



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:37 PM GMT

PDB ID : 1PX8
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
<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

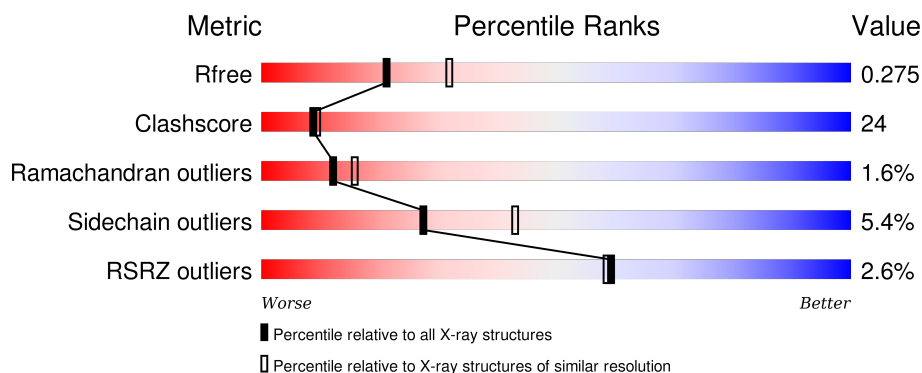
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (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 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	500	<div> <div>2%</div> <div> <div></div> <div>59%</div> <div>36%</div> <div>5%</div> </div> </div>
1	B	500	<div> <div>3%</div> <div> <div></div> <div>58%</div> <div>38%</div> <div>.</div> </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	XYP	A	601	-	-	-	X
2	XYP	B	701	-	-	-	X

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.

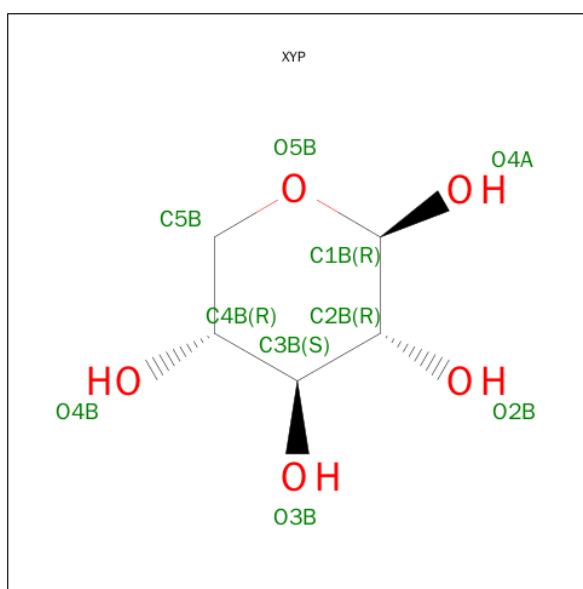
- Molecule 1 is a protein called Beta-xylosidase.

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 SUGAR (BETA-D-XYLOPYRANOSE) (three-letter code: 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		

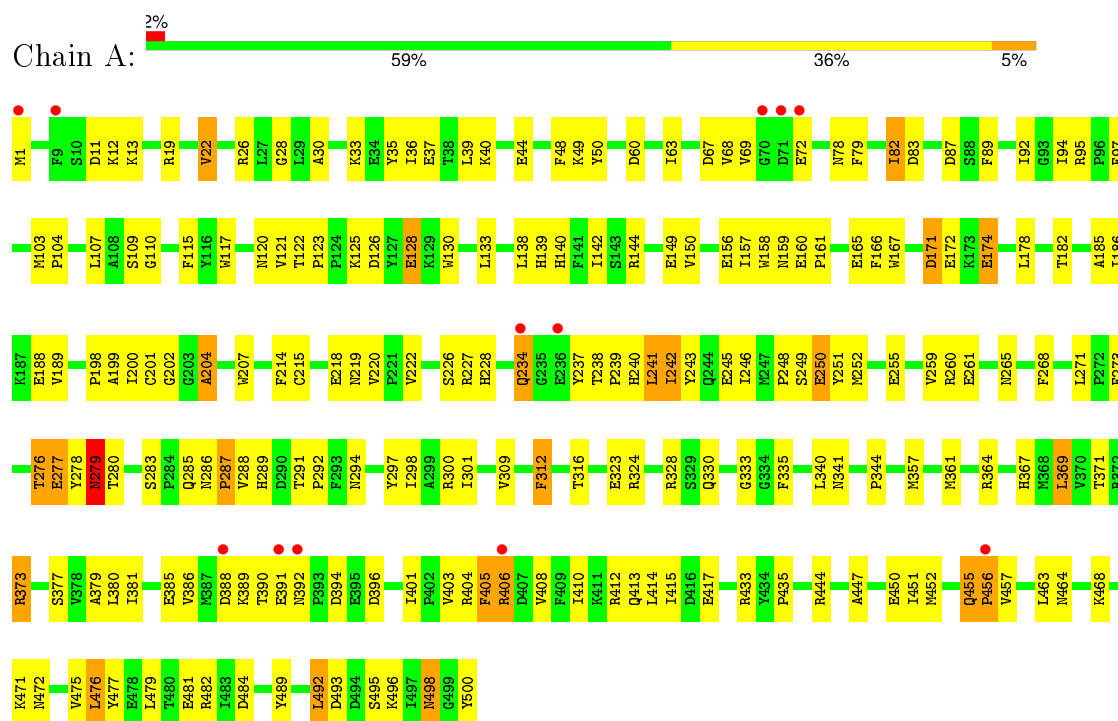
- Molecule 3 is water.

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

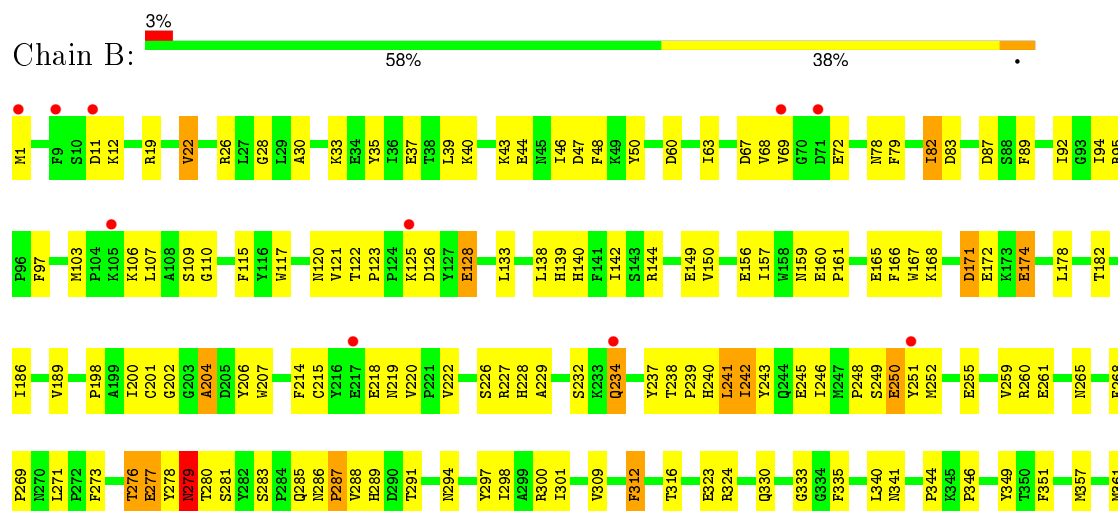
3 Residue-property plots

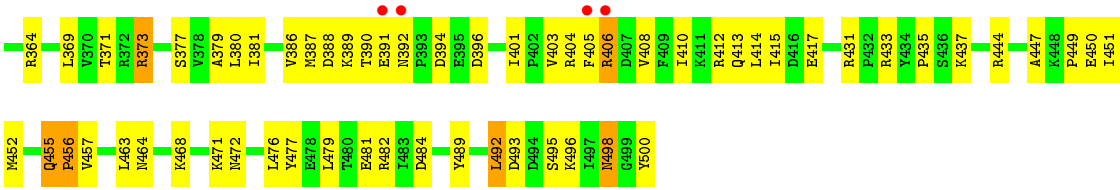
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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



• Molecule 1: Beta-xylosidase





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) 89.0 (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 0.229 , 0.275	Depositor DCC
R_{free} test set	3747 reflections (10.01%)	DCC
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 , 37.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 37437 reflections	Xtriage
F_o, F_c correlation	0.92	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, 0.375 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: 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	0.38	0/4278	0.61	0/5799
1	B	0.38	0/4278	0.61	0/5799
All	All	0.38	0/8556	0.61	0/11598

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	4154	0	3993	197	0
1	B	4154	0	3993	191	0
2	A	10	0	10	3	0
2	B	10	0	10	2	0
3	A	150	0	0	14	0
3	B	177	0	0	14	0
All	All	8655	0	8006	384	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 (384) 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:277:GLU:OE1	2:B:701:XYP:H1B	1.51	1.09
1:A:277:GLU:OE1	2:A:601:XYP:H1B	1.50	1.08
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:B:268:PHE:HA	3:B:1195:HOH:O	1.73	0.86
1:A:403:VAL:HG12	1:A:405:PHE:H	1.39	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
1:B:468:LYS:N	1:B:468:LYS:HD2	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:N	1:A:468:LYS:HD2	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: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:455:GLN:HG3	1:B:482:ARG:CD	2.19	0.71
1:A:252:MET:SD	1:A:301:ILE:HD13	2.31	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:MET:HG3	1:A:122:THR:O	1.90	0.71
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: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:N	1:B:498:ASN:HD22	1.92	0.67
1:B:412:ARG:HD3	1:B:452:MET:HE2	1.76	0.67
1:A:498:ASN:HD22	1:A:498:ASN:N	1.91	0.67
1:A:13:LYS:HE2	3:A:1300:HOH:O	1.95	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: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:138:LEU:HD11	1:A:186:ILE:HG12	1.78	0.65
1:A:202:GLY:CA	1:A:227:ARG:HH21	2.07	0.65
1:A:388:ASP:CG	1:A:389:LYS:H	1.99	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: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:388:ASP:CG	1:B:389:LYS:H	2.02	0.64
1:A:412:ARG:HD3	1:A:452:MET:HE2	1.79	0.64
1:B:471:LYS:HG2	1:B:472:ASN:ND2	2.13	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:172:GLU:HA	1:B:207:TRP:CH2	2.34	0.62
1:B:22:VAL:HG22	1:B:48:PHE:CG	2.34	0.62
1:A:404:ARG:HH11	1:A:404:ARG:HG3	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:406:ARG:O	1:B:457:VAL:HG13	1.99	0.61
1:B:404:ARG:HH11	1:B:404:ARG:HG3	1.64	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:121:VAL:HG13	1:A:166:PHE:C	2.21	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:121:VAL:O	1:B:121:VAL:HG12	2.01	0.60
1:A:121:VAL:O	1:A:121:VAL:HG12	2.00	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:121:VAL:CG1	1:B:121:VAL:O	2.50	0.60
1:B:121:VAL:HG13	1:B:166:PHE:C	2.21	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:238:THR:HG22	1:A:240:HIS:N	2.17	0.58
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
2:A:601:XYP:H2B	3:A:1290:HOH:O	2.03	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: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:388:ASP:CG	1:A:389:LYS:N	2.60	0.56
1:A:396:ASP:OD1	1:A:468:LYS:HG3	2.06	0.56
1:B:361:MET:HE3	1:B:364:ARG:HB3	1.87	0.55
1:B:238:THR:HG22	1:B:240:HIS:N	2.17	0.55
1:A:110:GLY:HA3	1:A:122:THR:HG21	1.88	0.55
1:B:103:MET:O	1:B:120:ASN:HB3	2.07	0.55
1:A:121:VAL:HG13	1:A:166:PHE:O	2.06	0.55
1:A:403:VAL:HA	3:A:1217:HOH:O	2.06	0.55
1:A:139:HIS:CE1	1:A:189:VAL:HG13	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:GLN:HA	1:A:234:GLN:HE21	1.72	0.54
1:A:227:ARG:HH11	1:A:259:VAL:CG2	2.20	0.54
1:B:406:ARG:HD3	3:B:1203:HOH:O	2.08	0.54
1:B:156:GLU:OE1	1:B:226:SER:OG	2.24	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:B:361:MET:HE3	1:B:364:ARG:CB	2.38	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:B:380:LEU:C	1:B:380:LEU:HD23	2.28	0.53
1:A:373:ARG:HD3	1:A:377:SER:OG	2.08	0.53
1:B:388:ASP:CG	1:B:389:LYS:N	2.62	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:HE21	1:B:234:GLN:HA	1.73	0.53
1:B:482:ARG:NH1	1:B:484:ASP:HB2	2.24	0.53
1:A:380:LEU:HD23	1:A:380:LEU:C	2.29	0.53
1:A:87:ASP:OD2	1:A:144:ARG:NH1	2.41	0.53
1:B:414:LEU:HD22	1:B:415:ILE:N	2.23	0.53
1:B:227:ARG:HH11	1:B:259:VAL:CG2	2.22	0.53
1:A:144:ARG:NH2	1:B:435:PRO:O	2.42	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:B:242:ILE:HD11	1:B:283:SER:OG	2.09	0.52
1:A:410:ILE:HG12	1:A:479:LEU:HD22	1.91	0.52
1:B:346:PRO:HB3	3:B:1078:HOH:O	2.09	0.52
1:A:103:MET:HE1	1:A:107:LEU:HB3	1.91	0.52
1:B:410:ILE:HG12	1:B:479:LEU:HD22	1.90	0.52
1:A:165:GLU:N	1:A:165:GLU:OE1	2.42	0.52
1:A:161:PRO:HA	1:A:167:TRP:HB2	1.92	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:O	1:B:68:VAL:HG23	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:403:VAL:HG13	1:A:405:PHE:CD2	2.46	0.51
1:A:386:VAL:HB	3:A:1160:HOH:O	2.11	0.51
1:B:161:PRO:HA	1:B:167:TRP:HB2	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:LEU:HD13	1:A:243:TYR:CE1	2.47	0.49
1:B:241:LEU:HD13	1:B:243:TYR:CE1	2.47	0.49
1:A:268:PHE:HB3	1:A:271:LEU:HG	1.93	0.49
1:B:386:VAL:HG12	1:B:388:ASP:O	2.13	0.49
1:B:168:LYS:HE3	3:B:1189:HOH:O	2.11	0.49
1:B:227:ARG:HG2	1:B:228:HIS:H	1.76	0.49
1:B:40:LYS:O	1:B:44:GLU:HG3	2.13	0.49
1:A:68:VAL:HG23	1:A:68:VAL:O	2.10	0.49
1:B:277:GLU:OE1	2:B:701:XYP:C1B	2.41	0.49
1:A:278:TYR:O	1:A:279:ASN:HB2	2.11	0.49
1:B:373:ARG:HD3	1:B:377:SER:OG	2.12	0.49
1:B:50:TYR:CD2	1:B:95:ARG:HB2	2.47	0.49
1:A:463:LEU:HD23	1:A:464:ASN:N	2.28	0.49
1:B:357:MET:HE2	1:B:357:MET:HA	1.94	0.49
1:A:433:ARG:HD2	3:B:1257:HOH:O	2.12	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: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:387:MET:HE1	3:B:1108:HOH:O	2.13	0.49
1:B:229:ALA:HB1	3:B:1106:HOH:O	2.12	0.49
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:B:28:GLY:HA3	1:B:60:ASP:OD2	2.13	0.48
1:A:11:ASP:OD2	1:A:12:LYS:HG3	2.12	0.48
1:A:361:MET:HE3	1:A:364:ARG:HB3	1.95	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:277:GLU:OE1	2:A:601:XYP:C1B	2.42	0.48
1:B:26:ARG:HD3	1:B:117:TRP:CE2	2.49	0.48
1:A:312:PHE:CD1	1:A:312:PHE:N	2.82	0.48
1:A:157:ILE:HD12	1:A:182:THR:HG21	1.96	0.48
1:B:206:TYR:HB3	3:B:1223:HOH:O	2.14	0.48
1:B:139:HIS:CE1	1:B:189:VAL:HG13	2.49	0.48
1:B:115:PHE:CG	1:B:323:GLU:HG2	2.49	0.48
1:A:115:PHE:CG	1:A:323:GLU:HG2	2.49	0.47
1:A:276:THR:O	1:A:277:GLU:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:THR:C	1:A:240:HIS:H	2.17	0.47
1:B:103:MET:HE1	1:B:107:LEU:HB3	1.95	0.47
1:B:403:VAL:HG12	1:B:405:PHE:N	2.20	0.47
1:A:50:TYR:CD2	1:A:95:ARG:HB2	2.49	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:B:69:VAL:CG2	1:B:72:GLU:HB3	2.43	0.47
1:A:171:ASP:HB3	1:A:174:GLU:HB2	1.97	0.47
1:B:288:VAL:O	1:B:294:ASN:HB2	2.14	0.47
1:A:89:PHE:O	1:A:94:ILE:HG22	2.15	0.47
1:B:165:GLU:OE1	1:B:165:GLU:N	2.43	0.47
1:B:215:CYS:SG	1:B:222:VAL:CG2	3.03	0.47
1:B:30:ALA:HA	1:B:35:TYR:CD2	2.50	0.46
1:A:401:ILE:HD12	1:A:401:ILE:N	2.30	0.46
1:B:312:PHE:N	1:B:312:PHE:CD1	2.82	0.46
1:A:289:HIS:HD2	1:A:333:GLY:O	1.97	0.46
1:B:89:PHE:O	1:B:94:ILE:HG22	2.14	0.46
1:A:142:ILE:HD13	1:A:150:VAL:HG21	1.97	0.46
1:A:404:ARG:NH1	1:A:404:ARG:HG3	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: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:B:142:ILE:HD13	1:B:150:VAL:HG21	1.98	0.46
1:A:28:GLY:HA3	1:A:60:ASP:OD2	2.15	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:A:380:LEU:HD23	1:A:381:ILE:N	2.30	0.46
1:B:238:THR:C	1:B:240:HIS:H	2.19	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:30:ALA:HA	1:A:35:TYR:CG	2.51	0.45
1:A:83:ASP:OD1	1:A:140:HIS:HE1	2.00	0.45
1:A:261:GLU:O	1:A:265:ASN:ND2	2.50	0.45
1:A:33:LYS:HE2	3:A:1273:HOH:O	2.15	0.45
1:A:482:ARG:HH12	1:A:484:ASP:HB2	1.82	0.45
1:A:245:GLU:C	1:A:246:ILE:HD12	2.36	0.45
1:A:110:GLY:CA	1:A:122:THR:HG21	2.47	0.45
1:B:341:ASN:O	1:B:444:ARG:NH2	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:26:ARG:HD3	1:A:117:TRP:CE2	2.51	0.45
1:B:278:TYR:O	1:B:279:ASN:HB2	2.16	0.45
1:A:63:ILE:HD11	1:A:82:ILE:HG12	1.99	0.45
1:B:248:PRO:HG2	1:B:251:TYR:CD1	2.52	0.45
1:A:156:GLU:OE1	1:A:226:SER:OG	2.29	0.45
1:B:289:HIS:HD2	1:B:333:GLY:O	1.99	0.45
1:A:361:MET:HE3	1:A:364:ARG:CB	2.46	0.45
1:A:22:VAL:CG2	1:A:48:PHE:CG	3.00	0.45
1:B:248:PRO:HA	1:B:387:MET:HE1	1.97	0.45
1:B:408:VAL:O	1:B:456:PRO:HD2	2.17	0.45
1:B:22:VAL:CG2	1:B:48:PHE:CG	3.00	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:455:GLN:HE21	1:B:455:GLN:HB3	1.53	0.45
1:A:410:ILE:HD11	1:A:456:PRO:HG3	1.99	0.45
1:B:346:PRO:HG2	3:B:1029:HOH:O	2.17	0.45
1:B:171:ASP:HB3	1:B:174:GLU:HB2	1.99	0.45
1:A:287:PRO:O	1:A:291:THR:HG23	2.16	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:227:ARG:NH2	1:A:255:GLU:OE1	2.50	0.44
1:A:237:TYR:HA	1:A:242:ILE:CG2	2.43	0.44
1:B:498:ASN:H	1:B:498:ASN:ND2	2.06	0.44
1:A:340:LEU:O	1:A:341:ASN:HB2	2.17	0.44
1:B:204:ALA:O	1:B:207:TRP:HB2	2.18	0.44
1:A:115:PHE:CD2	1:A:323:GLU:HG2	2.52	0.44
1:A:344:PRO:HG2	1:A:447:ALA:HB1	1.99	0.44
1:A:185:ALA:O	1:A:188:GLU:HB2	2.17	0.44
1:A:242:ILE:O	1:A:242:ILE:HD12	2.17	0.44
1:B:482:ARG:HH12	1:B:484:ASP:HB2	1.83	0.44
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:B:280:THR:HG22	1:B:297:TYR:CE2	2.53	0.44
1:A:130:TRP:HZ3	3:A:1017:HOH:O	1.97	0.44
1:B:245:GLU:C	1:B:246:ILE:HD12	2.38	0.44
1:A:413:GLN:HA	1:A:450:GLU:O	2.17	0.44
1:A:498:ASN:ND2	1:A:498:ASN:N	2.63	0.44
1:B:30:ALA:HA	1:B:35:TYR:CG	2.53	0.44
1:A:238:THR:HB	1:A:241:LEU:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:GLU:OE1	1:A:128:GLU:HA	2.18	0.43
1:B:404:ARG:HG3	1:B:404:ARG:NH1	2.30	0.43
1:A:167:TRP:HA	1:A:167:TRP:HE3	1.84	0.43
1:B:403:VAL:CG1	1:B:405:PHE:H	2.22	0.43
1:A:72:GLU:HG2	3:A:1161:HOH:O	2.18	0.43
1:A:408:VAL:O	1:A:456:PRO:HD2	2.18	0.43
1:A:361:MET:HA	1:A:371:THR:HG22	2.00	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:B:238:THR:HB	1:B:241:LEU:HD12	2.00	0.43
1:B:242:ILE:O	1:B:242:ILE:HD12	2.19	0.43
1:A:63:ILE:HA	1:A:78:ASN: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:B:276:THR:O	1:B:277:GLU:HB2	2.19	0.43
1:B:103:MET:HB3	1:B:103:MET:HE2	1.81	0.43
1:B:110:GLY:CA	1:B:122:THR:HG21	2.48	0.43
1:A:380:LEU:O	1:A:476:LEU:HA	2.18	0.43
1:B:463:LEU:HD23	1:B:463:LEU:C	2.39	0.43
1:A:49:LYS:HE3	1:A:49:LYS:HB3	1.92	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:341:ASN:O	1:A:444:ARG:NH2	2.46	0.43
1:B:92:ILE:O	1:B:92:ILE:HG22	2.17	0.43
1:A:160:GLU:OE2	1:A:201:CYS:HB3	2.19	0.43
1:A:280:THR:HG22	1:A:297:TYR:CE2	2.54	0.42
1:B:437:LYS:HE3	3:B:1011:HOH:O	2.19	0.42
1:B:379:ALA:HA	1:B:477:TYR:O	2.19	0.42
1:A:417:GLU:OE2	1:A:417:GLU:N	2.35	0.42
1:A:238:THR:HB	1:A:241:LEU:HD12	2.01	0.42
1:B:498:ASN:N	1:B:498:ASN:ND2	2.63	0.42
1:B:115:PHE:CD2	1:B:323:GLU:HG2	2.54	0.42
1:B:401:ILE:HD12	1:B:401:ILE:N	2.34	0.42
1:B:316:THR:N	1:B:335:PHE:HB3	2.35	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:128:GLU:OE1	1:B:128:GLU:HA	2.18	0.42
1:A:463:LEU:C	1:A:463:LEU:HD23	2.40	0.42
1:B:83:ASP:OD1	1:B:140:HIS:HE1	2.02	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:159:ASN:O	1:A:160:GLU:C	2.58	0.42
1:A:22:VAL:HG22	1:A:48:PHE:CD2	2.55	0.42
1:A:388:ASP:OD1	1:A:389:LYS:N	2.53	0.42
1:A:379:ALA:HA	1:A:477:TYR:O	2.20	0.42
1:A:455:GLN:HB3	1:A:455:GLN:HE21	1.51	0.41
1:A:33:LYS:O	1:A:37:GLU:HG3	2.19	0.41
1:A:238:THR:C	1:A:240:HIS:N	2.72	0.41
1:A:67:ASP:OD1	1:B:240:HIS:CE1	2.73	0.41
1:B:390:THR:HG22	1:B:391:GLU:N	2.36	0.41
1:B:167:TRP:HA	1:B:167:TRP:HE3	1.84	0.41
1:B:238:THR:C	1:B:240:HIS:N	2.74	0.41
1:A:373:ARG:HE	1:A:379:ALA:HB2	1.85	0.41
1:A:357:MET:HA	1:A:357:MET:HE2	2.01	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:92:ILE:HG22	1:A:92:ILE:O	2.19	0.41
1:A:498:ASN:ND2	1:A:498:ASN:H	2.06	0.41
1:B:349:TYR:CZ	1:B:449:PRO:HD3	2.55	0.41
1:B:43:LYS:NZ	1:B:47:ASP:OD2	2.49	0.41
1:A:316:THR:N	1:A:335:PHE:HB3	2.35	0.41
1:B:237:TYR:HA	1:B:242:ILE:CG2	2.43	0.41
1:A:103:MET:HA	1:A:104:PRO:HD2	1.92	0.41
1:B:79:PHE:CA	1:B:82:ILE:HD11	2.48	0.41
1:A:198:PRO:CG	1:A:200:ILE:HG23	2.47	0.41
1:A:361:MET:HE3	1:A:364:ARG:NE	2.36	0.41
1:A:215:CYS:HB3	1:A:220:VAL:O	2.21	0.41
1:A:249:SER:OG	1:A:300:ARG:HD3	2.21	0.41
1:A:242:ILE:CD1	1:A:286:ASN:HB2	2.51	0.41
1:B:412:ARG:HH11	1:B:452:MET:HE2	1.85	0.41
1:B:215:CYS:HB3	1:B:220:VAL:O	2.20	0.41
1:A:215:CYS:SG	1:A:222:VAL:CG2	3.09	0.41
1:A:40:LYS:O	1:A:44:GLU:HG3	2.20	0.41
1:B:159:ASN:O	1:B:160:GLU:C	2.59	0.41
1:B:46:ILE:HD13	1:B:351:PHE:HB3	2.03	0.41
1:A:198:PRO:O	1:A:199:ALA:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:414:LEU:C	1:B:414:LEU:HD13	2.41	0.41
1:B:232:SER:HB3	1:B:281:SER:HA	2.03	0.41
1:B:417:GLU:OE2	1:B:471:LYS:O	2.39	0.40
1:A:475:VAL:HG22	1:A:476:LEU:N	2.36	0.40
1:B:405:PHE:CD1	1:B:481:GLU:HB2	2.55	0.40
1:A:36:ILE:HD11	3:A:1100:HOH:O	2.21	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:227:ARG:NH1	1:B:259:VAL:CG2	2.84	0.40
1:A:456:PRO:HG2	1:A:463:LEU:HD11	2.03	0.40
1:A:361:MET:HE2	3:A:1269:HOH:O	2.21	0.40
1:B:160:GLU:OE2	1:B:201:CYS:HB3	2.21	0.40
1:A:367:HIS:HE1	1:A:385:GLU:OE1	2.05	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%)	12	16
1	B	498/500 (100%)	443 (89%)	47 (9%)	8 (2%)	12	16
All	All	996/1000 (100%)	890 (89%)	90 (9%)	16 (2%)	12	16

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	394	ASP
1	B	394	ASP
1	B	276	THR

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Mol	Chain	Res	Type
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%)	425 (94%)	25 (6%)	26	41
1	B	450/450 (100%)	426 (95%)	24 (5%)	28	44
All	All	900/900 (100%)	851 (95%)	49 (5%)	27	43

All (49) 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	97	PHE
1	A	128	GLU
1	A	133	LEU
1	A	149	GLU
1	A	174	GLU
1	A	178	LEU
1	A	219	ASN

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Mol	Chain	Res	Type
1	A	234	GLN
1	A	241	LEU
1	A	242	ILE
1	A	250	GLU
1	A	260	ARG
1	A	279	ASN
1	A	312	PHE
1	A	369	LEU
1	A	373	ARG
1	A	405	PHE
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	97	PHE
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	234	GLN
1	B	241	LEU
1	B	242	ILE
1	B	250	GLU
1	B	260	ARG
1	B	279	ASN
1	B	312	PHE
1	B	369	LEU
1	B	373	ARG
1	B	406	ARG
1	B	455	GLN
1	B	476	LEU
1	B	492	LEU
1	B	498	ASN

Some 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	455	GLN
1	A	498	ASN
1	B	140	HIS
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	367	HIS
1	B	384	ASN
1	B	421	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 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	XYP	A	601	-	10,10,10	0.58	0	12,14,14	0.38	0
2	XYP	B	701	-	10,10,10	0.52	0	12,14,14	0.40	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	A	601	-	-	0/0/17/17	0/1/1/1
2	XYP	B	701	-	-	0/0/17/17	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 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	XYP	3	0
2	B	701	XYP	2	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 ⓘ

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	500/500 (100%)	-0.09	12 (2%) 62 61	16, 36, 63, 89	0
1	B	500/500 (100%)	-0.13	14 (2%) 56 55	17, 36, 63, 89	0
All	All	1000/1000 (100%)	-0.11	26 (2%) 59 58	16, 36, 63, 89	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	71	ASP	4.5
1	A	9	PHE	4.5
1	B	71	ASP	4.3
1	A	70	GLY	4.2
1	A	1	MET	3.9
1	B	406	ARG	3.5
1	A	406	ARG	3.4
1	B	9	PHE	3.3
1	B	69	VAL	3.2
1	A	236	GLU	3.0
1	A	72	GLU	3.0
1	B	125	LYS	2.9
1	B	392	ASN	2.8
1	A	456	PRO	2.7
1	B	11	ASP	2.6
1	B	234	GLN	2.6
1	A	234	GLN	2.6
1	A	392	ASN	2.6
1	A	388	ASP	2.5
1	B	391	GLU	2.4
1	B	217	GLU	2.3
1	A	391	GLU	2.3
1	B	405	PHE	2.3
1	B	1	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	251	TYR	2.1
1	B	105	LYS	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	XYP	A	601	10/10	0.83	0.27	7.67	69,70,70,71	0
2	XYP	B	701	10/10	0.88	0.22	3.87	67,69,69,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.