



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:32 PM UTC

PDB ID : 2RF1 / pdb\_00002rf1  
Title : Crystal structure of ChoX in an unliganded closed conformation  
Authors : Oswald, C.; Smits, S.H.J.; Hoeing, M.; Sohn-Boeser, L.; Le Rudulier, D.; Schmitt, L.; Bremer, E.  
Deposited on : 2007-09-27  
Resolution : 2.00 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](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (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

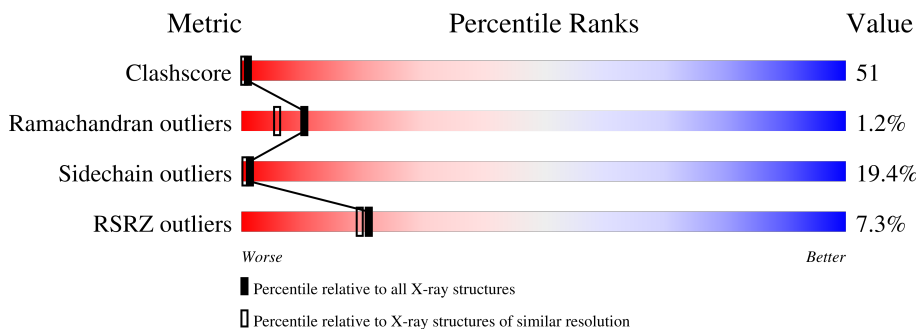
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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  $\geq 3$ , 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	298	
1	B	298	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4573 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 PUTATIVE GLYCINE BETAIN-BINDING ABC TRANSPORTER PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	290	Total 2192	C 1381	N 359	O 443	S 9	0	0	0
1	B	289	Total 2184	C 1375	N 358	O 442	S 9	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	251	ASP	GLY	engineered mutation	UNP Q92N37
A	319	GLU	-	expression tag	UNP Q92N37
A	320	HIS	-	expression tag	UNP Q92N37
A	321	HIS	-	expression tag	UNP Q92N37
A	322	HIS	-	expression tag	UNP Q92N37
A	323	HIS	-	expression tag	UNP Q92N37
A	324	HIS	-	expression tag	UNP Q92N37
A	325	HIS	-	expression tag	UNP Q92N37
B	251	ASP	GLY	engineered mutation	UNP Q92N37
B	319	GLU	-	expression tag	UNP Q92N37
B	320	HIS	-	expression tag	UNP Q92N37
B	321	HIS	-	expression tag	UNP Q92N37
B	322	HIS	-	expression tag	UNP Q92N37
B	323	HIS	-	expression tag	UNP Q92N37
B	324	HIS	-	expression tag	UNP Q92N37
B	325	HIS	-	expression tag	UNP Q92N37

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	105	Total 105	O 105	0	0
2	B	92	Total 92	O 92	0	0



D288	N289	P290	Q291	S292	I293	E294	F295	W296	L297	V300	A301	T302	K303	D304	G305	G306	D307	G308	L309	A310	A311	V312	K313	L316	G317	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS	HIS
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	30.90Å 196.20Å 42.80Å 90.00° 90.10° 90.00°	Depositor
Resolution (Å)	10.00 – 2.00 10.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	93.9 (10.00-2.00) 93.1 (10.00-2.00)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	8.83 (at 2.01Å)	Xtrriage
Refinement program	SHELX, SHELXL-97	Depositor
R, $R_{free}$	0.201 , 0.235 0.237 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.6	Xtrriage
Anisotropy	0.394	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.45 , 129.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.089 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	4573	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.57% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 i

### 5.1 Standard geometry i

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	0.30	1/2234 (0.0%)	0.66	1/3033 (0.0%)
1	B	0.85	3/2226 (0.1%)	1.15	6/3022 (0.2%)
All	All	0.63	4/4460 (0.1%)	0.94	7/6055 (0.1%)

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	B	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	226	PHE	C-N	-30.11	0.88	1.33
1	B	225	VAL	C-N	-21.27	1.06	1.33
1	A	262	GLN	CA-C	8.32	1.63	1.52
1	B	241	ALA	C-O	-6.52	1.15	1.24

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	226	PHE	O-C-N	-43.80	76.96	122.07
1	B	226	PHE	CA-C-N	14.64	144.85	121.87
1	B	226	PHE	C-N-CA	14.64	144.85	121.87
1	B	225	VAL	CA-C-N	9.17	132.37	120.44
1	B	225	VAL	C-N-CA	9.17	132.37	120.44
1	B	225	VAL	O-C-N	-8.39	112.08	122.57
1	A	262	GLN	N-CA-C	-5.28	105.52	111.28

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	225	VAL	Mainchain
1	B	226	PHE	Mainchain

## 5.2 Too-close contacts [i](#)

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	2192	0	2135	215	0
1	B	2184	0	2122	228	0
2	A	105	0	0	51	0
2	B	92	0	0	45	0
All	All	4573	0	4257	437	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 51.

All (437) 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:84:ASP:HA	1:B:240:ARG:HG2	1.44	0.99
1:B:38:PHE:HB2	1:B:66:VAL:HG22	1.49	0.94
1:A:252:LYS:HB3	1:A:300:VAL:HG22	1.50	0.93
1:B:162:ILE:HD11	1:B:203:LEU:HD21	1.53	0.90
1:B:89:ASN:HB2	1:B:238:ASN:HD21	1.37	0.88
1:A:302:THR:HG23	1:A:304:ASP:H	1.41	0.85
1:B:88:GLY:HA3	2:B:367:HOH:O	1.78	0.84
1:B:50:THR:HA	2:B:396:HOH:O	1.80	0.80
1:A:99:ALA:O	1:A:103:GLU:HG3	1.82	0.78
1:B:190:VAL:HG13	2:B:330:HOH:O	1.82	0.78
1:A:123:THR:OG1	1:A:127:GLY:HA3	1.84	0.78
1:A:133:LYS:HA	2:A:420:HOH:O	1.83	0.77
1:A:308:GLY:O	1:A:312:VAL:HG23	1.83	0.77
1:B:151:GLY:HA3	1:B:159:ASN:HD21	1.47	0.77
1:A:174:LYS:HB2	2:A:377:HOH:O	1.85	0.77
1:B:29:GLU:HG2	1:B:248:PRO:HD2	1.64	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:VAL:HA	1:B:76:THR:HB	1.67	0.76
1:B:271:ILE:HG22	1:B:272:LEU:HD23	1.66	0.76
1:B:302:THR:HG22	1:B:306:GLY:H	1.51	0.76
1:A:188:ALA:HB1	1:A:192:ARG:HH12	1.51	0.76
1:A:74:THR:O	1:A:78:LEU:HG	1.85	0.75
1:A:142:LYS:HD2	1:B:192:ARG:HH21	1.50	0.75
1:A:237:THR:HG21	2:A:350:HOH:O	1.86	0.75
1:B:188:ALA:HB1	1:B:192:ARG:HH12	1.50	0.75
1:B:58:GLU:HG3	2:B:387:HOH:O	1.87	0.75
1:A:152:ILE:H	1:A:159:ASN:HD21	1.32	0.75
1:A:81:LYS:HG2	2:A:403:HOH:O	1.85	0.75
1:A:103:GLU:HB2	2:A:425:HOH:O	1.87	0.74
1:A:311:ALA:HB3	2:A:336:HOH:O	1.88	0.73
1:A:78:LEU:HD23	1:A:83:ILE:HB	1.70	0.73
1:B:74:THR:O	1:B:78:LEU:HG	1.90	0.72
1:A:126:LYS:HG2	1:A:197:GLY:O	1.89	0.72
1:B:89:ASN:HB2	1:B:238:ASN:ND2	2.05	0.72
1:B:223:ASP:HB2	2:B:348:HOH:O	1.89	0.72
1:B:277:ASP:HB3	1:B:280:LYS:HG3	1.70	0.72
1:B:114:LEU:HD23	1:B:235:VAL:HG21	1.72	0.72
1:A:61:GLY:O	1:A:303:LYS:HD3	1.89	0.72
1:B:161:LEU:HD22	1:B:225:VAL:HG12	1.72	0.72
1:B:138:ILE:HG22	1:B:173:LEU:HD21	1.70	0.72
1:B:108:GLU:OE2	1:B:241:ALA:O	2.09	0.71
1:B:300:VAL:O	1:B:308:GLY:HA3	1.91	0.70
1:A:130:LEU:HD22	2:A:367:HOH:O	1.91	0.70
1:A:164:ASP:HB3	2:A:361:HOH:O	1.90	0.70
1:A:227:GLY:HA3	2:A:391:HOH:O	1.90	0.70
1:B:239:VAL:HB	1:B:243:TYR:HB3	1.72	0.70
1:B:290:PRO:O	1:B:293:ILE:HG23	1.91	0.70
1:B:302:THR:HG22	1:B:306:GLY:N	2.07	0.69
1:A:290:PRO:O	1:A:293:ILE:HG23	1.92	0.69
1:A:132:ILE:HG23	2:A:408:HOH:O	1.91	0.69
1:B:40:ASP:O	1:B:68:VAL:HA	1.93	0.69
1:B:44:THR:HG21	1:B:272:LEU:HG	1.74	0.69
1:B:44:THR:OG1	1:B:272:LEU:HD21	1.93	0.69
1:B:288:ASP:HA	2:B:413:HOH:O	1.92	0.68
1:B:184:GLN:HB3	2:B:383:HOH:O	1.94	0.68
1:B:242:GLY:O	2:B:329:HOH:O	2.11	0.67
1:B:71:VAL:O	1:B:74:THR:HB	1.95	0.67
1:B:95:GLU:O	1:B:99:ALA:HB2	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:ILE:HG22	2:B:341:HOH:O	1.95	0.66
1:A:307:ASP:HB3	2:A:369:HOH:O	1.95	0.66
1:B:204:GLY:HA3	2:B:354:HOH:O	1.94	0.66
1:A:141:HIS:HA	2:A:364:HOH:O	1.96	0.66
1:B:252:LYS:HB3	1:B:300:VAL:HG22	1.78	0.66
1:B:266:GLU:O	1:B:270:LYS:HG3	1.95	0.66
1:A:178:VAL:HB	2:A:396:HOH:O	1.95	0.66
1:B:114:LEU:HD22	1:B:264:GLU:OE2	1.96	0.66
1:A:40:ASP:OD1	1:A:46:ILE:HG23	1.95	0.65
1:B:40:ASP:OD1	1:B:46:ILE:HG23	1.97	0.65
1:A:292:SER:O	1:A:295:PRO:HD2	1.97	0.64
1:A:206:GLU:HG2	1:A:211:ASN:ND2	2.13	0.64
1:B:121:LEU:HD23	1:B:203:LEU:HD23	1.79	0.64
1:A:41:VAL:HG12	1:A:153:GLU:OE1	1.97	0.64
1:B:163:ILE:O	1:B:167:GLU:HG3	1.98	0.64
1:B:264:GLU:O	1:B:268:MET:HG3	1.98	0.63
1:A:302:THR:HG22	1:A:306:GLY:N	2.13	0.63
1:B:84:ASP:O	1:B:239:VAL:HA	1.98	0.63
1:B:69:LEU:HA	2:B:395:HOH:O	1.99	0.63
1:B:132:ILE:HD12	2:B:386:HOH:O	1.99	0.63
1:A:71:VAL:HB	1:A:72:PRO:HD3	1.81	0.62
1:A:163:ILE:O	1:A:167:GLU:HG3	1.98	0.62
1:A:126:LYS:HE3	1:A:197:GLY:O	1.99	0.62
1:B:37:ARG:HD2	1:B:82:ASP:O	1.99	0.62
1:B:313:LYS:HB2	2:B:382:HOH:O	1.99	0.62
1:A:83:ILE:O	1:A:240:ARG:HD3	2.00	0.62
1:A:175:GLY:HA3	1:B:192:ARG:HB3	1.81	0.62
1:B:251:ASP:O	1:B:255:GLN:HG3	1.99	0.62
1:B:67:LYS:HG2	2:B:364:HOH:O	2.00	0.62
1:B:45:ASP:O	1:B:49:THR:HG23	2.00	0.61
1:A:312:VAL:HG12	1:A:316:LEU:HD11	1.83	0.61
1:B:256:ASN:HB3	1:B:296:TRP:HA	1.82	0.61
1:B:246:GLU:HB2	2:B:329:HOH:O	2.00	0.60
1:A:121:LEU:HD12	1:A:135:PHE:CE1	2.36	0.60
1:B:169:GLY:HA2	2:B:360:HOH:O	2.01	0.60
1:A:270:LYS:O	1:A:274:ASP:HB2	2.02	0.60
1:A:152:ILE:HD11	1:A:156:ASN:ND2	2.17	0.60
1:A:165:MET:HE2	1:A:225:VAL:HG11	1.84	0.60
1:A:309:LEU:O	1:A:313:LYS:HG3	2.02	0.60
1:B:94:MET:HG3	1:B:157:ASP:HB3	1.84	0.60
1:A:260:SER:O	1:A:264:GLU:HG3	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:PRO:HD3	2:A:390:HOH:O	2.02	0.59
1:B:60:LEU:HG	2:B:341:HOH:O	2.01	0.59
1:B:83:ILE:O	1:B:240:ARG:HD3	2.00	0.59
1:A:95:GLU:O	1:A:99:ALA:HB2	2.02	0.59
1:B:110:VAL:HG23	1:B:237:THR:O	2.02	0.59
1:B:270:LYS:HA	1:B:274:ASP:OD2	2.01	0.59
1:B:151:GLY:HA3	1:B:159:ASN:ND2	2.16	0.59
1:A:290:PRO:HA	2:A:368:HOH:O	2.02	0.59
1:B:308:GLY:O	1:B:312:VAL:HG23	2.02	0.59
1:B:133:LYS:HA	2:B:328:HOH:O	2.03	0.59
1:A:189:GLN:HE21	1:A:189:GLN:HA	1.66	0.59
1:A:302:THR:HG22	1:A:306:GLY:H	1.67	0.59
1:A:254:LEU:HD22	2:A:350:HOH:O	2.02	0.58
1:B:309:LEU:O	1:B:313:LYS:HG3	2.02	0.58
1:A:145:LEU:HD22	1:A:200:ILE:HA	1.86	0.58
1:A:284:ALA:HB3	2:A:400:HOH:O	2.03	0.58
1:B:52:THR:O	1:B:56:ILE:HG13	2.03	0.58
1:A:142:LYS:CD	1:B:192:ARG:HH21	2.17	0.58
1:A:159:ASN:N	1:A:159:ASN:HD22	2.00	0.58
1:A:141:HIS:HA	1:A:144:GLU:OE2	2.03	0.58
1:B:70:SER:HB2	2:B:327:HOH:O	2.03	0.58
1:B:114:LEU:HB3	1:B:235:VAL:HB	1.85	0.57
1:A:281:ALA:HA	2:A:400:HOH:O	2.04	0.57
1:B:170:THR:HG22	1:B:171:PHE:CD1	2.39	0.57
1:A:132:ILE:HG22	1:A:219:LEU:HD21	1.86	0.57
1:A:185:GLY:O	1:A:188:ALA:HB3	2.03	0.57
1:B:119:TYR:CD1	1:B:205:TRP:HB3	2.39	0.57
1:B:110:VAL:HG21	1:B:239:VAL:HG13	1.85	0.57
1:A:162:ILE:HA	2:A:337:HOH:O	2.04	0.56
1:B:67:LYS:HA	2:B:364:HOH:O	2.05	0.56
1:B:119:TYR:HD1	1:B:205:TRP:HB3	1.68	0.56
1:B:60:LEU:HD21	1:B:308:GLY:HA2	1.87	0.56
1:B:53:ALA:HB3	2:B:396:HOH:O	2.06	0.56
1:B:288:ASP:HB3	2:B:352:HOH:O	2.05	0.56
1:A:154:PRO:HB2	2:A:399:HOH:O	2.05	0.56
1:A:130:LEU:HD23	1:A:199:PRO:HG3	1.87	0.56
1:B:134:ASP:HA	1:B:220:SER:O	2.06	0.56
1:A:310:ALA:HB3	2:A:369:HOH:O	2.05	0.56
1:B:293:ILE:HD12	1:B:312:VAL:CG1	2.36	0.56
1:A:312:VAL:O	1:A:316:LEU:HG	2.05	0.56
1:A:119:TYR:OH	1:A:203:LEU:HD13	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ASP:CA	1:A:160:ARG:HH11	2.19	0.55
1:B:60:LEU:HD13	1:B:301:ALA:O	2.06	0.55
1:B:142:LYS:HD2	2:B:399:HOH:O	2.06	0.55
1:A:126:LYS:O	1:A:129:GLU:HB3	2.06	0.55
1:A:38:PHE:HB2	1:A:66:VAL:HG22	1.88	0.55
1:A:138:ILE:HG21	1:A:173:LEU:HD21	1.88	0.55
1:A:145:LEU:HD13	2:A:429:HOH:O	2.07	0.55
1:A:191:ALA:O	1:A:194:GLU:HB2	2.06	0.55
1:B:86:PHE:HD2	1:B:238:ASN:HD22	1.55	0.55
1:B:112:GLU:HG3	1:B:236:HIS:CE1	2.41	0.55
1:A:233:ALA:HB1	2:A:370:HOH:O	2.06	0.55
1:B:161:LEU:HD22	1:B:225:VAL:CG1	2.36	0.55
1:B:36:VAL:HG21	1:B:57:LEU:HD13	1.89	0.55
1:B:29:GLU:OE1	1:B:33:CYS:HB3	2.07	0.54
1:A:94:MET:HG3	2:A:417:HOH:O	2.06	0.54
1:A:297:LEU:HD13	1:A:309:LEU:HA	1.89	0.54
1:A:308:GLY:HA2	2:A:336:HOH:O	2.06	0.54
1:B:157:ASP:HA	1:B:160:ARG:HH11	1.72	0.54
1:A:72:PRO:HD3	2:A:365:HOH:O	2.07	0.54
1:B:41:VAL:HA	1:B:69:LEU:O	2.08	0.54
1:A:312:VAL:CG1	1:A:316:LEU:HD21	2.38	0.54
1:A:210:MET:O	1:A:216:LEU:HD21	2.08	0.54
1:B:77:SER:HB2	1:B:83:ILE:HD12	1.89	0.54
1:A:98:ILE:HG12	1:A:98:ILE:O	2.08	0.53
1:A:300:VAL:O	1:A:308:GLY:HA3	2.08	0.53
1:A:301:ALA:HB1	1:A:306:GLY:O	2.08	0.53
1:B:239:VAL:HB	1:B:243:TYR:CB	2.39	0.53
1:B:270:LYS:O	1:B:274:ASP:HB2	2.08	0.53
1:A:50:THR:O	1:A:54:THR:HG23	2.08	0.53
1:A:52:THR:O	1:A:56:ILE:HG13	2.08	0.53
1:B:106:SER:O	1:B:107:VAL:HG23	2.07	0.53
1:B:138:ILE:CG2	1:B:173:LEU:HD21	2.37	0.53
1:B:242:GLY:O	1:B:245:THR:HG23	2.07	0.53
1:A:302:THR:HB	2:A:336:HOH:O	2.09	0.53
1:A:293:ILE:HD12	1:A:312:VAL:CG1	2.39	0.52
1:A:115:ALA:O	1:A:261:LEU:HD11	2.09	0.52
1:A:157:ASP:CB	1:A:160:ARG:HH11	2.22	0.52
1:A:186:MET:O	1:A:190:VAL:HG23	2.08	0.52
1:A:159:ASN:C	1:A:163:ILE:HD12	2.34	0.52
1:A:159:ASN:O	1:A:163:ILE:HD12	2.08	0.52
1:A:317:GLY:O	1:A:318:LEU:HB2	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:ILE:HG12	1:B:98:ILE:O	2.09	0.52
1:B:188:ALA:HB1	1:B:192:ARG:NH1	2.23	0.52
1:B:110:VAL:O	1:B:111:ARG:HB3	2.09	0.52
1:A:39:SER:HB2	1:A:83:ILE:HD13	1.91	0.52
1:A:121:LEU:HA	1:A:202:PHE:O	2.09	0.52
1:A:112:GLU:OE1	1:A:115:ALA:HB2	2.10	0.52
1:A:268:MET:HG3	2:A:341:HOH:O	2.09	0.52
1:A:67:LYS:HE3	2:A:372:HOH:O	2.09	0.52
1:B:108:GLU:HG2	2:B:392:HOH:O	2.09	0.52
1:A:78:LEU:CD2	1:A:83:ILE:HB	2.38	0.51
1:A:93:THR:HG23	2:A:335:HOH:O	2.10	0.51
1:B:94:MET:HA	1:B:160:ARG:HH12	1.73	0.51
1:A:157:ASP:HA	1:A:160:ARG:HH11	1.75	0.51
1:A:89:ASN:HB2	1:A:238:ASN:ND2	2.24	0.51
1:B:60:LEU:HD11	1:B:300:VAL:HG12	1.93	0.51
1:A:302:THR:HG23	1:A:304:ASP:N	2.18	0.51
1:B:228:PRO:O	1:B:229:ASN:HB2	2.10	0.51
1:A:165:MET:HB2	2:A:337:HOH:O	2.09	0.51
1:A:257:LEU:HD22	1:A:259:PHE:CE2	2.45	0.51
1:B:79:LYS:HG3	1:B:106:SER:OG	2.10	0.51
1:B:70:SER:OG	1:B:72:PRO:HD2	2.11	0.51
1:A:114:LEU:HD11	1:A:261:LEU:HD12	1.93	0.50
1:B:152:ILE:HG22	1:B:183:GLU:N	2.27	0.50
1:B:293:ILE:O	1:B:297:LEU:HD12	2.10	0.50
1:A:142:LYS:HD2	1:B:192:ARG:NH2	2.24	0.50
1:B:100:PRO:O	1:B:104:ASP:OD2	2.29	0.50
1:B:135:PHE:HE2	1:B:165:MET:HE1	1.77	0.50
1:B:145:LEU:HD21	1:B:199:PRO:HB2	1.93	0.50
1:B:253:LEU:O	1:B:257:LEU:HB2	2.12	0.50
1:A:60:LEU:HD11	1:A:300:VAL:HG12	1.93	0.50
1:A:162:ILE:HG23	2:A:337:HOH:O	2.11	0.50
1:A:250:VAL:O	1:A:254:LEU:HG	2.11	0.50
1:B:132:ILE:CD1	1:B:145:LEU:HD11	2.42	0.50
1:B:261:LEU:HD12	1:B:261:LEU:H	1.76	0.50
1:A:114:LEU:HB3	1:A:235:VAL:HG23	1.94	0.50
1:B:186:MET:HE1	2:B:410:HOH:O	2.12	0.50
1:B:269:GLY:O	1:B:273:ASN:HB2	2.12	0.50
1:B:114:LEU:HD23	1:B:235:VAL:CG2	2.41	0.50
1:A:124:ASN:HB3	2:A:356:HOH:O	2.11	0.49
1:B:46:ILE:HD13	2:B:367:HOH:O	2.12	0.49
1:B:153:GLU:O	1:B:159:ASN:OD1	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:ARG:NH2	1:A:258:SER:HB3	2.27	0.49
1:B:101:TYR:HA	1:B:104:ASP:OD2	2.11	0.49
1:B:146:ASP:OD1	1:B:146:ASP:O	2.30	0.49
1:A:219:LEU:HD23	2:A:420:HOH:O	2.11	0.49
1:A:166:VAL:HG22	1:A:173:LEU:HB3	1.93	0.49
1:A:252:LYS:NZ	1:A:255:GLN:HE21	2.10	0.49
1:B:174:LYS:N	2:B:360:HOH:O	2.44	0.49
1:A:30:PRO:HD2	1:A:33:CYS:SG	2.52	0.49
1:B:157:ASP:HA	1:B:160:ARG:NH1	2.28	0.49
1:B:301:ALA:HB1	1:B:306:GLY:O	2.12	0.49
1:A:44:THR:OG1	1:A:183:GLU:OE2	2.29	0.49
1:A:287:LYS:HG2	1:A:316:LEU:O	2.13	0.48
1:B:142:LYS:H	1:B:142:LYS:HG2	1.45	0.48
1:B:39:SER:HB2	1:B:83:ILE:HD13	1.94	0.48
1:A:71:VAL:O	1:A:74:THR:HB	2.13	0.48
1:A:138:ILE:CG2	1:A:173:LEU:HD21	2.43	0.48
1:A:264:GLU:O	1:A:268:MET:HG3	2.13	0.48
1:A:238:ASN:ND2	2:A:357:HOH:O	2.46	0.48
1:A:284:ALA:O	1:A:288:ASP:HB2	2.13	0.48
1:B:287:LYS:HG2	1:B:316:LEU:HB2	1.96	0.48
1:A:252:LYS:HZ2	1:A:255:GLN:HE21	1.61	0.48
1:B:43:TRP:HD1	2:B:400:HOH:O	1.94	0.48
1:B:271:ILE:O	1:B:275:GLY:HA2	2.14	0.48
1:A:110:VAL:O	1:A:111:ARG:HB3	2.14	0.48
1:A:37:ARG:NH1	1:A:81:LYS:O	2.47	0.48
1:B:31:GLU:HB2	2:B:370:HOH:O	2.12	0.48
1:B:93:THR:HG23	2:B:350:HOH:O	2.14	0.47
1:A:94:MET:N	2:A:417:HOH:O	2.47	0.47
1:A:259:PHE:HD2	1:A:263:MET:HE1	1.79	0.47
1:B:173:LEU:N	2:B:360:HOH:O	2.46	0.47
1:A:112:GLU:HG3	1:A:236:HIS:CE1	2.49	0.47
1:A:263:MET:HG3	1:A:285:TRP:CH2	2.49	0.47
1:B:71:VAL:HG23	2:B:327:HOH:O	2.14	0.47
1:A:163:ILE:HD11	2:A:396:HOH:O	2.15	0.47
1:A:202:PHE:HE2	2:A:356:HOH:O	1.96	0.47
1:A:312:VAL:HG12	1:A:316:LEU:HD21	1.95	0.47
1:B:95:GLU:N	2:B:408:HOH:O	2.48	0.47
1:B:208:HIS:HD2	1:B:210:MET:HB3	1.78	0.47
1:A:43:TRP:HA	1:A:183:GLU:OE1	2.14	0.47
1:A:114:LEU:HD23	1:A:235:VAL:HG21	1.96	0.47
1:B:78:LEU:HB3	2:B:384:HOH:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:ARG:NH1	2:B:356:HOH:O	2.47	0.47
1:B:252:LYS:HD2	1:B:255:GLN:NE2	2.30	0.47
1:B:43:TRP:HB2	1:B:45:ASP:OD1	2.15	0.47
1:B:72:PRO:HD3	1:B:155:GLY:O	2.15	0.47
1:B:73:VAL:CA	1:B:76:THR:HB	2.43	0.47
1:A:135:PHE:CE2	1:A:222:GLY:HA3	2.50	0.47
1:A:189:GLN:HA	1:A:192:ARG:HG3	1.96	0.47
1:A:293:ILE:O	1:A:297:LEU:HG	2.15	0.47
1:B:87:LEU:HD23	1:B:259:PHE:HZ	1.79	0.47
1:A:45:ASP:O	1:A:49:THR:HG23	2.14	0.46
1:A:298:SER:O	1:A:298:SER:OG	2.29	0.46
1:A:150:TYR:CE2	1:A:189:GLN:HG2	2.50	0.46
1:A:157:ASP:N	1:A:157:ASP:OD1	2.48	0.46
1:B:126:LYS:HE2	1:B:197:GLY:O	2.16	0.46
1:A:46:ILE:HD12	1:A:46:ILE:O	2.16	0.46
1:A:309:LEU:HD21	1:A:313:LYS:NZ	2.31	0.46
1:B:99:ALA:H	1:B:100:PRO:HD2	1.80	0.46
1:A:40:ASP:O	1:A:68:VAL:HA	2.14	0.46
1:A:94:MET:O	1:A:98:ILE:HG22	2.15	0.46
1:A:243:TYR:OH	1:A:250:VAL:HG11	2.14	0.46
1:B:32:SER:N	2:B:370:HOH:O	2.48	0.46
1:B:121:LEU:HD12	1:B:135:PHE:CE2	2.50	0.46
1:B:310:ALA:HA	1:B:313:LYS:HE3	1.97	0.46
1:A:187:LEU:HA	1:A:190:VAL:HG23	1.98	0.46
1:A:269:GLY:O	1:A:273:ASN:HB2	2.16	0.46
1:A:118:LYS:O	1:A:205:TRP:HA	2.16	0.46
1:A:309:LEU:HD21	1:A:313:LYS:HZ1	1.80	0.46
1:B:108:GLU:OE2	1:B:242:GLY:HA2	2.15	0.46
1:B:162:ILE:HD11	1:B:203:LEU:CD2	2.36	0.46
1:B:170:THR:O	1:B:171:PHE:HB2	2.15	0.46
1:B:35:THR:HA	1:B:63:GLU:O	2.15	0.46
1:B:40:ASP:OD2	1:B:47:THR:OG1	2.30	0.46
1:A:149:ILE:HD12	1:A:162:ILE:HG23	1.98	0.45
1:B:145:LEU:CD2	1:B:199:PRO:HB2	2.45	0.45
1:B:215:LYS:HD2	1:B:215:LYS:HA	1.77	0.45
1:B:234:THR:HG22	2:B:373:HOH:O	2.16	0.45
1:A:141:HIS:ND1	1:A:144:GLU:OE2	2.49	0.45
1:B:208:HIS:HB3	1:B:210:MET:HG2	1.97	0.45
1:A:294:GLU:HA	1:A:309:LEU:HD13	1.99	0.45
1:B:30:PRO:HD2	1:B:33:CYS:SG	2.57	0.45
1:A:71:VAL:O	1:A:74:THR:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:TRP:O	1:A:94:MET:HB2	2.17	0.45
1:A:271:ILE:O	1:A:275:GLY:HA2	2.16	0.45
1:B:84:ASP:HB3	1:B:243:TYR:CZ	2.52	0.45
1:B:167:GLU:HG2	2:B:381:HOH:O	2.17	0.45
1:A:170:THR:O	1:A:171:PHE:HB2	2.17	0.45
1:A:254:LEU:HB3	2:A:350:HOH:O	2.17	0.45
1:A:302:THR:HB	2:A:416:HOH:O	2.16	0.45
1:B:144:GLU:OE2	1:B:144:GLU:N	2.50	0.45
1:A:138:ILE:N	2:A:408:HOH:O	2.50	0.45
1:A:293:ILE:HD13	1:A:316:LEU:HD11	1.99	0.45
1:B:290:PRO:C	1:B:293:ILE:HG23	2.41	0.45
1:A:149:ILE:O	1:A:178:VAL:HA	2.17	0.45
1:A:170:THR:HG22	1:A:171:PHE:CD1	2.51	0.45
1:A:194:GLU:HA	2:A:329:HOH:O	2.16	0.45
1:B:293:ILE:HD12	1:B:312:VAL:HG12	1.98	0.45
1:B:223:ASP:OD1	1:B:228:PRO:HA	2.18	0.44
1:A:38:PHE:HD2	2:A:383:HOH:O	2.00	0.44
1:A:235:VAL:HB	2:A:331:HOH:O	2.17	0.44
1:B:110:VAL:CG2	1:B:239:VAL:HG13	2.47	0.44
1:B:117:ALA:HB1	1:B:206:GLU:O	2.16	0.44
1:B:294:GLU:HG3	1:B:309:LEU:HD11	1.98	0.44
1:A:181:SER:O	1:A:182:SER:HB3	2.18	0.44
1:A:186:MET:HE2	1:A:186:MET:HB3	1.82	0.44
1:B:37:ARG:O	1:B:83:ILE:HG23	2.17	0.44
1:B:44:THR:OG1	1:B:272:LEU:HD11	2.18	0.44
1:B:89:ASN:ND2	2:B:332:HOH:O	2.50	0.44
1:B:289:ASN:O	1:B:292:SER:OG	2.33	0.44
1:B:147:GLY:N	2:B:389:HOH:O	2.50	0.44
1:B:148:LYS:HB3	1:B:179:VAL:CG2	2.47	0.44
1:B:257:LEU:HD22	1:B:259:PHE:CE2	2.51	0.44
1:B:294:GLU:O	1:B:297:LEU:N	2.50	0.44
1:A:293:ILE:HD12	1:A:312:VAL:HG11	1.98	0.44
1:B:316:LEU:H	1:B:316:LEU:HG	1.53	0.44
1:A:70:SER:N	2:A:371:HOH:O	2.50	0.44
1:A:208:HIS:HB3	1:A:210:MET:HG2	1.99	0.44
1:B:111:ARG:NH2	1:B:112:GLU:O	2.50	0.44
1:A:252:LYS:HA	1:A:252:LYS:HD2	1.72	0.44
1:B:269:GLY:O	1:B:273:ASN:N	2.51	0.44
1:A:71:VAL:HG23	2:A:365:HOH:O	2.17	0.44
1:B:114:LEU:HB3	1:B:235:VAL:CG2	2.48	0.44
1:A:190:VAL:O	1:A:194:GLU:N	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:PHE:HB3	1:B:238:ASN:HB2	1.99	0.43
1:B:142:LYS:O	1:B:146:ASP:N	2.51	0.43
1:A:43:TRP:HB2	1:A:46:ILE:HG22	2.00	0.43
1:B:254:LEU:HA	1:B:257:LEU:HB2	2.00	0.43
1:B:152:ILE:HD11	1:B:156:ASN:ND2	2.33	0.43
1:B:163:ILE:HG22	1:B:164:ASP:N	2.33	0.43
1:B:187:LEU:O	1:B:190:VAL:HB	2.18	0.43
1:B:188:ALA:CB	1:B:192:ARG:HH12	2.26	0.43
1:B:302:THR:HG23	1:B:304:ASP:H	1.82	0.43
1:A:139:ALA:HB3	2:A:389:HOH:O	2.18	0.43
1:B:213:ASN:N	1:B:213:ASN:HD22	2.17	0.43
1:A:62:TYR:OH	1:A:249:ASN:ND2	2.50	0.43
1:A:251:ASP:O	1:A:255:GLN:HG3	2.18	0.43
1:B:126:LYS:O	1:B:129:GLU:HB3	2.19	0.43
1:B:254:LEU:HD23	1:B:257:LEU:HD12	2.00	0.43
1:A:110:VAL:HG23	1:A:237:THR:O	2.19	0.43
1:A:73:VAL:HA	1:A:76:THR:HB	1.99	0.43
1:B:207:PRO:HB2	1:B:268:MET:HE1	2.00	0.43
1:A:113:ASN:O	1:A:259:PHE:N	2.50	0.43
1:A:187:LEU:HA	1:A:190:VAL:CG2	2.49	0.43
1:A:261:LEU:HD12	1:A:261:LEU:N	2.33	0.43
1:B:97:ASP:OD2	1:B:160:ARG:NH1	2.52	0.43
1:B:287:LYS:NZ	1:B:316:LEU:HB3	2.34	0.43
1:B:287:LYS:CE	1:B:316:LEU:HB3	2.49	0.43
1:B:297:LEU:CD1	1:B:312:VAL:HG21	2.49	0.43
1:A:58:GLU:HG2	1:A:64:THR:HG23	2.01	0.43
1:B:84:ASP:HA	1:B:240:ARG:CG	2.32	0.43
1:B:126:LYS:HB2	2:B:346:HOH:O	2.19	0.42
1:B:287:LYS:O	1:B:290:PRO:HD3	2.19	0.42
1:A:107:VAL:O	1:A:107:VAL:HG12	2.18	0.42
1:A:163:ILE:HG22	1:A:164:ASP:N	2.33	0.42
1:B:99:ALA:HB3	1:B:100:PRO:HD3	2.02	0.42
1:B:247:CYS:HB3	1:B:250:VAL:HG12	2.01	0.42
1:A:81:LYS:HZ3	1:A:240:ARG:HH11	1.66	0.42
1:A:87:LEU:HG	1:A:237:THR:HG23	2.01	0.42
1:B:263:MET:HA	1:B:285:TRP:CZ2	2.54	0.42
1:A:138:ILE:HD11	1:A:201:VAL:HG11	2.01	0.42
1:A:302:THR:HG23	1:A:303:LYS:N	2.33	0.42
1:B:75:TYR:HB3	1:B:101:TYR:CE1	2.55	0.42
1:A:57:LEU:CD2	1:A:250:VAL:HG23	2.50	0.42
1:B:138:ILE:HD11	1:B:219:LEU:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:LYS:HG3	2:B:372:HOH:O	2.19	0.42
1:A:142:LYS:HZ2	1:B:189:GLN:NE2	2.17	0.42
1:B:46:ILE:HA	1:B:49:THR:OG1	2.20	0.42
1:B:79:LYS:HD2	1:B:101:TYR:HE2	1.84	0.42
1:B:43:TRP:HE1	1:B:153:GLU:CD	2.27	0.42
1:B:302:THR:HG23	1:B:303:LYS:N	2.33	0.42
1:A:142:LYS:O	1:A:147:GLY:N	2.53	0.42
1:B:240:ARG:HA	2:B:384:HOH:O	2.20	0.42
1:B:90:TRP:O	1:B:94:MET:HB2	2.19	0.42
1:B:70:SER:HB3	2:B:357:HOH:O	2.20	0.41
1:B:222:GLY:HA3	2:B:342:HOH:O	2.20	0.41
1:A:160:ARG:O	1:A:163:ILE:HB	2.20	0.41
1:B:85:VAL:HG12	1:B:87:LEU:HD12	2.01	0.41
1:B:114:LEU:HB3	1:B:235:VAL:CB	2.50	0.41
1:A:267:ILE:O	1:A:270:LYS:HB2	2.19	0.41
1:A:288:ASP:C	1:A:290:PRO:HD3	2.45	0.41
1:B:94:MET:HG3	1:B:157:ASP:CB	2.48	0.41
1:B:108:GLU:CD	1:B:241:ALA:O	2.63	0.41
1:A:318:LEU:HD22	1:A:318:LEU:HA	1.89	0.41
1:B:139:ALA:HB1	1:B:172:ASP:O	2.20	0.41
1:A:92:PRO:HG3	2:A:391:HOH:O	2.19	0.41
1:A:206:GLU:HG2	1:A:211:ASN:HD21	1.84	0.41
1:B:94:MET:CG	1:B:157:ASP:HB3	2.50	0.41
1:B:196:SER:HB2	1:B:198:ASP:OD2	2.21	0.41
1:A:60:LEU:HD21	1:A:308:GLY:HA2	2.02	0.41
1:A:69:LEU:CD1	1:A:83:ILE:HD11	2.50	0.41
1:A:229:ASN:O	1:A:230:TYR:HB2	2.20	0.41
1:A:261:LEU:HD12	1:A:261:LEU:H	1.86	0.41
1:A:294:GLU:HG3	1:A:309:LEU:HD11	2.02	0.41
1:B:252:LYS:HA	1:B:255:GLN:CD	2.46	0.41
1:A:283:ALA:O	1:A:287:LYS:HG3	2.21	0.41
1:A:77:SER:HB3	1:A:83:ILE:HG13	2.02	0.40
1:A:81:LYS:NZ	1:A:240:ARG:HH11	2.19	0.40
1:A:106:SER:HA	1:A:241:ALA:HB2	2.03	0.40
1:A:165:MET:HE3	2:A:337:HOH:O	2.21	0.40
1:A:202:PHE:HD1	1:A:203:LEU:O	2.03	0.40
1:B:57:LEU:HD22	1:B:62:TYR:CD1	2.56	0.40
1:B:173:LEU:O	1:B:176:PHE:HB2	2.21	0.40
1:A:83:ILE:HG22	1:A:84:ASP:N	2.37	0.40
1:A:142:LYS:HD2	1:B:192:ARG:HE	1.85	0.40
1:B:152:ILE:HB	1:B:153:GLU:H	1.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:MET:O	1:B:216:LEU:HD21	2.20	0.40
1:A:85:VAL:HG12	1:A:87:LEU:HD12	2.03	0.40
1:B:261:LEU:HD12	1:B:261:LEU:N	2.34	0.40
1:A:312:VAL:HG13	1:A:316:LEU:HD21	2.03	0.40
1:B:120:THR:HG23	1:B:121:LEU:O	2.20	0.40
1:A:67:LYS:HG3	2:A:340:HOH:O	2.21	0.40
1:A:68:VAL:N	2:A:344:HOH:O	2.50	0.40
1:A:289:ASN:O	1:A:292:SER:OG	2.29	0.40
1:B:110:VAL:HG22	1:B:239:VAL:HG22	2.02	0.40
1:B:186:MET:HE2	1:B:186:MET:HB3	1.77	0.40
1:B:292:SER:C	1:B:295:PRO:HD2	2.47	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	288/298 (97%)	268 (93%)	17 (6%)	3 (1%)	12   8
1	B	287/298 (96%)	266 (93%)	17 (6%)	4 (1%)	9   4
All	All	575/596 (96%)	534 (93%)	34 (6%)	7 (1%)	10   6

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	241	ALA
1	A	152	ILE
1	B	181	SER
1	B	70	SER
1	B	152	ILE
1	A	181	SER
1	A	30	PRO

### 5.3.2 Protein sidechains [i](#)

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	232/240 (97%)	182 (78%)	50 (22%)	1	0
1	B	231/240 (96%)	191 (83%)	40 (17%)	2	1
All	All	463/480 (96%)	373 (81%)	90 (19%)	1	1

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	GLU
1	A	32	SER
1	A	36	VAL
1	A	37	ARG
1	A	46	ILE
1	A	52	THR
1	A	60	LEU
1	A	67	LYS
1	A	69	LEU
1	A	74	THR
1	A	105	LYS
1	A	107	VAL
1	A	108	GLU
1	A	110	VAL
1	A	112	GLU
1	A	126	LYS
1	A	130	LEU
1	A	133	LYS
1	A	142	LYS
1	A	152	ILE
1	A	153	GLU
1	A	159	ASN
1	A	163	ILE
1	A	167	GLU
1	A	168	LYS
1	A	174	LYS
1	A	189	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	190	VAL
1	A	192	ARG
1	A	195	LYS
1	A	215	LYS
1	A	216	LEU
1	A	235	VAL
1	A	244	THR
1	A	245	THR
1	A	252	LYS
1	A	253	LEU
1	A	257	LEU
1	A	258	SER
1	A	262	GLN
1	A	263	MET
1	A	266	GLU
1	A	288	ASP
1	A	291	GLN
1	A	293	ILE
1	A	298	SER
1	A	302	THR
1	A	313	LYS
1	A	316	LEU
1	A	318	LEU
1	B	32	SER
1	B	36	VAL
1	B	37	ARG
1	B	47	THR
1	B	52	THR
1	B	60	LEU
1	B	67	LYS
1	B	69	LEU
1	B	74	THR
1	B	77	SER
1	B	94	MET
1	B	105	LYS
1	B	110	VAL
1	B	126	LYS
1	B	130	LEU
1	B	132	ILE
1	B	133	LYS
1	B	142	LYS
1	B	163	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	167	GLU
1	B	174	LYS
1	B	179	VAL
1	B	192	ARG
1	B	195	LYS
1	B	196	SER
1	B	215	LYS
1	B	216	LEU
1	B	244	THR
1	B	245	THR
1	B	252	LYS
1	B	253	LEU
1	B	257	LEU
1	B	262	GLN
1	B	263	MET
1	B	266	GLU
1	B	293	ILE
1	B	294	GLU
1	B	302	THR
1	B	313	LYS
1	B	316	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	89	ASN
1	A	159	ASN
1	A	184	GLN
1	A	189	GLN
1	A	211	ASN
1	A	213	ASN
1	A	238	ASN
1	A	255	GLN
1	A	262	GLN
1	A	289	ASN
1	A	291	GLN
1	B	159	ASN
1	B	189	GLN
1	B	208	HIS
1	B	213	ASN
1	B	238	ASN
1	B	262	GLN

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Mol	Chain	Res	Type
1	B	273	ASN
1	B	289	ASN
1	B	291	GLN

### 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](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	225:VAL	C	226:PHE	N	1.06
1	B	226:PHE	C	227:GLY	N	0.88

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	290/298 (97%)	0.81	14 (4%) 35 34	10, 22, 33, 41	0
1	B	289/298 (96%)	1.00	28 (9%) 13 12	12, 25, 36, 46	0
All	All	579/596 (97%)	0.90	42 (7%) 21 19	10, 23, 36, 46	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	302	THR	4.2
1	A	301	ALA	4.2
1	B	59	ALA	4.0
1	B	292	SER	3.4
1	A	305	GLY	3.2
1	B	283	ALA	3.2
1	B	296	TRP	3.1
1	B	36	VAL	3.1
1	B	288	ASP	3.0
1	A	296	TRP	3.0
1	B	122	ALA	2.9
1	A	245	THR	2.8
1	A	290	PRO	2.8
1	A	193	ALA	2.8
1	B	83	ILE	2.7
1	B	228	PRO	2.6
1	B	247	CYS	2.6
1	B	284	ALA	2.6
1	B	163	ILE	2.5
1	B	54	THR	2.5
1	B	32	SER	2.4
1	B	114	LEU	2.4
1	B	66	VAL	2.4
1	A	235	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	217	THR	2.4
1	B	128	ALA	2.3
1	A	316	LEU	2.3
1	B	169	GLY	2.3
1	A	259	PHE	2.3
1	B	98	ILE	2.3
1	B	100	PRO	2.3
1	B	290	PRO	2.3
1	B	307	ASP	2.2
1	A	256	ASN	2.2
1	B	30	PRO	2.2
1	A	163	ILE	2.1
1	B	99	ALA	2.1
1	B	227	GLY	2.1
1	B	85	VAL	2.1
1	A	30	PRO	2.1
1	B	293	ILE	2.1
1	A	306	GLY	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.