET:HE2	1:B:357:MET:HA	1.93	0.49
1:A:288:VAL:O	1:A:294:ASN:HB2	2.13	0.49
1:B:157:ILE:HD12	1:B:182:THR:HG21	1.94	0.49
1:B:361:MET:HE3	1:B:364:ARG:CB	2.43	0.49
1:A:123:PRO:HB3	1:A:167:TRP:CH2	2.48	0.49
1:B:167:TRP:HA	1:B:167:TRP:CE3	2.47	0.49
1:B:463:LEU:HD23	1:B:464:ASN:N	2.27	0.49
1:A:167:TRP:HA	1:A:167:TRP:CE3	2.46	0.49
1:B:229:ALA:HB1	3:B:1106:HOH:O	2.12	0.49
1:B:245:GLU:C	1:B:246:ILE:HD12	2.38	0.49
1:A:11:ASP:OD2	1:A:12:LYS:HG3	2.12	0.48
1:B:28:GLY:HA3	1:B:60:ASP:OD2	2.13	0.48
1:B:268:PHE:HB3	1:B:271:LEU:HG	1.93	0.48
1:B:468:LYS:HD2	1:B:468:LYS:H	1.76	0.48
1:A:297:TYR:HD2	1:A:298:ILE:HD12	1.79	0.48
1:B:297:TYR:HD2	1:B:298:ILE:HD12	1.77	0.48
1:B:340:LEU:O	1:B:341:ASN:HB2	2.14	0.48
1:B:63:ILE:HD11	1:B:82:ILE:HG12	1.96	0.48
1:A:157:ILE:HD12	1:A:182:THR:HG21	1.96	0.48
1:A:312:PHE:CD1	1:A:312:PHE:N	2.82	0.48
1:B:26:ARG:HD3	1:B:117:TRP:CE2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:206:TYR:HB3	3:B:1223:HOH:O	2.14	0.48
1:B:103:MET:HE2	1:B:108:ALA:HA	1.95	0.48
1:B:115:PHE:CG	1:B:323:GLU:HG2	2.49	0.48
1:B:139:HIS:CE1	1:B:189:VAL:HG13	2.49	0.48
1:A:115:PHE:CG	1:A:323:GLU:HG2	2.49	0.47
1:B:463:LEU:HD23	1:B:463:LEU:C	2.39	0.47
1:A:276:THR:O	1:A:277:GLU:HB2	2.14	0.47
1:A:50:TYR:CD2	1:A:95:ARG:HB2	2.49	0.47
1:B:403:VAL:HG12	1:B:405:PHE:N	2.20	0.47
1:A:19:ARG:O	1:A:48:PHE:HA	2.14	0.47
1:A:79:PHE:HD2	1:A:82:ILE:HD11	1.79	0.47
1:A:386:VAL:HG12	1:A:388:ASP:O	2.14	0.47
1:A:1:MET:HB3	1:A:396:ASP:HB2	1.96	0.47
1:A:103:MET:HE2	1:A:108:ALA:HA	1.96	0.47
1:A:171:ASP:HB3	1:A:174:GLU:HB2	1.97	0.47
1:B:69:VAL:CG2	1:B:72:GLU:HB3	2.43	0.47
1:A:89:PHE:O	1:A:94:ILE:HG22	2.15	0.47
1:A:463:LEU:HD23	1:A:463:LEU:C	2.40	0.47
1:B:288:VAL:O	1:B:294:ASN:HB2	2.14	0.47
1:B:165:GLU:N	1:B:165:GLU:OE1	2.43	0.47
1:B:215:CYS:SG	1:B:222:VAL:CG2	3.03	0.47
1:A:289:HIS:HD2	1:A:333:GLY:O	1.97	0.46
1:A:401:ILE:HD12	1:A:401:ILE:N	2.30	0.46
1:B:30:ALA:HA	1:B:35:TYR:CD2	2.50	0.46
1:B:89:PHE:O	1:B:94:ILE:HG22	2.14	0.46
1:B:312:PHE:CD1	1:B:312:PHE:N	2.82	0.46
1:A:142:ILE:HD13	1:A:150:VAL:HG21	1.97	0.46
1:A:404:ARG:HG3	1:A:404:ARG:NH1	2.30	0.46
1:B:121:VAL:HG21	1:B:165:GLU:O	2.15	0.46
1:B:380:LEU:HD23	1:B:381:ILE:N	2.31	0.46
1:A:158:TRP:CG	1:A:159:ASN:H	2.33	0.46
1:B:123:PRO:HB3	1:B:167:TRP:CH2	2.49	0.46
1:A:26:ARG:NH1	1:A:60:ASP:OD2	2.48	0.46
1:A:28:GLY:HA3	1:A:60:ASP:OD2	2.15	0.46
1:B:142:ILE:HD13	1:B:150:VAL:HG21	1.98	0.46
1:A:380:LEU:HD23	1:A:381:ILE:N	2.30	0.46
1:B:1:MET:HB3	1:B:396:ASP:HB2	1.98	0.46
1:B:198:PRO:CG	1:B:200:ILE:HG23	2.45	0.46
1:B:227:ARG:NH2	1:B:255:GLU:OE1	2.49	0.46
1:A:30:ALA:HA	1:A:35:TYR:CD2	2.51	0.45
1:A:159:ASN:O	1:A:160:GLU:C	2.58	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:159:ASN:O	1:B:160:GLU:C	2.59	0.45
1:A:30:ALA:HA	1:A:35:TYR:CG	2.51	0.45
1:A:33:LYS:HE2	3:A:1273:HOH:O	2.15	0.45
1:A:83:ASP:OD1	1:A:140:HIS:HE1	2.00	0.45
1:A:238:THR:C	1:A:240:HIS:N	2.72	0.45
1:A:261:GLU:O	1:A:265:ASN:ND2	2.50	0.45
1:B:412:ARG:HD3	1:B:452:MET:HE2	1.97	0.45
1:A:482:ARG:HH12	1:A:484:ASP:HB2	1.82	0.45
1:B:158:TRP:CG	1:B:159:ASN:H	2.35	0.45
1:A:26:ARG:HD3	1:A:117:TRP:CE2	2.51	0.45
1:A:110:GLY:CA	1:A:122:THR:HG21	2.47	0.45
1:A:121:VAL:HG21	1:A:165:GLU:O	2.16	0.45
1:B:79:PHE:HD2	1:B:82:ILE:HD11	1.81	0.45
1:B:341:ASN:O	1:B:444:ARG:NH2	2.45	0.45
1:A:63:ILE:HD11	1:A:82:ILE:HG12	1.99	0.45
1:A:156:GLU:OE1	1:A:226:SER:OG	2.29	0.45
1:B:248:PRO:HG2	1:B:251:TYR:CD1	2.52	0.45
1:B:278:TYR:O	1:B:279:ASN:HB2	2.16	0.45
1:B:289:HIS:HD2	1:B:333:GLY:O	1.99	0.45
1:B:414:LEU:C	1:B:414:LEU:HD13	2.41	0.45
1:A:22:VAL:CG2	1:A:48:PHE:CG	3.00	0.45
1:B:408:VAL:O	1:B:456:PRO:HD2	2.17	0.45
1:A:204:ALA:O	1:A:207:TRP:HB2	2.17	0.45
1:A:489:TYR:HB2	1:A:492:LEU:HB2	1.99	0.45
1:B:22:VAL:CG2	1:B:48:PHE:CG	3.00	0.45
1:A:287:PRO:O	1:A:291:THR:HG23	2.16	0.45
1:A:410:ILE:HD11	1:A:456:PRO:HG3	1.99	0.45
1:B:171:ASP:HB3	1:B:174:GLU:HB2	1.99	0.45
1:B:346:PRO:HG2	3:B:1029:HOH:O	2.17	0.45
1:B:455:GLN:HE21	1:B:455:GLN:HB3	1.53	0.45
1:A:248:PRO:HG2	1:A:251:TYR:CD1	2.52	0.44
1:A:273:PHE:CD2	1:A:309:VAL:HG12	2.52	0.44
1:A:357:MET:HE2	1:A:357:MET:HA	1.99	0.44
1:A:227:ARG:NH2	1:A:255:GLU:OE1	2.50	0.44
1:A:115:PHE:CD2	1:A:323:GLU:HG2	2.52	0.44
1:A:185:ALA:O	1:A:188:GLU:HB2	2.17	0.44
1:A:237:TYR:HA	1:A:242:ILE:CG2	2.43	0.44
1:A:344:PRO:HG2	1:A:447:ALA:HB1	1.99	0.44
1:B:204:ALA:O	1:B:207:TRP:HB2	2.18	0.44
1:A:242:ILE:HD12	1:A:242:ILE:O	2.17	0.44
1:B:482:ARG:HH12	1:B:484:ASP:HB2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:VAL:CG2	1:A:72:GLU:HB3	2.43	0.44
1:B:26:ARG:NH1	1:B:60:ASP:OD2	2.50	0.44
1:A:130:TRP:HZ3	3:A:1017:HOH:O	1.97	0.44
1:B:280:THR:HG22	1:B:297:TYR:CE2	2.53	0.44
1:A:340:LEU:O	1:A:341:ASN:HB2	2.17	0.44
1:A:413:GLN:HA	1:A:450:GLU:O	2.17	0.44
1:A:498:ASN:N	1:A:498:ASN:ND2	2.63	0.44
1:B:30:ALA:HA	1:B:35:TYR:CG	2.53	0.44
1:A:121:VAL:CG1	1:A:166:PHE:C	2.91	0.43
1:A:128:GLU:OE1	1:A:128:GLU:HA	2.18	0.43
1:A:238:THR:HB	1:A:241:LEU:O	2.17	0.43
1:A:167:TRP:HA	1:A:167:TRP:HE3	1.84	0.43
1:B:404:ARG:HG3	1:B:404:ARG:NH1	2.30	0.43
1:A:72:GLU:HG2	3:A:1161:HOH:O	2.18	0.43
1:A:361:MET:HA	1:A:371:THR:HG22	2.00	0.43
1:A:408:VAL:O	1:A:456:PRO:HD2	2.18	0.43
1:B:238:THR:C	1:B:240:HIS:N	2.74	0.43
1:B:403:VAL:CG1	1:B:405:PHE:H	2.22	0.43
1:A:240:HIS:HE1	1:B:67:ASP:OD1	2.00	0.43
1:B:287:PRO:O	1:B:291:THR:HG23	2.19	0.43
1:A:63:ILE:HA	1:A:78:ASN:O	2.19	0.43
1:B:238:THR:HB	1:B:241:LEU:HD12	2.00	0.43
1:B:242:ILE:HD12	1:B:242:ILE:O	2.19	0.43
1:B:261:GLU:O	1:B:265:ASN:ND2	2.52	0.43
1:B:344:PRO:HG2	1:B:447:ALA:HB1	2.01	0.43
1:A:380:LEU:O	1:A:476:LEU:HA	2.18	0.43
1:B:110:GLY:CA	1:B:122:THR:HG21	2.48	0.43
1:B:276:THR:O	1:B:277:GLU:HB2	2.19	0.43
1:A:49:LYS:HE3	1:A:49:LYS:HB3	1.92	0.43
1:A:160:GLU:OE2	1:A:201:CYS:HB3	2.19	0.43
1:A:341:ASN:O	1:A:444:ARG:NH2	2.46	0.43
1:A:403:VAL:HG12	1:A:405:PHE:N	2.21	0.43
1:B:249:SER:OG	1:B:300:ARG:HD3	2.19	0.43
1:B:413:GLN:HA	1:B:450:GLU:O	2.19	0.43
1:A:280:THR:HG22	1:A:297:TYR:CE2	2.54	0.42
1:B:171:ASP:CG	1:B:174:GLU:HB2	2.44	0.42
1:B:437:LYS:HE3	3:B:1011:HOH:O	2.19	0.42
1:A:417:GLU:OE2	1:A:417:GLU:N	2.35	0.42
1:B:379:ALA:HA	1:B:477:TYR:O	2.19	0.42
1:A:238:THR:HB	1:A:241:LEU:HD12	2.01	0.42
1:B:115:PHE:CD2	1:B:323:GLU:HG2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:316:THR:N	1:B:335:PHE:HB3	2.35	0.42
1:B:401:ILE:N	1:B:401:ILE:HD12	2.34	0.42
1:B:498:ASN:N	1:B:498:ASN:ND2	2.63	0.42
1:B:238:THR:HB	1:B:241:LEU:O	2.20	0.42
1:A:228:HIS:CD2	1:A:277:GLU:HB3	2.55	0.42
1:A:405:PHE:CD1	1:A:481:GLU:HB2	2.55	0.42
1:B:22:VAL:HG22	1:B:48:PHE:CD2	2.54	0.42
1:B:361:MET:HA	1:B:371:THR:HG22	2.01	0.42
1:A:390:THR:HG22	1:A:391:GLU:N	2.35	0.42
1:B:83:ASP:OD1	1:B:140:HIS:HE1	2.02	0.42
1:B:92:ILE:O	1:B:92:ILE:HG22	2.17	0.42
1:B:128:GLU:OE1	1:B:128:GLU:HA	2.18	0.42
1:A:171:ASP:CG	1:A:174:GLU:HB2	2.44	0.42
1:A:361:MET:HE1	1:A:364:ARG:CZ	2.50	0.42
1:B:63:ILE:HA	1:B:78:ASN:O	2.19	0.42
1:B:273:PHE:CD2	1:B:309:VAL:HG12	2.55	0.42
1:A:455:GLN:HG3	1:A:482:ARG:HE	1.79	0.42
1:A:22:VAL:HG22	1:A:48:PHE:CD2	2.55	0.42
1:A:379:ALA:HA	1:A:477:TYR:O	2.20	0.42
1:A:388:ASP:OD1	1:A:389:LYS:N	2.53	0.42
1:A:33:LYS:O	1:A:37:GLU:HG3	2.19	0.41
1:A:455:GLN:HE21	1:A:455:GLN:HB3	1.51	0.41
1:A:67:ASP:OD1	1:B:240:HIS:CE1	2.73	0.41
1:B:167:TRP:HA	1:B:167:TRP:HE3	1.84	0.41
1:B:390:THR:HG22	1:B:391:GLU:N	2.36	0.41
1:A:373:ARG:HE	1:A:379:ALA:HB2	1.85	0.41
1:A:92:ILE:HG22	1:A:92:ILE:O	2.19	0.41
1:A:227:ARG:NH1	1:A:259:VAL:CG2	2.83	0.41
1:B:373:ARG:HE	1:B:379:ALA:HB2	1.86	0.41
1:A:316:THR:N	1:A:335:PHE:HB3	2.35	0.41
1:A:498:ASN:H	1:A:498:ASN:ND2	2.06	0.41
1:B:43:LYS:NZ	1:B:47:ASP:OD2	2.49	0.41
1:B:349:TYR:CZ	1:B:449:PRO:HD3	2.55	0.41
1:A:103:MET:HA	1:A:104:PRO:HD2	1.92	0.41
1:B:237:TYR:HA	1:B:242:ILE:CG2	2.43	0.41
1:A:198:PRO:CG	1:A:200:ILE:HG23	2.47	0.41
1:A:215:CYS:HB3	1:A:220:VAL:O	2.21	0.41
1:A:416:ASP:C	1:A:416:ASP:OD2	2.63	0.41
1:B:79:PHE:CA	1:B:82:ILE:HD11	2.48	0.41
1:B:498:ASN:H	1:B:498:ASN:ND2	2.06	0.41
1:A:40:LYS:O	1:A:44:GLU:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:CYS:SG	1:A:222:VAL:CG2	3.09	0.41
1:A:242:ILE:CD1	1:A:286:ASN:HB2	2.51	0.41
1:A:249:SER:OG	1:A:300:ARG:HD3	2.21	0.41
1:B:46:ILE:HD13	1:B:351:PHE:HB3	2.03	0.41
1:B:121:VAL:CG1	1:B:166:PHE:C	2.91	0.41
1:B:215:CYS:HB3	1:B:220:VAL:O	2.20	0.41
1:A:198:PRO:O	1:A:199:ALA:HB3	2.21	0.41
1:B:232:SER:HB3	1:B:281:SER:HA	2.03	0.41
1:A:475:VAL:HG22	1:A:476:LEU:N	2.36	0.40
1:B:417:GLU:OE2	1:B:471:LYS:O	2.39	0.40
1:A:36:ILE:HD11	3:A:1100:HOH:O	2.21	0.40
1:A:165:GLU:H	1:A:165:GLU:CD	2.29	0.40
1:B:405:PHE:CD1	1:B:481:GLU:HB2	2.55	0.40
1:A:384:ASN:C	1:A:384:ASN:ND2	2.79	0.40
1:B:489:TYR:HB2	1:B:492:LEU:HB2	2.02	0.40
1:A:79:PHE:CA	1:A:82:ILE:HD11	2.50	0.40
1:A:369:LEU:HD22	1:A:371:THR:HG23	2.03	0.40
1:B:33:LYS:O	1:B:37:GLU:HG3	2.21	0.40
1:B:298:ILE:O	1:B:299:ALA:C	2.65	0.40
1:A:367:HIS:HE1	1:A:385:GLU:OE1	2.05	0.40
1:A:456:PRO:HG2	1:A:463:LEU:HD11	2.03	0.40
1:B:160:GLU:OE2	1:B:201:CYS:HB3	2.21	0.40
1:B:227:ARG:NH1	1:B:259:VAL:CG2	2.84	0.40
1:B:329:SER:O	1:B:330:GLN:C	2.63	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	498/500 (100%)	447 (90%)	43 (9%)	8 (2%)	7 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	498/500 (100%)	443 (89%)	47 (9%)	8 (2%)	7	11
All	All	996/1000 (100%)	890 (89%)	90 (9%)	16 (2%)	7	11

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	394	ASP
1	B	394	ASP
1	B	276	THR
1	A	171	ASP
1	A	276	THR
1	A	277	GLU
1	A	279	ASN
1	B	171	ASP
1	B	204	ALA
1	B	277	GLU
1	A	287	PRO
1	A	456	PRO
1	B	279	ASN
1	B	456	PRO
1	A	204	ALA
1	B	287	PRO

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	450/450 (100%)	429 (95%)	21 (5%)	23	41
1	B	450/450 (100%)	429 (95%)	21 (5%)	23	41
All	All	900/900 (100%)	858 (95%)	42 (5%)	23	41

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	VAL
1	A	39	LEU
1	A	82	ILE
1	A	128	GLU
1	A	133	LEU
1	A	149	GLU
1	A	174	GLU
1	A	178	LEU
1	A	219	ASN
1	A	238	THR
1	A	241	LEU
1	A	242	ILE
1	A	250	GLU
1	A	260	ARG
1	A	312	PHE
1	A	369	LEU
1	A	406	ARG
1	A	455	GLN
1	A	476	LEU
1	A	492	LEU
1	A	498	ASN
1	B	22	VAL
1	B	39	LEU
1	B	82	ILE
1	B	128	GLU
1	B	133	LEU
1	B	149	GLU
1	B	174	GLU
1	B	178	LEU
1	B	219	ASN
1	B	238	THR
1	B	241	LEU
1	B	242	ILE
1	B	250	GLU
1	B	260	ARG
1	B	312	PHE
1	B	369	LEU
1	B	406	ARG
1	B	455	GLN
1	B	476	LEU
1	B	492	LEU
1	B	498	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	HIS
1	A	228	HIS
1	A	234	GLN
1	A	240	HIS
1	A	265	ASN
1	A	279	ASN
1	A	289	HIS
1	A	294	ASN
1	A	330	GLN
1	A	367	HIS
1	A	384	ASN
1	A	421	ASN
1	A	428	HIS
1	A	455	GLN
1	A	498	ASN
1	B	228	HIS
1	B	234	GLN
1	B	240	HIS
1	B	265	ASN
1	B	279	ASN
1	B	289	HIS
1	B	294	ASN
1	B	330	GLN
1	B	384	ASN
1	B	421	ASN
1	B	441	ASN
1	B	455	GLN
1	B	498	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 oligosaccharides 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	XYP	B	701	-	10,10,10	0.52	0	14,14,14	0.33	0
2	XYP	A	601	-	10,10,10	0.57	0	14,14,14	0.33	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	XYP	B	701	-	-	-	0/1/1/1
2	XYP	A	601	-	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	XYP	1	0
2	A	601	XYP	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

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	500/500 (100%)	-0.13	4 (0%) 82 80	16, 36, 63, 89	0
1	B	500/500 (100%)	-0.10	5 (1%) 79 76	17, 36, 63, 89	0
All	All	1000/1000 (100%)	-0.12	9 (0%) 81 78	16, 36, 63, 89	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	456	PRO	2.6
1	B	405	PHE	2.5
1	A	417	GLU	2.5
1	B	9	PHE	2.4
1	B	125	LYS	2.4
1	A	1	MET	2.2
1	B	406	ARG	2.1
1	A	406	ARG	2.0
1	B	73	VAL	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(Å ²)	Q<0.9
2	XYP	A	601	10/10	0.78	0.14	69,70,70,71	0
2	XYP	B	701	10/10	0.87	0.14	67,69,69,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.