Full wwPDB X-ray Structure Validation Report (i)

Aug 3, 2023 – 06:03 AM EDT

PDB ID	:	1I7X
Title	:	BETA-CATENIN/E-CADHERIN COMPLEX
Authors	:	Huber, A.H.; Weis, W.I.
Deposited on	:	2001-03-10
Resolution	:	3.00 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

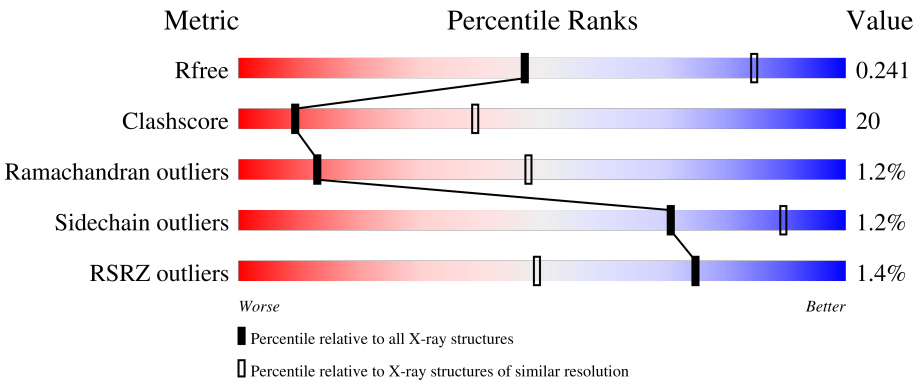
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.34
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.34

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 3.00 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))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 >=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 <=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	538	2% 64% 33%
1	C	538	62% 33%
2	B	151	2% 20% 16% 62%
2	D	151	% 25% 17% 58%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8930 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-CATENIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	522	3988	2503	723	736	26	0	0	0
1	C	521	3978	2500	721	731	26	0	0	0

- Molecule 2 is a protein called EPITHELIAL-CADHERIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	57	442	277	72	92	1	0	0	0
2	D	63	502	314	77	110	1	0	0	0

- Molecule 3 is water.

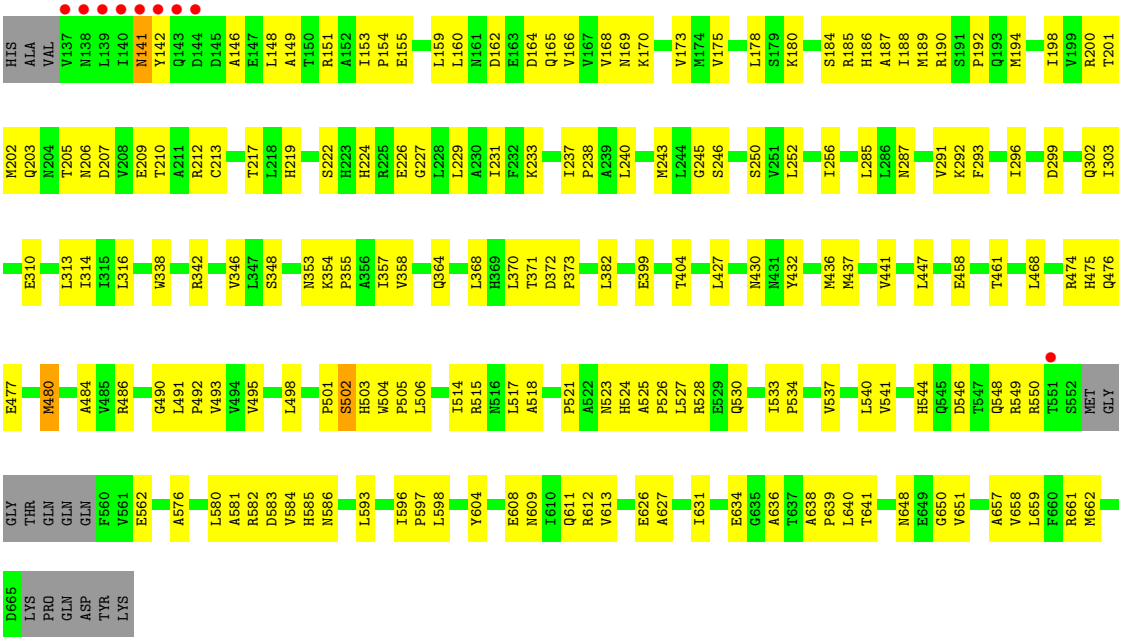
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	11	11	11	0	0
3	C	9	9	9	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

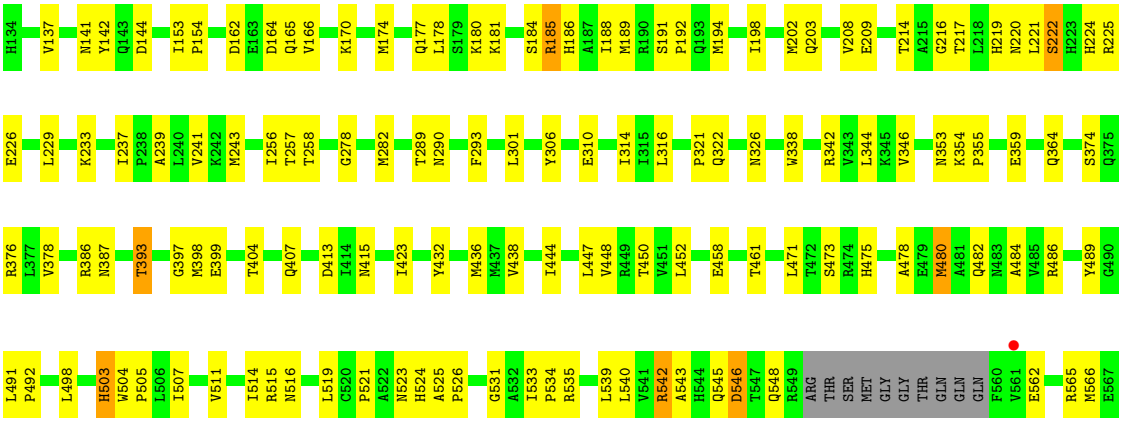
• Molecule 1: BETA-CATENIN

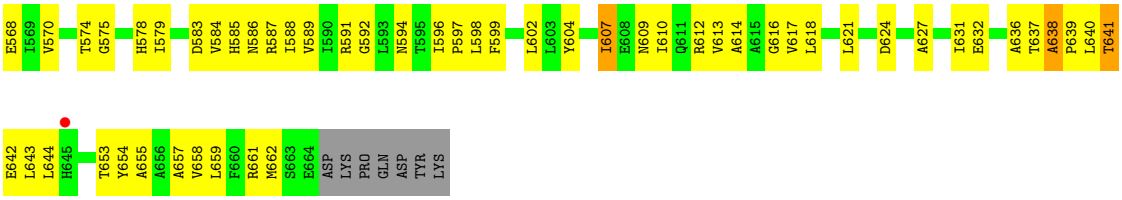
Chain A: 2% 64% 33%



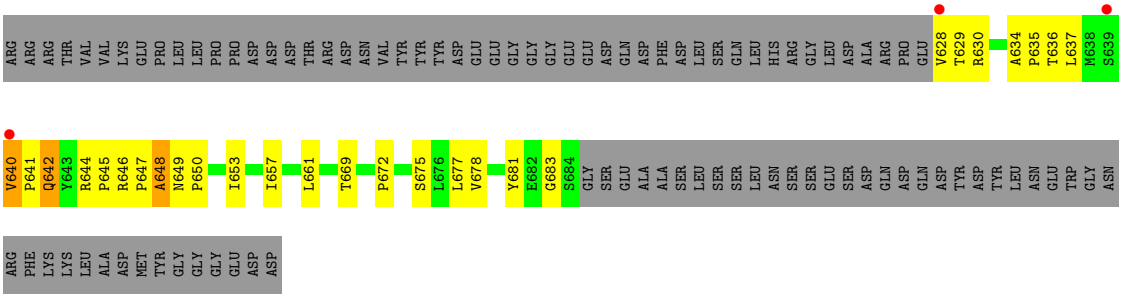
• Molecule 1: BETA-CATENIN

Chain C: 62% 33%

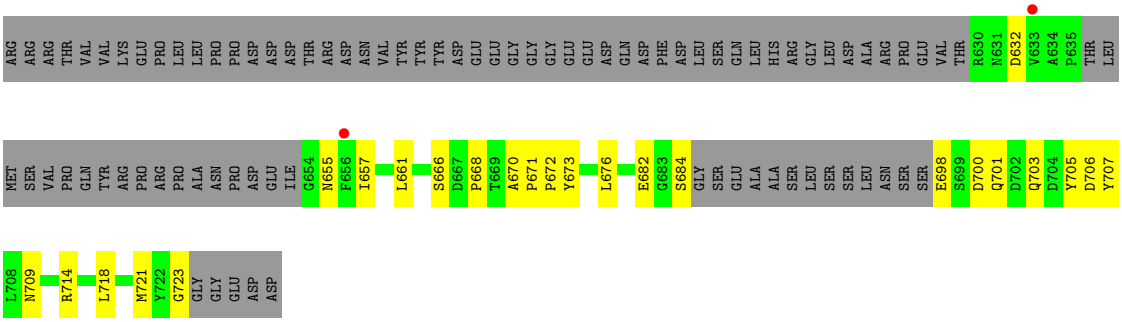




• Molecule 2: EPITHELIAL-CADHERIN



• Molecule 2: EPITHELIAL-CADHERIN



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	180.80Å 134.20Å 94.20Å 90.00° 94.30° 90.00°	Depositor
Resolution (Å)	30.00 – 3.00 29.71 – 2.99	Depositor EDS
% Data completeness (in resolution range)	94.5 (30.00-3.00) 94.0 (29.71-2.99)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.97 (at 3.00Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.196 , 0.242 0.194 , 0.241	Depositor DCC
R_{free} test set	3449 reflections (7.75%)	wwPDB-VP
Wilson B-factor (Å^2)	50.3	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 63.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	8930	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.34	0/4043	0.59	0/5487
1	C	0.34	0/4034	0.60	0/5476
2	B	0.36	0/454	0.63	0/624
2	D	0.32	0/513	0.52	0/695
All	All	0.34	0/9044	0.59	0/12282

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 (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	3988	0	4125	149	0
1	C	3978	0	4117	179	0
2	B	442	0	413	26	0
2	D	502	0	432	23	0
3	A	11	0	0	0	0
3	C	9	0	0	1	0
All	All	8930	0	9087	356	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 20.

All (356) 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:C:638:ALA:HB3	1:C:639:PRO:HD3	1.47	0.95
1:C:473:SER:HB3	1:C:516:ASN:ND2	1.82	0.95
1:C:637:THR:HA	1:C:659:LEU:HD21	1.52	0.91
2:D:632:ASP:OD1	2:D:673:TYR:HB2	1.70	0.91
1:C:583:ASP:HB3	1:C:586:ASN:HD22	1.36	0.90
1:A:229:LEU:HD11	1:A:233:LYS:HE3	1.56	0.87
1:C:583:ASP:HB3	1:C:586:ASN:ND2	1.91	0.85
1:C:640:LEU:HD11	1:C:655:ALA:HA	1.56	0.85
2:B:628:VAL:HG22	2:B:629:THR:H	1.41	0.85
1:C:637:THR:HG22	1:C:659:LEU:HD22	1.59	0.85
1:A:153:ILE:HB	1:A:154:PRO:HD3	1.61	0.82
1:A:165:GLN:HE21	1:A:169:ASN:HD21	1.26	0.80
1:C:219:HIS:O	1:C:222:SER:HB3	1.81	0.80
1:C:225:ARG:NH1	1:C:225:ARG:HB2	1.97	0.80
1:C:525:ALA:HB3	1:C:526:PRO:HD3	1.64	0.79
1:C:640:LEU:HD21	1:C:658:VAL:HB	1.65	0.78
2:B:640:VAL:H	2:B:641:PRO:CD	1.97	0.78
2:B:637:LEU:HD11	2:B:669:THR:CG2	2.14	0.77
1:C:189:MET:HG2	1:C:221:LEU:HD22	1.65	0.77
2:B:640:VAL:H	2:B:641:PRO:HD3	1.50	0.77
1:C:225:ARG:HB2	1:C:225:ARG:HH11	1.49	0.77
1:C:599:PHE:CZ	1:C:617:VAL:HG11	2.20	0.76
1:A:604:TYR:CE2	1:A:639:PRO:HB3	2.21	0.75
1:A:576:ALA:O	1:A:580:LEU:HB2	1.86	0.75
2:D:657:ILE:O	2:D:661:LEU:HB2	1.87	0.74
1:C:354:LYS:HB3	1:C:355:PRO:HD3	1.67	0.74
1:C:542:ARG:HE	1:C:542:ARG:HA	1.51	0.74
1:A:523:ASN:O	1:A:527:LEU:HB2	1.88	0.74
1:A:657:ALA:O	1:A:661:ARG:HG2	1.88	0.74
1:C:478:ALA:O	1:C:482:GLN:HG3	1.88	0.74
1:A:299:ASP:O	1:A:303:ILE:HG13	1.89	0.72
1:C:482:GLN:HE22	1:C:519:LEU:HB2	1.55	0.72
1:A:316:LEU:HD21	1:C:489:TYR:CE2	2.26	0.71
1:C:482:GLN:NE2	1:C:519:LEU:HB2	2.05	0.71
1:C:178:LEU:O	1:C:184:SER:HB2	1.90	0.70
1:C:185:ARG:NH1	1:C:224:HIS:NE2	2.41	0.69
1:A:458:GLU:HG2	1:A:506:LEU:HD22	1.74	0.69
1:C:153:ILE:HB	1:C:154:PRO:HD3	1.75	0.69
1:C:637:THR:HA	1:C:659:LEU:CD2	2.22	0.69
1:C:613:VAL:O	1:C:617:VAL:HG23	1.92	0.69
1:C:654:TYR:O	1:C:658:VAL:HG23	1.94	0.68
2:B:628:VAL:HG22	2:B:629:THR:N	2.09	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:GLU:HA	1:A:212:ARG:HG2	1.77	0.65
1:C:473:SER:HB3	1:C:516:ASN:HD22	1.61	0.65
1:A:190:ARG:O	1:A:192:PRO:HD3	1.97	0.64
1:A:188:ILE:HG23	1:A:194:MET:CG	2.28	0.64
1:A:474:ARG:HG3	1:A:474:ARG:HH11	1.62	0.64
2:B:628:VAL:HG13	2:B:629:THR:N	2.13	0.64
1:A:166:VAL:HG12	1:A:170:LYS:HE3	1.81	0.63
1:C:507:ILE:O	1:C:511:VAL:HG23	1.99	0.62
1:C:584:VAL:HG22	1:C:587:ARG:HH12	1.63	0.62
1:A:474:ARG:HG3	1:A:474:ARG:NH1	2.14	0.62
1:C:607:ILE:HD12	1:C:610:ILE:HD12	1.81	0.62
1:C:609:ASN:HD22	2:D:671:PRO:HG2	1.64	0.62
1:A:178:LEU:O	1:A:184:SER:HB2	2.00	0.61
1:A:212:ARG:HH12	1:A:250:SER:CB	2.13	0.61
1:C:202:MET:HB2	1:C:214:THR:HB	1.83	0.61
1:A:169:ASN:O	1:A:173:VAL:HG23	2.00	0.61
2:B:650:PRO:HA	2:B:653:ILE:HG13	1.81	0.61
1:C:584:VAL:HA	1:C:587:ARG:NH1	2.15	0.61
1:A:480:MET:HE2	1:A:484:ALA:HB2	1.81	0.61
1:C:604:TYR:CE1	1:C:639:PRO:HG2	2.35	0.61
1:A:185:ARG:HD2	1:A:224:HIS:NE2	2.17	0.60
1:C:208:VAL:HG23	1:C:209:GLU:H	1.67	0.60
1:C:338:TRP:CE2	1:C:376:ARG:HD2	2.37	0.59
1:A:165:GLN:HE21	1:A:169:ASN:ND2	1.99	0.59
1:A:515:ARG:HG2	1:A:515:ARG:HH11	1.67	0.59
1:A:437:MET:O	1:A:441:VAL:HG22	2.03	0.59
1:C:282:MET:HB2	1:C:301:LEU:HD21	1.84	0.59
1:C:542:ARG:HE	1:C:542:ARG:CA	2.15	0.59
1:C:316:LEU:HD13	1:C:321:PRO:HG2	1.85	0.59
1:C:578:HIS:CD2	1:C:616:GLY:HA3	2.37	0.59
1:A:153:ILE:CB	1:A:154:PRO:HD3	2.33	0.59
1:A:515:ARG:HD3	2:B:672:PRO:HD3	1.84	0.58
1:C:491:LEU:HB2	1:C:492:PRO:HD3	1.85	0.58
1:A:141:ASN:HD22	1:A:142:TYR:N	2.01	0.58
1:A:188:ILE:HG23	1:A:194:MET:HG3	1.85	0.58
1:C:290:ASN:HB3	1:C:293:PHE:HB3	1.85	0.58
1:C:657:ALA:HB2	2:D:657:ILE:CG2	2.34	0.58
1:A:626:GLU:CD	1:A:626:GLU:H	2.03	0.58
1:C:521:PRO:HA	1:C:524:HIS:CE1	2.39	0.58
1:A:515:ARG:HG2	1:A:515:ARG:NH1	2.18	0.58
1:C:540:LEU:CD2	1:C:574:THR:HG22	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:614:ALA:O	1:C:618:LEU:HG	2.03	0.58
1:C:638:ALA:CB	1:C:639:PRO:HD3	2.29	0.58
1:C:322:GLN:HG3	1:C:326:ASN:HD21	1.68	0.58
1:A:202:MET:O	1:A:205:THR:HG22	2.04	0.58
1:C:585:HIS:O	1:C:589:VAL:HG23	2.04	0.58
1:A:237:ILE:HB	1:A:238:PRO:HD3	1.86	0.57
1:A:514:ILE:HA	1:A:517:LEU:HD12	1.87	0.57
1:C:208:VAL:HG23	1:C:209:GLU:N	2.19	0.57
1:C:540:LEU:HD22	1:C:574:THR:HG22	1.85	0.57
1:C:653:THR:HG22	2:D:661:LEU:HD13	1.85	0.57
1:A:338:TRP:CE2	1:A:342:ARG:HD2	2.40	0.57
1:A:641:THR:HA	1:A:659:LEU:HD11	1.86	0.57
1:A:640:LEU:HD13	1:A:658:VAL:HB	1.86	0.57
1:A:458:GLU:OE2	1:A:503:HIS:HD2	1.88	0.57
2:B:640:VAL:N	2:B:641:PRO:CD	2.67	0.57
2:B:681:TYR:CZ	2:B:683:GLY:HA2	2.40	0.56
1:A:189:MET:SD	1:A:226:GLU:HB2	2.45	0.56
1:A:165:GLN:NE2	1:A:169:ASN:HD21	2.01	0.56
1:C:565:ARG:HG2	1:C:568:GLU:OE1	2.06	0.56
1:A:314:ILE:HD11	1:C:452:LEU:HB3	1.89	0.55
1:C:202:MET:HB2	1:C:214:THR:CB	2.37	0.55
1:C:316:LEU:HB2	1:C:353:ASN:OD1	2.06	0.55
1:C:594:ASN:HD21	1:C:597:PRO:HG2	1.72	0.55
1:C:222:SER:HB2	1:C:258:THR:HG23	1.89	0.55
2:D:718:LEU:HA	2:D:721:MET:HE3	1.87	0.55
1:A:310:GLU:H	1:A:310:GLU:CD	2.11	0.55
1:C:533:ILE:HB	1:C:534:PRO:HD3	1.88	0.55
1:A:546:ASP:O	1:A:550:ARG:HG2	2.07	0.54
1:A:490:GLY:O	1:A:493:VAL:HG12	2.07	0.54
1:C:473:SER:HB3	1:C:516:ASN:HD21	1.69	0.54
1:C:637:THR:HG22	1:C:659:LEU:CD2	2.33	0.54
1:A:528:ARG:HD3	1:A:586:ASN:OD1	2.06	0.54
1:C:594:ASN:ND2	1:C:597:PRO:HG2	2.23	0.54
1:C:638:ALA:HB3	1:C:639:PRO:CD	2.31	0.54
1:A:609:ASN:O	1:A:613:VAL:HG22	2.08	0.54
1:A:475:HIS:CE1	1:A:477:GLU:HB2	2.43	0.53
1:C:587:ARG:HD2	1:C:624:ASP:OD2	2.09	0.53
1:A:188:ILE:HG23	1:A:194:MET:HG2	1.90	0.53
1:A:354:LYS:HB3	1:A:355:PRO:CD	2.38	0.53
1:A:205:THR:C	1:A:206:ASN:HD22	2.11	0.53
1:C:640:LEU:HD23	1:C:659:LEU:CD2	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:TRP:O	1:A:342:ARG:HG3	2.09	0.53
1:C:631:ILE:HG22	1:C:636:ALA:HB2	1.91	0.53
1:C:181:LYS:HD2	1:C:181:LYS:N	2.24	0.53
2:B:641:PRO:O	2:B:642:GLN:HB3	2.10	0.52
2:D:666:SER:O	2:D:668:PRO:HD3	2.08	0.52
2:B:637:LEU:HD11	2:B:669:THR:HG21	1.90	0.52
1:C:399:GLU:H	1:C:399:GLU:CD	2.13	0.52
1:C:153:ILE:HG23	1:C:194:MET:CE	2.38	0.52
1:C:162:ASP:OD2	2:D:714:ARG:NH1	2.41	0.52
1:C:584:VAL:HA	1:C:587:ARG:HH11	1.75	0.52
1:C:188:ILE:HG23	1:C:194:MET:HG3	1.92	0.52
1:C:322:GLN:HE21	1:C:326:ASN:ND2	2.08	0.52
1:A:521:PRO:HA	1:A:524:HIS:CE1	2.45	0.52
1:C:504:TRP:N	1:C:505:PRO:HD2	2.25	0.52
1:A:155:GLU:O	1:A:159:LEU:HD13	2.11	0.51
1:A:583:ASP:OD2	1:A:585:HIS:HB2	2.10	0.51
1:C:475:HIS:CD2	1:C:478:ALA:HB2	2.45	0.51
1:C:519:LEU:HD23	1:C:579:ILE:HG21	1.92	0.51
1:C:226:GLU:CD	1:C:226:GLU:H	2.13	0.51
1:A:525:ALA:HB3	1:A:526:PRO:HD3	1.92	0.51
1:C:177:GLN:HG2	1:C:181:LYS:NZ	2.25	0.51
1:C:216:GLY:O	1:C:219:HIS:HB3	2.10	0.51
2:B:677:LEU:HD12	2:B:678:VAL:H	1.75	0.51
1:C:306:TYR:OH	2:D:684:SER:HA	2.10	0.51
1:A:480:MET:CE	1:A:484:ALA:HB2	2.41	0.50
1:A:458:GLU:HA	1:A:461:THR:OG1	2.11	0.50
1:A:537:VAL:O	1:A:541:VAL:HG23	2.10	0.50
1:C:640:LEU:HD23	1:C:659:LEU:HG	1.93	0.50
1:A:198:ILE:HD13	1:A:217:THR:HG21	1.92	0.50
1:A:546:ASP:HA	1:A:549:ARG:HG2	1.94	0.50
1:C:545:GLN:HA	1:C:548:GLN:OE1	2.10	0.50
1:A:200:ARG:HA	1:A:203:GLN:HE21	1.77	0.50
1:A:292:LYS:O	1:A:296:ILE:HG12	2.12	0.50
1:A:584:VAL:HG13	1:A:585:HIS:N	2.27	0.49
1:A:597:PRO:HA	1:A:634:GLU:HG2	1.93	0.49
1:A:146:ALA:O	1:A:149:ALA:HB3	2.12	0.49
1:A:399:GLU:CD	1:A:399:GLU:H	2.15	0.49
1:C:607:ILE:HD12	1:C:610:ILE:CD1	2.43	0.49
1:C:657:ALA:O	1:C:661:ARG:HG3	2.13	0.49
1:A:291:VAL:HG23	1:A:292:LYS:N	2.28	0.49
1:A:432:TYR:O	1:A:436:MET:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:617:VAL:HG12	1:C:621:LEU:CD1	2.43	0.49
1:C:387:ASN:ND2	3:C:6:HOH:O	2.45	0.49
2:D:701:GLN:CD	2:D:701:GLN:H	2.16	0.49
2:B:630:ARG:HD3	2:B:675:SER:OG	2.12	0.49
1:C:397:GLY:HA2	1:C:399:GLU:OE1	2.13	0.49
1:A:209:GLU:O	1:A:212:ARG:HG2	2.13	0.48
1:C:444:ILE:HG21	1:C:484:ALA:HB3	1.95	0.48
1:C:515:ARG:CD	2:D:672:PRO:HD3	2.43	0.48
1:C:278:GLY:O	1:C:282:MET:HG3	2.13	0.48
1:C:599:PHE:O	1:C:602:LEU:HB2	2.13	0.48
1:C:174:MET:CE	1:C:178:LEU:HD21	2.44	0.48
1:A:544:HIS:O	1:A:548:GLN:HG2	2.13	0.48
1:C:546:ASP:C	1:C:548:GLN:H	2.14	0.48
1:C:404:THR:O	1:C:407:GLN:HB2	2.13	0.48
1:C:447:LEU:O	1:C:450:THR:HB	2.14	0.48
1:A:447:LEU:HB2	1:A:468:LEU:HD21	1.96	0.48
1:C:346:VAL:HG13	2:D:682:GLU:OE2	2.14	0.48
1:C:640:LEU:CD2	1:C:659:LEU:HG	2.44	0.48
1:A:458:GLU:HG2	1:A:506:LEU:CD2	2.42	0.47
1:C:480:MET:HE2	1:C:484:ALA:HB2	1.95	0.47
1:A:627:ALA:O	1:A:631:ILE:HG13	2.14	0.47
1:A:212:ARG:CZ	1:A:212:ARG:HB2	2.45	0.47
1:C:531:GLY:O	1:C:534:PRO:HD2	2.14	0.47
1:A:160:LEU:HA	1:A:168:VAL:HG13	1.95	0.47
1:A:148:LEU:O	1:A:151:ARG:HB3	2.14	0.47
2:B:653:ILE:HG22	2:B:653:ILE:O	2.14	0.47
1:C:185:ARG:HG2	1:C:185:ARG:HH11	1.78	0.47
1:A:648:ASN:HB3	1:A:651:VAL:HB	1.97	0.47
1:C:632:GLU:HB3	1:C:662:MET:SD	2.55	0.47
2:D:705:TYR:HA	2:D:707:TYR:CE2	2.49	0.47
1:A:474:ARG:HH11	1:A:474:ARG:CG	2.28	0.47
1:C:642:GLU:C	1:C:644:LEU:H	2.18	0.47
1:A:580:LEU:HD12	1:A:580:LEU:HA	1.82	0.47
1:C:137:VAL:HG12	1:C:141:ASN:ND2	2.29	0.46
1:C:322:GLN:HG3	1:C:326:ASN:ND2	2.30	0.46
1:C:393:THR:HG21	2:D:676:LEU:HD21	1.97	0.46
1:C:535:ARG:NH2	1:C:539:LEU:HD21	2.30	0.46
1:C:164:ASP:CG	1:C:166:VAL:HG12	2.34	0.46
1:A:212:ARG:HB2	1:A:212:ARG:NH1	2.30	0.46
1:A:207:ASP:HB3	1:A:210:THR:OG1	2.16	0.46
1:A:596:ILE:N	1:A:597:PRO:HD2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:189:MET:CG	1:C:221:LEU:HD22	2.40	0.46
1:C:531:GLY:C	1:C:534:PRO:HD2	2.36	0.46
1:A:638:ALA:HB3	1:A:639:PRO:CD	2.46	0.46
1:A:498:LEU:HD11	1:A:514:ILE:HD12	1.97	0.46
1:C:640:LEU:HD11	1:C:655:ALA:CA	2.38	0.46
1:A:503:HIS:HB3	1:A:562:GLU:OE1	2.16	0.46
1:C:591:ARG:HH11	1:C:627:ALA:HB2	1.80	0.46
1:A:364:GLN:OE1	1:A:364:GLN:N	2.41	0.46
1:C:413:ASP:OD1	1:C:413:ASP:C	2.55	0.46
1:A:246:SER:O	1:A:252:LEU:HD21	2.16	0.46
1:A:501:PRO:O	1:A:502:SER:C	2.54	0.46
1:C:503:HIS:HB3	1:C:562:GLU:OE1	2.15	0.46
1:C:586:ASN:O	1:C:587:ARG:C	2.55	0.45
1:A:523:ASN:C	1:A:526:PRO:HD2	2.37	0.45
1:A:533:ILE:HB	1:A:534:PRO:HD3	1.98	0.45
1:C:338:TRP:CE2	1:C:342:ARG:HD2	2.51	0.45
1:C:458:GLU:HA	1:C:461:THR:OG1	2.17	0.45
1:C:575:GLY:O	1:C:578:HIS:HB3	2.17	0.45
1:A:207:ASP:OD1	1:A:209:GLU:HB2	2.16	0.45
1:C:498:LEU:HD11	1:C:514:ILE:HD12	1.99	0.45
1:C:637:THR:O	1:C:641:THR:OG1	2.34	0.45
1:C:515:ARG:NH1	1:C:515:ARG:HG2	2.32	0.45
1:C:239:ALA:O	1:C:243:MET:HG2	2.17	0.45
1:A:207:ASP:HB3	1:A:210:THR:CB	2.46	0.45
1:A:436:MET:HE3	1:A:476:GLN:HB2	1.99	0.45
1:C:413:ASP:OD1	1:C:415:ASN:N	2.49	0.45
1:C:480:MET:CE	1:C:484:ALA:HB2	2.47	0.45
1:C:640:LEU:HD23	1:C:659:LEU:HD23	1.99	0.45
1:A:155:GLU:O	1:A:159:LEU:CD1	2.65	0.45
1:A:178:LEU:HD22	1:A:184:SER:HB3	1.99	0.44
1:A:180:LYS:O	1:A:185:ARG:NH2	2.50	0.44
1:A:243:MET:C	1:A:245:GLY:H	2.21	0.44
1:A:316:LEU:CD2	1:C:489:TYR:CE2	3.00	0.44
1:A:474:ARG:O	1:A:475:HIS:HB3	2.16	0.44
1:A:636:ALA:O	1:A:639:PRO:HG2	2.18	0.44
1:A:658:VAL:HG12	1:A:662:MET:HE2	1.98	0.44
1:C:198:ILE:HD13	1:C:217:THR:HG21	1.99	0.44
1:C:616:GLY:HA2	1:C:654:TYR:CD1	2.52	0.44
1:A:584:VAL:CG1	1:A:585:HIS:N	2.81	0.44
1:C:632:GLU:HA	1:C:636:ALA:HB3	1.99	0.44
1:C:177:GLN:HG2	1:C:181:LYS:HZ3	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:191:SER:HA	1:C:192:PRO:HD2	1.91	0.44
2:B:644:ARG:HG2	2:B:645:PRO:CD	2.48	0.44
1:C:432:TYR:O	1:C:436:MET:HG2	2.18	0.44
1:C:515:ARG:HD3	2:D:672:PRO:HD3	1.99	0.44
1:A:313:LEU:HD11	1:C:492:PRO:HB2	2.00	0.44
2:B:649:ASN:OD1	2:B:649:ASN:O	2.36	0.44
2:B:677:LEU:HD12	2:B:678:VAL:N	2.33	0.44
1:A:162:ASP:OD1	1:A:164:ASP:N	2.50	0.43
1:C:310:GLU:O	1:C:314:ILE:HG13	2.18	0.43
1:C:338:TRP:NE1	1:C:376:ARG:HD2	2.32	0.43
1:C:535:ARG:HH21	1:C:539:LEU:HD21	1.83	0.43
1:C:657:ALA:HB2	2:D:657:ILE:HG22	2.00	0.43
2:B:628:VAL:HG13	2:B:629:THR:H	1.80	0.43
1:C:364:GLN:NE2	1:C:398:MET:SD	2.91	0.43
1:A:186:HIS:O	1:A:190:ARG:HG3	2.18	0.43
1:C:137:VAL:O	1:C:141:ASN:ND2	2.52	0.43
1:C:256:ILE:HG23	1:C:257:THR:N	2.33	0.43
1:C:599:PHE:CE2	1:C:617:VAL:HG11	2.53	0.43
1:A:184:SER:O	1:A:187:ALA:N	2.51	0.43
1:A:491:LEU:HB2	1:A:492:PRO:HD3	2.00	0.43
1:A:514:ILE:HG23	1:A:527:LEU:HD21	2.00	0.43
1:A:612:ARG:NH1	1:A:650:GLY:HA3	2.34	0.43
2:D:709:ASN:ND2	2:D:723:GLY:O	2.51	0.43
1:A:504:TRP:N	1:A:505:PRO:HD2	2.34	0.43
1:C:153:ILE:HG23	1:C:194:MET:HE2	2.00	0.43
1:C:374:SER:O	1:C:378:VAL:HG23	2.18	0.43
1:C:186:HIS:HA	1:C:189:MET:CE	2.48	0.43
1:C:220:ASN:OD1	2:D:698:GLU:HG3	2.18	0.43
1:A:240:LEU:O	1:A:243:MET:HB2	2.18	0.43
1:A:436:MET:CE	1:A:476:GLN:HB2	2.49	0.43
1:A:342:ARG:O	1:A:346:VAL:HG23	2.19	0.43
1:A:430:ASN:HD21	2:B:636:THR:H	1.66	0.43
1:A:640:LEU:HD12	1:A:662:MET:HE1	2.00	0.43
1:C:498:LEU:HD11	1:C:514:ILE:CD1	2.49	0.43
1:C:166:VAL:O	1:C:170:LYS:HG3	2.19	0.42
1:A:313:LEU:O	1:A:316:LEU:HB3	2.19	0.42
1:C:438:VAL:HG11	1:C:471:LEU:HD11	2.01	0.42
1:A:175:VAL:HG11	1:A:198:ILE:HD11	2.01	0.42
1:A:382:LEU:HD23	1:A:382:LEU:HA	1.86	0.42
1:A:598:LEU:HD12	1:A:598:LEU:O	2.19	0.42
1:C:355:PRO:O	1:C:359:GLU:HG2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:444:ILE:O	1:C:448:VAL:HG23	2.18	0.42
1:C:523:ASN:C	1:C:526:PRO:HD2	2.40	0.42
1:A:227:GLY:O	1:A:231:ILE:HG13	2.20	0.42
1:A:285:LEU:HD13	1:A:293:PHE:HZ	1.84	0.42
1:A:486:ARG:NE	1:A:523:ASN:OD1	2.52	0.42
1:C:174:MET:HE2	1:C:178:LEU:HD21	2.01	0.42
1:A:427:LEU:HD23	1:A:427:LEU:HA	1.75	0.42
2:B:637:LEU:HD11	2:B:669:THR:HG23	1.99	0.42
1:C:399:GLU:CD	1:C:399:GLU:N	2.72	0.42
1:C:543:ALA:HA	1:C:566:MET:HE3	2.02	0.42
1:A:141:ASN:HD22	1:A:141:ASN:C	2.20	0.42
2:B:657:ILE:O	2:B:661:LEU:N	2.48	0.42
1:C:224:HIS:HB3	1:C:226:GLU:OE1	2.20	0.42
1:C:237:ILE:O	1:C:241:VAL:HG23	2.20	0.42
1:C:473:SER:O	1:C:475:HIS:HD2	2.03	0.42
1:C:596:ILE:N	1:C:597:PRO:CD	2.83	0.42
1:A:354:LYS:O	1:A:358:VAL:HG23	2.20	0.41
2:B:646:ARG:HA	2:B:647:PRO:HD3	1.88	0.41
1:A:219:HIS:O	1:A:222:SER:OG	2.29	0.41
1:A:285:LEU:C	1:A:287:ASN:H	2.23	0.41
1:A:353:ASN:O	1:A:357:ILE:HG13	2.20	0.41
1:A:338:TRP:CZ2	1:A:342:ARG:HD2	2.55	0.41
2:B:642:GLN:O	2:B:642:GLN:HG3	2.21	0.41
2:B:648:ALA:O	2:B:649:ASN:C	2.57	0.41
1:C:256:ILE:CG2	1:C:257:THR:N	2.83	0.41
1:C:636:ALA:HB1	1:C:662:MET:HE1	2.02	0.41
1:C:659:LEU:O	1:C:662:MET:HB3	2.19	0.41
2:D:670:ALA:HA	2:D:671:PRO:HD3	1.89	0.41
1:A:608:GLU:O	1:A:611:GLN:HB2	2.21	0.41
1:A:638:ALA:O	1:A:641:THR:HB	2.20	0.41
1:A:527:LEU:HD12	1:A:527:LEU:HA	1.83	0.41
1:A:518:ALA:HB2	1:A:580:LEU:HD13	2.03	0.41
1:C:189:MET:HB2	1:C:189:MET:HE3	1.92	0.41
1:C:386:ARG:HA	1:C:423:ILE:HG12	2.02	0.41
1:C:515:ARG:NE	2:D:672:PRO:HD3	2.35	0.41
1:C:533:ILE:HD11	1:C:586:ASN:OD1	2.20	0.41
2:D:655:ASN:OD1	2:D:655:ASN:C	2.58	0.41
1:A:212:ARG:HG3	1:A:213:CYS:N	2.36	0.41
1:C:180:LYS:HD3	2:D:700:ASP:HB2	2.02	0.41
1:C:344:LEU:HD23	1:C:344:LEU:HA	1.90	0.41
1:C:486:ARG:HA	1:C:491:LEU:HG	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:588:ILE:O	1:C:592:GLY:N	2.51	0.41
1:A:201:THR:O	1:A:205:THR:HB	2.20	0.41
1:A:372:ASP:HA	1:A:373:PRO:HD3	1.93	0.41
1:A:209:GLU:CA	1:A:212:ARG:HG2	2.48	0.41
1:A:371:THR:O	1:A:371:THR:HG22	2.20	0.41
1:A:593:LEU:HD23	1:A:593:LEU:HA	1.93	0.41
2:B:634:ALA:HA	2:B:635:PRO:HD3	1.91	0.41
1:C:515:ARG:HG2	1:C:515:ARG:HH11	1.85	0.41
1:A:314:ILE:CD1	1:C:452:LEU:HB3	2.51	0.41
1:A:370:LEU:HB2	1:A:404:THR:HG21	2.03	0.41
1:A:540:LEU:HD12	1:A:540:LEU:O	2.21	0.41
1:C:640:LEU:HD23	1:C:659:LEU:CG	2.50	0.41
1:A:243:MET:C	1:A:245:GLY:N	2.74	0.40
1:A:348:SER:O	1:A:354:LYS:HE2	2.21	0.40
1:A:495:VAL:HG11	1:A:530:GLN:O	2.21	0.40
1:C:229:LEU:HD11	1:C:233:LYS:HE2	2.03	0.40
1:C:354:LYS:CB	1:C:355:PRO:HD3	2.44	0.40
1:A:285:LEU:C	1:A:287:ASN:N	2.75	0.40
1:A:580:LEU:C	1:A:582:ARG:H	2.24	0.40
1:C:540:LEU:HG	1:C:598:LEU:HD21	2.03	0.40
1:A:515:ARG:HH11	1:A:515:ARG:CG	2.32	0.40
1:C:181:LYS:HE2	2:D:703:GLN:OE1	2.20	0.40
1:C:570:VAL:O	1:C:574:THR:HG23	2.21	0.40
1:C:661:ARG:HG2	1:C:661:ARG:HH11	1.86	0.40
1:A:256:ILE:HG21	1:A:293:PHE:CE1	2.57	0.40
1:A:534:PRO:HA	1:A:593:LEU:HD11	2.02	0.40
1:C:203:GLN:HB3	1:C:239:ALA:HB1	2.03	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	518/538 (96%)	473 (91%)	42 (8%)	3 (1%)	25	64
1	C	517/538 (96%)	459 (89%)	50 (10%)	8 (2%)	10	42
2	B	55/151 (36%)	45 (82%)	7 (13%)	3 (6%)	2	10
2	D	57/151 (38%)	52 (91%)	5 (9%)	0	100	100
All	All	1147/1378 (83%)	1029 (90%)	104 (9%)	14 (1%)	13	48

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	640	VAL
2	B	642	GLN
1	C	643	LEU
1	A	368	LEU
1	A	502	SER
1	A	581	ALA
1	C	393	THR
1	C	607	ILE
2	B	648	ALA
1	C	165	GLN
1	C	222	SER
1	C	142	TYR
1	C	612	ARG
1	C	638	ALA

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	434/447 (97%)	431 (99%)	3 (1%)	84	94
1	C	432/447 (97%)	424 (98%)	8 (2%)	57	84
2	B	50/131 (38%)	50 (100%)	0	100	100
2	D	53/131 (40%)	52 (98%)	1 (2%)	57	84
All	All	969/1156 (84%)	957 (99%)	12 (1%)	71	90

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	141	ASN
1	A	302	GLN
1	A	480	MET
1	C	144	ASP
1	C	185	ARG
1	C	289	THR
1	C	480	MET
1	C	503	HIS
1	C	542	ARG
1	C	546	ASP
1	C	641	THR
2	D	706	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	141	ASN
1	A	161	ASN
1	A	169	ASN
1	A	203	GLN
1	A	206	ASN
1	A	220	ASN
1	A	302	GLN
1	A	326	ASN
1	A	353	ASN
1	A	415	ASN
1	A	430	ASN
1	A	499	HIS
1	A	503	HIS
2	B	631	ASN
2	B	642	GLN
1	C	138	ASN
1	C	141	ASN
1	C	165	GLN
1	C	169	ASN
1	C	223	HIS
1	C	302	GLN
1	C	309	GLN
1	C	322	GLN
1	C	326	ASN
1	C	387	ASN

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Mol	Chain	Res	Type
1	C	415	ASN
1	C	482	GLN
1	C	516	ASN
1	C	594	ASN
1	C	601	GLN
1	C	609	ASN
2	D	660	ASN
2	D	709	ASN

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 monosaccharides 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)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	522/538 (97%)	-0.73	9 (1%)	70	41	13, 40, 114, 201	0
1	C	521/538 (96%)	-0.70	2 (0%)	92	79	16, 43, 122, 201	0
2	B	57/151 (37%)	0.23	3 (5%)	26	10	34, 78, 165, 195	0
2	D	63/151 (41%)	0.23	2 (3%)	47	20	38, 91, 141, 151	0
All	All	1163/1378 (84%)	-0.62	16 (1%)	75	49	13, 46, 131, 201	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	138	ASN	5.8
1	A	137	VAL	5.2
1	C	645	HIS	4.4
1	A	140	ILE	4.0
1	A	139	LEU	3.4
1	A	142	TYR	2.7
1	A	144	ASP	2.7
1	A	551	THR	2.5
2	D	633	VAL	2.5
1	A	141	ASN	2.5
1	A	143	GLN	2.5
2	B	640	VAL	2.3
2	B	628	VAL	2.2
2	B	639	SER	2.2
1	C	561	VAL	2.2
2	D	656	PHE	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 monosaccharides 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.