WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 12:52 AM GMT

PDB ID	:	2C1C
Title	:	Structural basis of the resistance of an insect carboxypeptidase to plant protease inhibitors
Authors	:	Bayes, A.; Comellas-Bigler, M.; Rodriguez de la Vega, M.; Maskos, K.; Bode, W.; Aviles, F.X.; Jongsma, M.A.; Beekwilder, J.; Vendrell, J.
Deposited on	:	2005-09-12
Resolution	:	2.30 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
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 (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	Percentile Ranks	Value
Clashscore		25
Ramachandran outliers		0.6%
Sidechain outliers		5.6%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
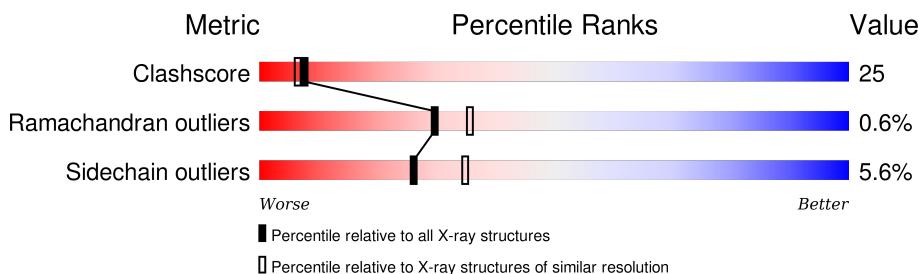
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)

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 <=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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	312	57% 39% •
1	B	312	60% 36% •
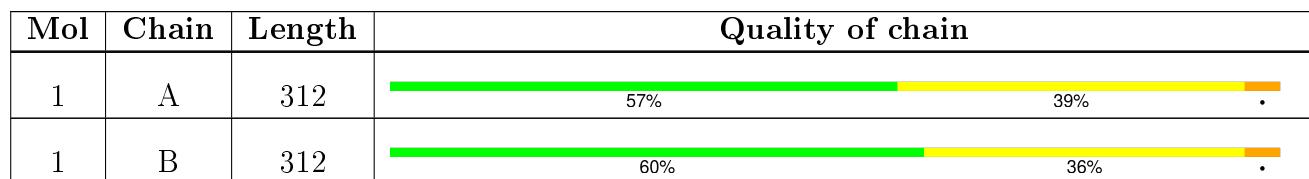
2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5255 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 CARBOXYPEPTIDASE B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	312	Total	C	N	O	S	0	0	0
			2455	1573	405	470	7			
1	B	312	Total	C	N	O	S	0	0	0
			2449	1573	402	467	7			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is YTTRIUM ION (three-letter code: Y1) (formula: Y).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Y	0	0
			1	1		
3	A	1	Total	Y	0	0
			1	1		

- Molecule 4 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	171	Total	O	0	0
			171	171		
4	B	176	Total	O	0	0
			176	176		

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.

Note EDS was not executed.

- Molecule 1: CARBOXYPEPTIDASE B
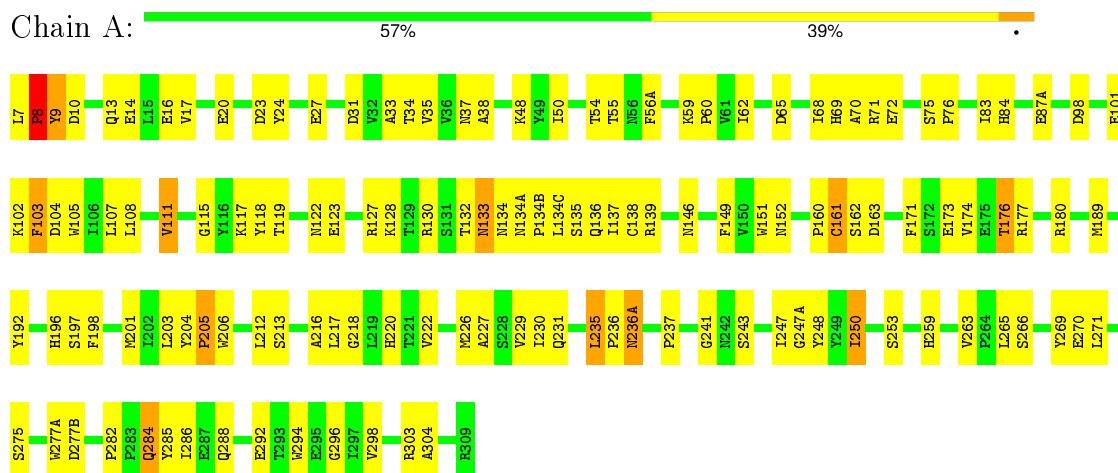
- Molecule 1: CARBOXYPEPTIDASE B
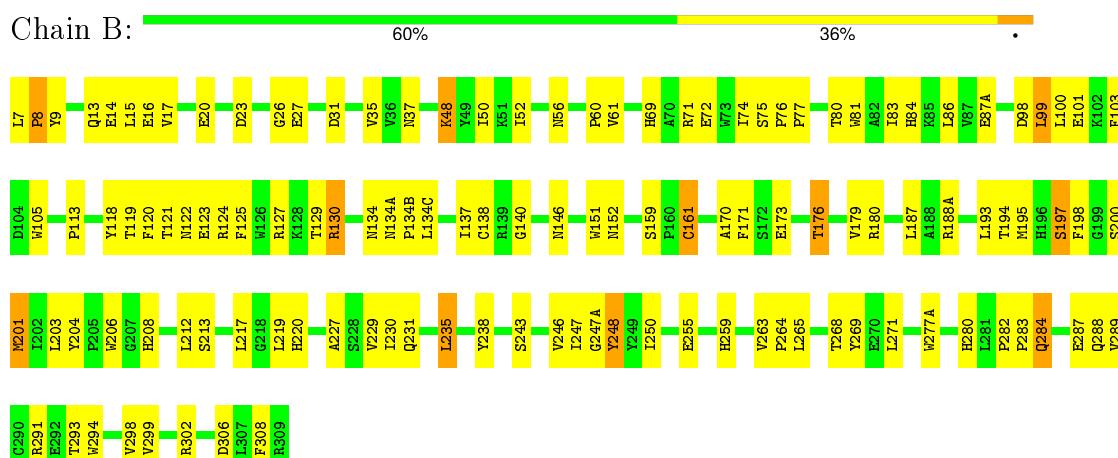
4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	42.01Å　　58.34Å　　146.56Å 90.00°　　89.87°　　90.00°	Depositor
Resolution (Å)	20.00　–　2.30	Depositor
% Data completeness (in resolution range)	91.4 (20.00-2.30)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.215　,　0.292	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5255	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: Y1, ZN

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	0.48	0/2528	0.72	2/3453 (0.1%)
1	B	0.44	0/2520	0.72	0/3442
All	All	0.46	0/5048	0.72	2/6895 (0.0%)

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	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	205	PRO	O-C-N	-6.69	111.99	122.70
1	A	9	TYR	N-CA-C	-5.20	96.95	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	248	TYR	Sidechain

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	2455	0	2306	136	59
1	B	2449	0	2305	105	57
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	171	0	0	38	5
4	B	176	0	0	23	5
All	All	5255	0	4611	241	103

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 25.

All (241) 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:123:GLU:CD	4:B:2074:HOH:O	1.74	1.24
1:A:160:PRO:HG2	4:A:2095:HOH:O	1.11	1.23
1:A:102:LYS:HG3	4:A:2060:HOH:O	1.46	1.13
1:A:23:ASP:OD1	4:A:2026:HOH:O	1.69	1.10
1:A:220:HIS:HB3	4:A:2134:HOH:O	1.50	1.09
1:A:160:PRO:CG	4:A:2095:HOH:O	1.73	1.08
1:A:37:ASN:HD21	1:A:48:LYS:HE2	1.26	0.98
1:A:102:LYS:CA	4:A:2060:HOH:O	2.09	0.98
1:A:160:PRO:CB	4:A:2095:HOH:O	1.97	0.97
1:A:23:ASP:CG	4:A:2026:HOH:O	1.98	0.97
1:B:16:GLU:OE2	4:B:2013:HOH:O	1.81	0.96
1:A:235:LEU:HD22	1:A:288:GLN:HG2	1.47	0.95
1:A:102:LYS:N	4:A:2060:HOH:O	2.02	0.92
1:A:203:LEU:HD11	1:A:247:ILE:HD13	1.51	0.92
1:A:23:ASP:OD2	4:A:2026:HOH:O	1.86	0.91
1:A:162:SER:C	4:A:2094:HOH:O	2.09	0.91
1:A:138:CYS:CB	4:A:2095:HOH:O	2.18	0.91
1:A:284:GLN:H	1:A:284:GLN:HE21	1.19	0.88
1:B:171:PHE:HD2	1:B:176:THR:HG23	1.40	0.87
1:A:236(A):ASN:H	1:A:236(A):ASN:HD22	1.13	0.87
1:A:102:LYS:HA	4:A:2060:HOH:O	1.73	0.84
1:A:68:ILE:HA	1:A:111:VAL:HG22	1.59	0.82
1:A:250:ILE:HD11	1:A:253:SER:HB3	1.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:170:ALA:HA	4:B:2093:HOH:O	1.81	0.80
1:B:227:ALA:O	1:B:231:GLN:HG2	1.81	0.80
1:B:284:GLN:H	1:B:284:GLN:HE21	1.29	0.80
1:A:37:ASN:ND2	1:A:48:LYS:HE2	1.99	0.78
1:B:20:GLU:CG	4:B:2014:HOH:O	2.29	0.78
1:A:171:PHE:HD2	1:A:176:THR:HG23	1.49	0.77
1:A:54:THR:C	4:A:2033:HOH:O	2.24	0.76
1:A:236(A):ASN:HD22	1:A:236(A):ASN:N	1.85	0.75
1:B:171:PHE:CD2	1:B:176:THR:HG23	2.24	0.73
1:A:284:GLN:H	1:A:284:GLN:NE2	1.88	0.71
1:B:7:LEU:O	1:B:8:PRO:N	2.24	0.70
1:B:8:PRO:HB3	4:B:2003:HOH:O	1.92	0.70
1:A:160:PRO:C	4:A:2095:HOH:O	2.29	0.70
1:A:235:LEU:HB3	1:A:236(A):ASN:ND2	2.07	0.70
1:A:72:GLU:HG2	1:A:197:SER:OG	1.91	0.70
1:B:284:GLN:H	1:B:284:GLN:NE2	1.90	0.69
1:A:216:ALA:O	4:A:2134:HOH:O	2.09	0.69
1:A:213:SER:OG	1:A:259:HIS:HE1	1.76	0.69
1:A:138:CYS:HB2	4:A:2095:HOH:O	1.84	0.69
1:B:231:GLN:HE22	1:B:238:TYR:H	1.40	0.69
1:A:236(A):ASN:H	1:A:236(A):ASN:ND2	1.90	0.68
1:B:69:HIS:CE1	1:B:127:ARG:HH21	2.11	0.68
1:B:171:PHE:HA	1:B:176:THR:HG21	1.75	0.68
1:B:98:ASP:CG	1:B:302:ARG:HH12	1.96	0.68
1:B:98:ASP:OD1	1:B:302:ARG:NH1	2.27	0.67
1:A:133:ASN:HD22	1:A:134(A):ASN:H	1.43	0.67
1:B:75:SER:HB3	1:B:76:PRO:HD3	1.77	0.67
1:B:229:VAL:HG21	1:B:299:VAL:HG21	1.77	0.67
1:A:275:SER:HB2	1:A:277(B):ASP:HB2	1.76	0.66
1:A:294:TRP:O	1:A:298:VAL:HG23	1.96	0.66
1:A:161:CYS:O	4:A:2094:HOH:O	2.12	0.66
1:B:23:ASP:O	1:B:27:GLU:HG3	1.96	0.66
1:A:212:LEU:HD12	1:A:212:LEU:N	2.10	0.66
1:B:123:GLU:OE2	4:B:2074:HOH:O	1.97	0.65
1:B:20:GLU:HG3	4:B:2014:HOH:O	1.94	0.64
1:A:160:PRO:CA	4:A:2095:HOH:O	2.40	0.64
1:B:74:ILE:HG22	4:B:2044:HOH:O	1.98	0.63
1:A:173:GLU:O	1:A:176:THR:HG22	1.99	0.63
1:A:220:HIS:CB	4:A:2134:HOH:O	2.26	0.62
1:B:302:ARG:HH11	1:B:302:ARG:HG2	1.64	0.62
1:B:287:GLU:O	1:B:291:ARG:HG3	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:THR:HA	1:A:123:GLU:O	1.98	0.62
1:A:84:HIS:CD2	1:A:87(A):GLU:HB2	2.35	0.61
1:A:247:ILE:HG23	1:A:248:TYR:CE2	2.36	0.61
1:A:55:THR:N	4:A:2033:HOH:O	2.33	0.61
1:B:72:GLU:HB3	1:B:197:SER:HB3	1.83	0.61
1:A:56(A):PHE:HA	1:A:104:ASP:OD2	2.01	0.61
1:A:205:PRO:HB3	1:A:206:TRP:CE3	2.36	0.60
1:B:306:ASP:OD1	4:B:2176:HOH:O	0.61	0.60
1:B:130:ARG:NH1	4:B:2085:HOH:O	2.31	0.60
1:B:20:GLU:CB	4:B:2018:HOH:O	2.49	0.60
1:A:171:PHE:CD2	1:A:176:THR:HG23	2.34	0.60
1:A:235:LEU:HB3	1:A:236(A):ASN:HD21	1.65	0.60
1:A:102:LYS:CG	4:A:2060:HOH:O	2.19	0.60
1:A:177:ARG:HG2	1:A:180:ARG:CZ	2.32	0.59
1:B:37:ASN:OD1	1:B:48:LYS:HE3	2.02	0.59
1:A:250:ILE:HD13	1:A:250:ILE:O	2.03	0.59
1:B:213:SER:OG	1:B:259:HIS:HE1	1.85	0.59
1:B:7:LEU:O	1:B:7:LEU:HD23	2.02	0.59
1:B:171:PHE:HD2	1:B:176:THR:CG2	2.14	0.59
1:B:7:LEU:O	1:B:8:PRO:C	2.42	0.58
1:A:68:ILE:HG21	1:A:196:HIS:CE1	2.38	0.58
1:B:201:MET:CE	1:B:246:VAL:HG12	2.33	0.58
1:A:220:HIS:CD2	4:A:2123:HOH:O	2.56	0.58
1:B:134:ASN:CB	4:B:2089:HOH:O	2.52	0.58
1:A:59:LYS:HD3	4:A:2037:HOH:O	2.02	0.57
1:A:204:TYR:OH	1:A:220:HIS:HD2	1.86	0.57
1:B:259:HIS:HD2	1:B:263:VAL:O	1.87	0.57
1:B:231:GLN:NE2	1:B:238:TYR:H	2.01	0.57
1:A:133:ASN:HD21	1:A:134(A):ASN:HB2	1.69	0.56
1:A:226:MET:O	1:A:230:ILE:HG12	2.05	0.56
1:A:83:ILE:HG12	1:A:107:LEU:HD13	1.87	0.56
1:A:174:VAL:HG12	4:A:2109:HOH:O	2.05	0.56
1:A:7:LEU:N	1:A:8:PRO:HD2	2.22	0.55
1:B:146:ASN:HA	4:B:2093:HOH:O	2.06	0.55
1:A:230:ILE:HD11	1:A:296:GLY:HA3	1.89	0.55
1:A:133:ASN:ND2	1:A:134(A):ASN:HB2	2.21	0.55
1:B:23:ASP:OD1	1:B:48:LYS:NZ	2.35	0.55
1:B:271:LEU:HD22	1:B:293:THR:HG21	1.89	0.55
1:A:71:ARG:NH1	1:A:277(A):TRP:HZ3	2.04	0.54
1:A:235:LEU:CD2	1:A:288:GLN:HG2	2.30	0.54
1:A:33:ALA:HB1	1:A:50:ILE:HD11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:TYR:OH	1:A:220:HIS:CD2	2.60	0.54
1:A:226:MET:O	1:A:229:VAL:HG12	2.08	0.54
1:B:193:LEU:HB3	1:B:195:MET:CE	2.39	0.53
1:A:247:ILE:HG23	1:A:248:TYR:CD2	2.43	0.53
1:A:231:GLN:OE1	1:A:237:PRO:HA	2.08	0.53
1:B:294:TRP:O	1:B:298:VAL:HG23	2.08	0.53
1:B:171:PHE:HA	1:B:176:THR:CG2	2.37	0.53
1:A:34:THR:C	1:A:50:ILE:HD12	2.29	0.53
1:B:248:TYR:CE1	1:B:250:ILE:HD11	2.44	0.53
1:B:171:PHE:CE2	1:B:180:ARG:HB2	2.44	0.53
1:A:230:ILE:HG23	1:A:292:GLU:HG3	1.90	0.53
1:B:284:GLN:N	1:B:284:GLN:HE21	2.03	0.52
1:A:160:PRO:HB2	4:A:2095:HOH:O	1.84	0.52
1:A:162:SER:O	4:A:2094:HOH:O	2.17	0.52
1:A:69:HIS:CE1	1:A:127:ARG:HH11	2.28	0.52
1:A:68:ILE:HA	1:A:111:VAL:CG2	2.35	0.52
1:B:203:LEU:HB3	1:B:243:SER:HA	1.92	0.52
1:A:60:PRO:HG2	1:A:103:PHE:HD2	1.74	0.52
1:A:68:ILE:CG2	1:A:196:HIS:CE1	2.93	0.51
1:A:284:GLN:N	1:A:284:GLN:HE21	1.98	0.51
1:B:151:TRP:NE1	4:B:2093:HOH:O	2.35	0.51
1:B:203:LEU:HB2	1:B:268:THR:CG2	2.40	0.51
1:A:146:ASN:OD1	1:A:176:THR:HG21	2.11	0.51
1:A:177:ARG:HG2	1:A:180:ARG:NH2	2.26	0.51
1:A:75:SER:HB3	1:A:76:PRO:HD3	1.92	0.51
1:B:20:GLU:HB2	4:B:2018:HOH:O	2.10	0.50
1:A:201:MET:SD	1:A:247:ILE:HD12	2.51	0.50
1:B:20:GLU:HB2	4:B:2014:HOH:O	2.10	0.50
1:A:203:LEU:CD1	1:A:247:ILE:HD13	2.34	0.50
1:A:127:ARG:HD3	1:A:163:ASP:HB3	1.93	0.50
1:B:14:GLU:HG2	1:B:120:PHE:CD1	2.46	0.50
1:B:8:PRO:HA	4:B:2001:HOH:O	2.12	0.50
1:B:204:TYR:OH	1:B:220:HIS:HD2	1.95	0.50
1:B:20:GLU:CB	4:B:2014:HOH:O	2.59	0.50
1:A:171:PHE:HA	1:A:176:THR:HG21	1.94	0.49
1:B:201:MET:HE1	1:B:246:VAL:HG12	1.94	0.49
1:A:24:TYR:HB2	4:A:2013:HOH:O	2.12	0.49
1:A:196:HIS:HB2	1:A:270:GLU:OE1	2.12	0.49
1:B:248:TYR:HE1	1:B:250:ILE:HD11	1.77	0.49
1:B:80:THR:HA	1:B:83:ILE:HD12	1.94	0.49
1:A:68:ILE:HG21	1:A:196:HIS:HE1	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:SER:CB	1:A:277(B):ASP:HB2	2.43	0.49
1:A:220:HIS:HD2	4:A:2123:HOH:O	1.92	0.49
1:B:230:ILE:HG21	1:B:238:TYR:CE1	2.48	0.49
1:A:132:THR:HG22	1:A:135:SER:O	2.12	0.49
1:A:265:LEU:HD12	1:A:304:ALA:CB	2.43	0.49
1:B:101:GLU:OE1	4:B:2062:HOH:O	0.49	0.48
1:A:34:THR:O	1:A:50:ILE:HD12	2.13	0.48
1:B:229:VAL:HG12	1:B:229:VAL:O	2.13	0.48
1:B:302:ARG:HD2	4:B:2170:HOH:O	2.13	0.48
1:B:119:THR:HA	1:B:123:GLU:O	2.14	0.47
1:A:35:VAL:CG2	1:A:50:ILE:HD13	2.43	0.47
1:A:68:ILE:HG22	4:A:2120:HOH:O	2.14	0.47
1:A:212:LEU:HB3	1:A:216:ALA:HB2	1.96	0.47
1:B:86:LEU:O	1:B:100:LEU:HD11	2.14	0.47
1:A:138:CYS:HB3	4:A:2095:HOH:O	1.98	0.47
1:A:213:SER:CB	1:A:259:HIS:HE1	2.28	0.47
1:A:222:VAL:O	1:A:226:MET:HG3	2.15	0.47
1:A:171:PHE:HA	1:A:176:THR:CG2	2.45	0.47
1:B:125:PHE:CE2	1:B:277(A):TRP:HB3	2.49	0.47
1:B:84:HIS:CD2	1:B:87(A):GLU:HB2	2.49	0.47
1:A:37:ASN:ND2	1:A:48:LYS:HG2	2.30	0.47
1:B:231:GLN:HE22	1:B:238:TYR:N	2.09	0.47
1:B:248:TYR:CD2	1:B:248:TYR:N	2.83	0.47
1:B:134(A):ASN:ND2	1:B:134(A):ASN:N	2.63	0.47
1:A:117:LYS:HA	4:A:2007:HOH:O	2.14	0.46
1:A:23:ASP:O	1:A:27:GLU:HG3	2.15	0.46
1:B:204:TYR:OH	1:B:220:HIS:CD2	2.69	0.46
1:B:60:PRO:HB3	1:B:308:PHE:CD2	2.50	0.46
1:B:201:MET:HE2	1:B:246:VAL:HG12	1.96	0.46
1:A:71:ARG:NH1	1:A:277(A):TRP:CZ3	2.83	0.46
1:B:235:LEU:HD13	1:B:288:GLN:CD	2.35	0.46
1:A:101:GLU:C	4:A:2060:HOH:O	2.49	0.46
1:A:212:LEU:N	1:A:212:LEU:CD1	2.77	0.46
1:A:69:HIS:CE1	1:A:127:ARG:NH1	2.84	0.46
1:B:130:ARG:HD3	4:B:2087:HOH:O	2.15	0.46
1:B:134(A):ASN:ND2	1:B:134(A):ASN:H	2.13	0.46
1:A:48:LYS:O	1:A:108:LEU:HD12	2.15	0.45
1:B:193:LEU:HB3	1:B:195:MET:HE1	1.98	0.45
1:A:241:GLY:HA2	4:A:2123:HOH:O	2.17	0.45
1:A:192:TYR:O	1:A:266:SER:HA	2.17	0.45
1:B:61:VAL:HG23	1:B:188(A):ARG:NH1	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:GLU:OE1	4:B:2074:HOH:O	2.09	0.45
1:A:37:ASN:HD21	1:A:48:LYS:CE	2.13	0.45
1:B:213:SER:CB	1:B:259:HIS:HE1	2.29	0.44
1:B:121:THR:OG1	1:B:122:ASN:ND2	2.51	0.44
1:A:8:PRO:C	1:A:10:ASP:H	2.14	0.44
1:B:134(A):ASN:HD22	1:B:134(A):ASN:N	2.16	0.44
1:A:189:MET:HE1	1:A:263:VAL:HG21	1.99	0.44
1:A:161:CYS:N	4:A:2095:HOH:O	2.48	0.44
1:B:71:ARG:NH1	1:B:277(A):TRP:HZ3	2.14	0.44
1:A:31:ASP:HA	4:A:2018:HOH:O	2.17	0.44
1:B:206:TRP:HB3	1:B:208:HIS:CE1	2.53	0.44
1:A:282:PRO:HB2	1:A:285:TYR:CD1	2.52	0.43
1:A:128:LYS:HE3	1:A:139:ARG:O	2.18	0.43
1:A:220:HIS:N	4:A:2134:HOH:O	2.51	0.43
1:A:70:ALA:HB1	1:A:115:GLY:O	2.18	0.43
1:B:268:THR:HG23	1:B:268:THR:O	2.19	0.43
1:A:149:PHE:C	1:A:151:TRP:N	2.71	0.43
1:B:197:SER:HA	1:B:198:PHE:HA	1.87	0.43
1:B:200:SER:C	1:B:201:MET:HG3	2.39	0.43
1:A:62:ILE:HG21	1:A:105:TRP:CZ3	2.54	0.43
1:B:151:TRP:CE3	1:B:152:ASN:HB2	2.54	0.43
1:B:129:THR:O	1:B:140:GLY:HA3	2.19	0.43
1:A:65:ASP:OD2	1:A:65:ASP:C	2.57	0.43
1:A:198:PHE:HA	1:A:271:LEU:O	2.19	0.42
1:B:15:LEU:HD21	1:B:113:PRO:HB2	2.01	0.42
1:B:194:THR:HG23	1:B:268:THR:HA	2.01	0.42
1:B:9:TYR:N	1:B:9:TYR:CD1	2.87	0.42
1:B:146:ASN:OD1	1:B:173:GLU:HG2	2.20	0.42
1:A:203:LEU:HB3	1:A:243:SER:HA	2.02	0.42
1:A:98:ASP:HB2	1:A:102:LYS:HD2	2.00	0.42
1:A:9:TYR:O	1:A:286:ILE:HB	2.20	0.42
1:B:219:LEU:HD23	1:B:265:LEU:HD23	2.02	0.41
1:B:264:PRO:HB2	4:B:2042:HOH:O	2.19	0.41
1:B:52:ILE:HB	1:B:105:TRP:HB2	2.02	0.41
1:A:133:ASN:ND2	1:A:134(A):ASN:ND2	2.68	0.41
1:B:282:PRO:HA	1:B:283:PRO:HD3	1.76	0.41
1:A:119:THR:HA	4:A:2078:HOH:O	2.20	0.41
1:A:7:LEU:O	1:A:8:PRO:C	2.59	0.41
1:B:99:LEU:HG	1:B:105:TRP:HZ2	1.86	0.41
1:A:68:ILE:CA	1:A:111:VAL:HG22	2.40	0.41
1:B:99:LEU:HG	1:B:105:TRP:CZ2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:LEU:HA	1:A:236:PRO:HD3	1.93	0.41
1:B:289:VAL:O	1:B:293:THR:HG23	2.19	0.41
1:A:35:VAL:HG23	1:A:50:ILE:HD13	2.03	0.40
1:B:194:THR:O	1:B:194:THR:HG23	2.21	0.40
1:B:69:HIS:CE1	1:B:127:ARG:NH2	2.85	0.40
1:B:81:TRP:O	1:B:84:HIS:HB3	2.20	0.40
1:A:222:VAL:HG22	1:A:303:ARG:HB3	2.03	0.40
1:A:235:LEU:HD22	1:A:288:GLN:CG	2.35	0.40
1:B:76:PRO:HB2	1:B:77:PRO:HD3	2.03	0.40
1:B:26:GLY:HA3	1:B:35:VAL:HG23	2.03	0.40
1:A:227:ALA:O	1:A:231:GLN:HG2	2.21	0.40
1:A:60:PRO:HG2	1:A:103:PHE:CD2	2.56	0.40
1:B:124:ARG:HH21	1:B:280:HIS:CD2	2.39	0.40

All (103) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:TYR:CE1	4:A:2011:HOH:O[2_556]	0.30	1.90
1:A:217:LEU:CD2	1:B:212:LEU:CD2[2_555]	0.66	1.54
1:B:31:ASP:OD2	1:B:248:TYR:CA[1_565]	0.70	1.50
1:A:8:PRO:CG	1:A:134(B):PRO:CB[2_546]	0.79	1.41
1:A:31:ASP:OD1	1:A:248:TYR:CA[1_545]	0.84	1.36
1:A:13:GLN:CD	1:A:134(C):LEU:CD1[2_546]	0.92	1.28
1:A:217:LEU:CG	1:B:212:LEU:CD2[2_555]	0.95	1.25
1:A:8:PRO:CG	1:A:134(B):PRO:CA[2_546]	0.98	1.22
1:B:13:GLN:CD	1:B:134(C):LEU:CD1[2_555]	1.01	1.19
1:B:17:VAL:CG1	1:B:137:ILE:CB[2_555]	1.18	1.02
1:A:212:LEU:CD2	1:B:217:LEU:CB[2_555]	1.23	0.97
1:A:17:VAL:CG1	1:A:137:ILE:CB[2_546]	1.27	0.93
1:B:13:GLN:NE2	1:B:134(C):LEU:CD1[2_555]	1.34	0.86
1:B:134(B):PRO:CG	4:B:2003:HOH:O[2_545]	1.35	0.85
1:A:217:LEU:CD2	1:B:212:LEU:CG[2_555]	1.39	0.81
1:B:20:GLU:OE1	1:B:130:ARG:CZ[2_555]	1.42	0.78
1:A:13:GLN:OE1	1:A:134(C):LEU:CD1[2_546]	1.42	0.78
1:A:13:GLN:NE2	1:A:134(C):LEU:CD1[2_546]	1.45	0.75
1:A:17:VAL:CG2	1:A:138:CYS:SG[2_546]	1.46	0.74
1:B:17:VAL:CG2	1:B:138:CYS:SG[2_555]	1.49	0.71
1:B:7:LEU:CG	1:B:137:ILE:CD1[2_555]	1.50	0.70
1:B:13:GLN:OE1	1:B:134(C):LEU:CD1[2_555]	1.51	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:GLU:CD	1:B:130:ARG:NH2[2_555]	1.52	0.68
1:A:31:ASP:OD1	1:A:248:TYR:N[1_545]	1.55	0.65
1:B:20:GLU:OE1	1:B:130:ARG:NH2[2_555]	1.56	0.64
1:B:13:GLN:OE1	1:B:134(C):LEU:CG[2_555]	1.56	0.64
1:A:13:GLN:OE1	1:A:134(C):LEU:CG[2_546]	1.56	0.64
1:A:118:TYR:CD1	4:A:2011:HOH:O[2_556]	1.56	0.64
1:A:20:GLU:OE2	1:A:130:ARG:NH1[2_546]	1.62	0.58
1:A:212:LEU:CG	1:B:217:LEU:CD2[2_555]	1.63	0.57
1:A:17:VAL:CG2	1:A:138:CYS:CB[2_546]	1.64	0.56
1:A:8:PRO:CB	1:A:134(B):PRO:CB[2_546]	1.65	0.55
1:B:31:ASP:OD2	1:B:248:TYR:CB[1_565]	1.66	0.54
1:A:17:VAL:CG1	1:A:137:ILE:CA[2_546]	1.66	0.54
1:B:20:GLU:OE1	1:B:130:ARG:NH1[2_555]	1.67	0.53
1:B:14:GLU:CD	1:B:159:SER:OG[2_555]	1.67	0.53
1:B:31:ASP:OD2	1:B:248:TYR:N[1_565]	1.67	0.53
1:B:17:VAL:CG1	1:B:137:ILE:CA[2_555]	1.67	0.53
1:B:134(B):PRO:CB	4:B:2003:HOH:O[2_545]	1.68	0.52
1:B:14:GLU:OE1	1:B:159:SER:OG[2_555]	1.69	0.51
1:A:17:VAL:CG1	1:A:137:ILE:C[2_546]	1.75	0.45
1:A:20:GLU:CD	1:A:130:ARG:NH1[2_546]	1.75	0.45
4:B:2017:HOH:O	4:B:2074:HOH:O[2_555]	1.76	0.44
1:B:17:VAL:CG2	1:B:138:CYS:CB[2_555]	1.76	0.44
1:A:212:LEU:CG	1:B:217:LEU:CB[2_555]	1.76	0.44
1:B:17:VAL:CG1	1:B:137:ILE:C[2_555]	1.77	0.43
1:A:14:GLU:CB	1:A:161:CYS:CB[2_546]	1.78	0.42
1:A:20:GLU:OE2	1:A:130:ARG:CZ[2_546]	1.78	0.42
4:B:2022:HOH:O	4:B:2087:HOH:O[2_555]	1.79	0.41
1:B:23:ASP:OD2	1:B:118:TYR:OH[2_555]	1.79	0.41
1:A:31:ASP:CG	1:A:248:TYR:CA[1_545]	1.80	0.40
1:B:7:LEU:CD2	1:B:137:ILE:CD1[2_555]	1.80	0.40
1:B:7:LEU:CG	1:B:137:ILE:CG1[2_555]	1.82	0.38
1:B:17:VAL:CB	1:B:137:ILE:CG2[2_555]	1.83	0.37
1:A:212:LEU:CG	1:B:217:LEU:CG[2_555]	1.84	0.36
1:B:17:VAL:CG1	1:B:137:ILE:CG2[2_555]	1.84	0.36
1:B:8:PRO:CB	1:B:134(B):PRO:CB[2_555]	1.85	0.35
1:A:17:VAL:CG1	1:A:138:CYS:N[2_546]	1.85	0.35
1:A:7:LEU:N	1:A:136:GLN:CG[2_546]	1.86	0.34
1:A:118:TYR:CZ	4:A:2011:HOH:O[2_556]	1.89	0.31
1:A:8:PRO:CG	1:A:134(B):PRO:CG[2_546]	1.92	0.28
1:B:31:ASP:CG	1:B:248:TYR:CA[1_565]	1.92	0.28
1:A:220:HIS:ND1	1:B:220:HIS:ND1[2_555]	1.93	0.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:16:GLU:OE1	1:B:161:CYS:O[2_555]	1.93	0.27
1:B:8:PRO:CD	1:B:134(B):PRO:O[2_555]	1.98	0.22
1:A:17:VAL:CG1	1:A:137:ILE:CG2[2_546]	1.99	0.21
1:A:8:PRO:CB	1:A:134(B):PRO:C[2_546]	1.99	0.21
1:B:17:VAL:CG1	1:B:138:CYS:N[2_555]	1.99	0.21
1:A:27:GLU:OE1	1:A:122:ASN:ND2[2_546]	2.00	0.20
1:A:31:ASP:OD1	1:A:248:TYR:C[1_545]	2.00	0.20
1:A:17:VAL:CB	1:A:137:ILE:CG2[2_546]	2.01	0.19
1:A:217:LEU:CG	1:B:212:LEU:CG[2_555]	2.02	0.18
1:A:212:LEU:CD2	1:B:217:LEU:CA[2_555]	2.02	0.18
1:A:220:HIS:CE1	1:B:220:HIS:ND1[2_555]	2.02	0.18
1:B:20:GLU:CG	1:B:130:ARG:NH2[2_555]	2.03	0.17
1:A:8:PRO:CD	1:A:134(B):PRO:CB[2_546]	2.03	0.17
1:B:20:GLU:OE2	1:B:118:TYR:OH[2_555]	2.03	0.17
1:A:8:PRO:CG	1:A:134(B):PRO:C[2_546]	2.04	0.16
1:A:217:LEU:CB	1:B:212:LEU:CD1[2_555]	2.05	0.15
1:B:8:PRO:CG	1:B:134(B):PRO:O[2_555]	2.06	0.14
1:A:17:VAL:CG2	1:A:138:CYS:CA[2_546]	2.06	0.14
1:A:220:HIS:ND1	1:B:220:HIS:CE1[2_555]	2.07	0.13
1:B:13:GLN:CD	1:B:134(C):LEU:CG[2_555]	2.07	0.13
1:A:13:GLN:CD	1:A:134(C):LEU:CG[2_546]	2.08	0.12
1:A:13:GLN:CG	1:A:134(C):LEU:CD1[2_546]	2.09	0.11
1:A:16:GLU:OE1	1:A:161:CYS:O[2_546]	2.11	0.09
1:A:218:GLY:N	1:B:212:LEU:CD1[2_555]	2.11	0.09
4:A:2008:HOH:O	4:A:2027:HOH:O[2_546]	2.11	0.09
1:B:20:GLU:OE2	4:B:2074:HOH:O[2_555]	2.12	0.08
1:A:137:ILE:CD1	4:A:2049:HOH:O[2_556]	2.12	0.08
1:A:8:PRO:CG	1:A:134(B):PRO:N[2_546]	2.12	0.08
1:A:217:LEU:CD1	1:B:212:LEU:CD2[2_555]	2.13	0.07
1:A:20:GLU:OE2	1:A:130:ARG:NH2[2_546]	2.13	0.07
1:B:17:VAL:CA	1:B:137:ILE:O[2_555]	2.14	0.06
1:B:31:ASP:OD2	1:B:247(A):GLY:C[1_565]	2.14	0.06
1:A:217:LEU:CB	1:B:212:LEU:CD2[2_555]	2.14	0.06
1:A:23:ASP:OD2	1:A:118:TYR:OH[2_546]	2.18	0.02
1:A:20:GLU:OE1	1:A:118:TYR:OH[2_546]	2.18	0.02
1:B:8:PRO:CG	1:B:134(B):PRO:CB[2_555]	2.18	0.02
1:B:8:PRO:CG	1:B:134(B):PRO:CA[2_555]	2.18	0.02
1:A:31:ASP:OD1	1:A:247(A):GLY:C[1_545]	2.18	0.02
1:B:17:VAL:CG2	1:B:138:CYS:CA[2_555]	2.19	0.01
1:A:13:GLN:CG	1:A:137:ILE:CD1[2_546]	2.19	0.01

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	310/312 (99%)	289 (93%)	18 (6%)	3 (1%)	19	21
1	B	309/312 (99%)	281 (91%)	27 (9%)	1 (0%)	46	57
All	All	619/624 (99%)	570 (92%)	45 (7%)	4 (1%)	30	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	PRO
1	A	38	ALA
1	B	56	ASN
1	A	134	ASN

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	261/269 (97%)	249 (95%)	12 (5%)	33	44
1	B	259/269 (96%)	242 (93%)	17 (7%)	21	27
All	All	520/538 (97%)	491 (94%)	29 (6%)	26	35

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	PRO
1	A	103	PHE

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Mol	Chain	Res	Type
1	A	111	VAL
1	A	133	ASN
1	A	152	ASN
1	A	161	CYS
1	A	176	THR
1	A	235	LEU
1	A	236(A)	ASN
1	A	250	ILE
1	A	269	TYR
1	A	284	GLN
1	B	8	PRO
1	B	48	LYS
1	B	50	ILE
1	B	99	LEU
1	B	103	PHE
1	B	130	ARG
1	B	161	CYS
1	B	176	THR
1	B	179	VAL
1	B	187	LEU
1	B	197	SER
1	B	201	MET
1	B	235	LEU
1	B	247	ILE
1	B	255	GLU
1	B	269	TYR
1	B	284	GLN

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

Mol	Chain	Res	Type
1	A	37	ASN
1	A	84	HIS
1	A	133	ASN
1	A	134(A)	ASN
1	A	152	ASN
1	A	158	ASN
1	A	220	HIS
1	A	236(A)	ASN
1	A	259	HIS
1	A	284	GLN
1	A	288	GLN

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Mol	Chain	Res	Type
1	B	84	HIS
1	B	122	ASN
1	B	134(A)	ASN
1	B	152	ASN
1	B	158	ASN
1	B	220	HIS
1	B	233	ASN
1	B	259	HIS
1	B	280	HIS
1	B	284	GLN
1	B	288	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates (i)

EDS was not executed - this section will therefore be empty.

6.4 Ligands (i)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers (i)

EDS was not executed - this section will therefore be empty.