Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:15 PM GMT

PDB ID	:	1WUP
Title	:	Crystal structure of metallo-beta-lactamase IMP-1 mutant (D81E)
Authors	:	Yamaguchi, Y.; Yamagata, Y.; Goto, M.
Deposited on	:	2004-12-08
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
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:

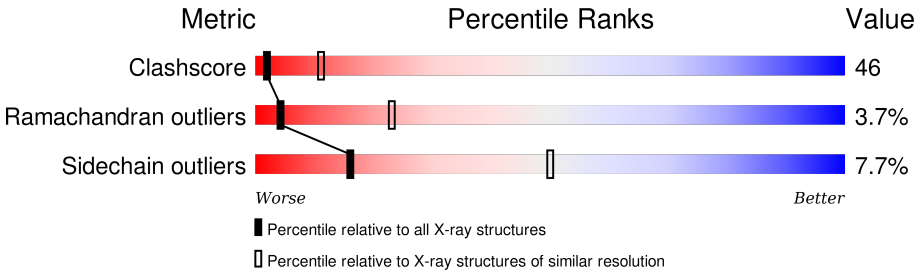
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 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))
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (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 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	228	34% 55% 6% 5%
1	B	228	31% 55% 8% 5%
1	C	228	36% 51% 8% 5%
1	D	228	35% 54% 7% 5%

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
3	ACY	A	401	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6810 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-lactamase IMP-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1698	1102	279	316	1			
1	B	216	Total	C	N	O	S	0	0	0
			1692	1099	278	314	1			
1	C	217	Total	C	N	O	S	0	0	0
			1698	1102	279	316	1			
1	D	217	Total	C	N	O	S	0	0	0
			1698	1102	279	316	1			

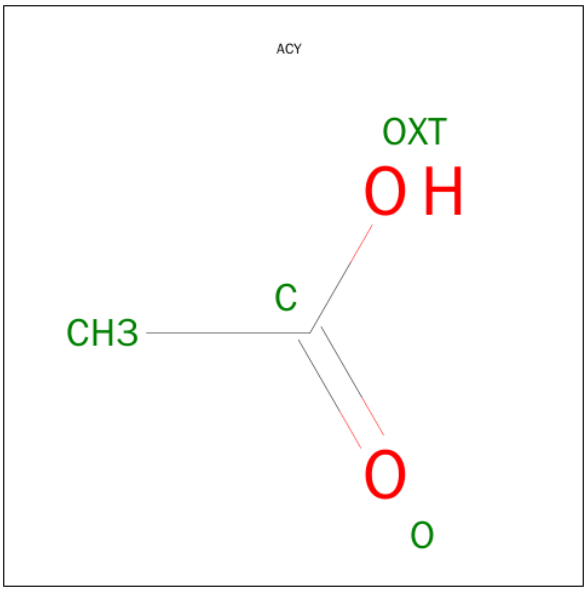
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	81	GLU	ASP	ENGINEERED	UNP P52699
B	81	GLU	ASP	ENGINEERED	UNP P52699
C	81	GLU	ASP	ENGINEERED	UNP P52699
D	81	GLU	ASP	ENGINEERED	UNP P52699

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

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

- Molecule 3 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0

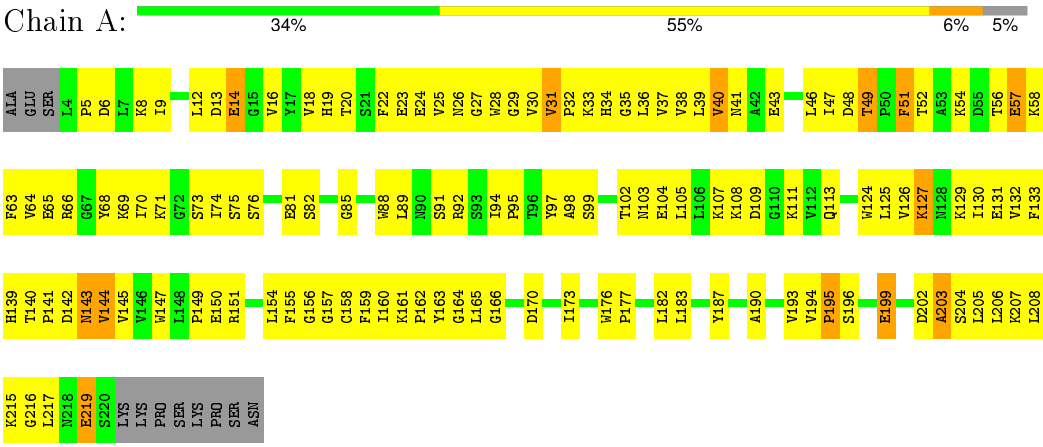
3 Residue-property plots (i)

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.

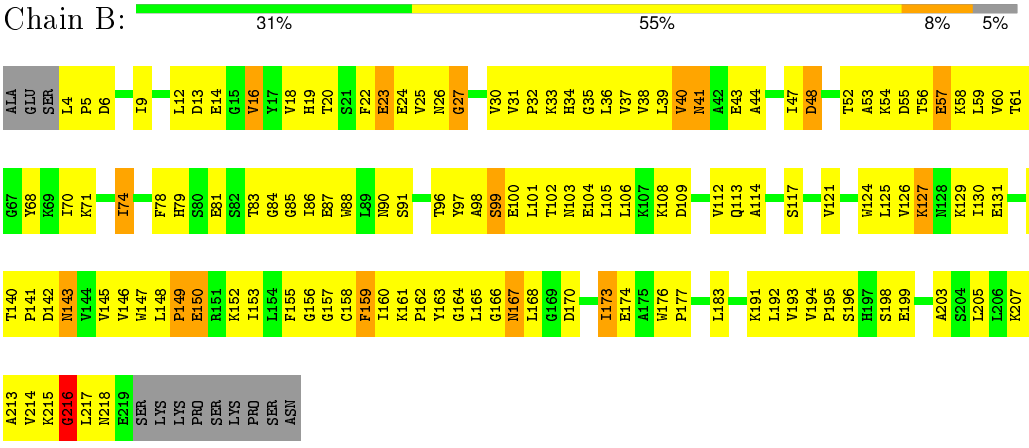
- Molecule 1: Beta-lactamase IMP-1

Chain A:



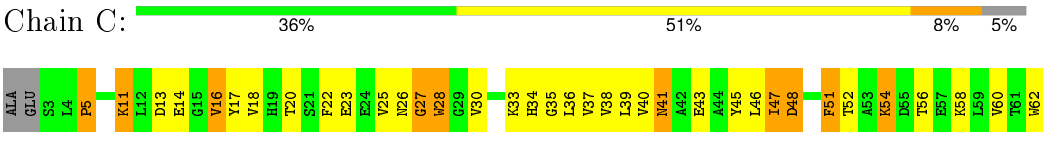
- Molecule 1: Beta-lactamase IMP-1

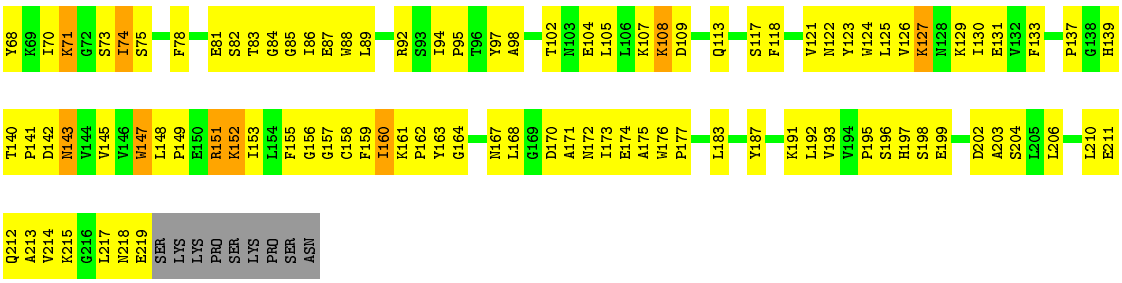
Chain B:



- Molecule 1: Beta-lactamase IMP-1

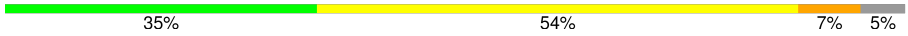
Chain C:

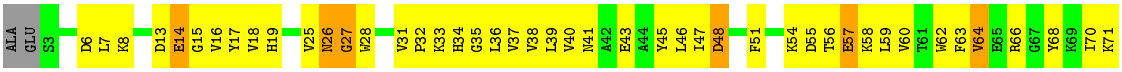




- Molecule 1: Beta-lactamase IMP-1

Chain D:





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	Depositor
Cell constants a, b, c, α, β, γ	49.21Å 73.06Å 80.89Å 84.81° 76.10° 74.00°	Depositor
Resolution (Å)	19.73 – 3.00	Depositor
% Data completeness (in resolution range)	88.7 (19.73-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.224 , 0.295	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6810	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.44	0/1742	0.72	0/2365
1	B	0.40	0/1736	0.73	1/2357 (0.0%)
1	C	0.42	0/1742	0.73	1/2365 (0.0%)
1	D	0.42	0/1742	0.71	0/2365
All	All	0.42	0/6962	0.72	2/9452 (0.0%)

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	B	216	GLY	N-CA-C	-7.57	94.17	113.10
1	C	47	ILE	N-CA-C	-5.08	97.28	111.00

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	1698	0	1707	147	0
1	B	1692	0	1702	163	0
1	C	1698	0	1707	177	0
1	D	1698	0	1707	163	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	4	0	3	5	0
3	B	4	0	3	1	0
3	C	4	0	3	0	0
3	D	4	0	3	1	0
All	All	6810	0	6835	633	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 46.

All (633) 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:40:VAL:HG12	1:B:41:ASN:H	1.11	1.07
1:C:145:VAL:HG23	1:C:156:GLY:HA2	1.39	1.01
1:C:164:GLY:N	1:C:212:GLN:HE22	1.61	0.98
1:C:43:GLU:HB3	1:C:71:LYS:HB2	1.49	0.94
1:B:40:VAL:HG12	1:B:41:ASN:N	1.85	0.92
1:A:102:THR:HG22	1:A:142:ASP:OD1	1.69	0.91
1:C:152:LYS:HB2	1:C:191:LYS:HE3	1.52	0.91
1:C:151:ARG:HE	1:C:151:ARG:HA	1.35	0.90
1:C:54:LYS:HD3	1:C:58:LYS:HD2	1.53	0.89
1:B:211:GLU:O	1:B:214:VAL:HG22	1.72	0.89
1:A:60:VAL:HG13	1:A:70:ILE:HD12	1.55	0.87
1:B:157:GLY:C	1:B:196:SER:HB2	1.95	0.87
1:B:210:LEU:O	1:B:214:VAL:HG13	1.74	0.85
1:C:147:TRP:CZ2	1:C:149:PRO:HB3	2.12	0.84
1:C:211:GLU:O	1:C:214:VAL:HG22	1.78	0.84
1:B:166:GLY:HA2	1:D:28:TRP:CZ3	2.12	0.84
1:D:157:GLY:C	1:D:196:SER:HB2	1.99	0.83
1:B:23:GLU:HG3	1:B:24:GLU:H	1.44	0.82
1:A:89:LEU:HD22	1:A:94:ILE:HG21	1.63	0.81
1:A:145:VAL:HG23	1:A:156:GLY:HA2	1.61	0.81
1:A:43:GLU:HB3	1:A:71:LYS:HG2	1.62	0.80
1:B:126:VAL:HA	1:B:127:LYS:HZ3	1.47	0.80
1:D:74:ILE:HD13	1:D:75:SER:N	1.96	0.80
1:C:127:LYS:HE2	1:C:127:LYS:HA	1.64	0.79
1:C:54:LYS:O	1:C:58:LYS:HG3	1.83	0.79
1:B:174:GLU:HA	1:B:217:LEU:HD13	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:VAL:HA	1:B:127:LYS:NZ	1.99	0.78
1:C:102:THR:HA	1:C:142:ASP:OD1	1.84	0.78
1:C:210:LEU:O	1:C:214:VAL:HG13	1.85	0.77
1:D:64:VAL:HA	1:D:68:TYR:O	1.84	0.77
1:A:163:TYR:HB3	1:C:30:VAL:HB	1.67	0.77
1:C:98:ALA:HB1	1:C:102:THR:OG1	1.86	0.76
1:D:140:THR:HG23	1:D:141:PRO:HD2	1.68	0.75
1:A:12:LEU:HB2	1:A:18:VAL:HG23	1.68	0.75
1:A:157:GLY:C	1:A:196:SER:HB2	2.07	0.74
1:A:61:THR:HA	1:A:64:VAL:HB	1.69	0.74
1:D:62:TRP:O	1:D:66:ARG:HG3	1.87	0.73
1:A:102:THR:HG22	1:A:142:ASP:CG	2.09	0.73
1:D:193:VAL:HB	1:D:205:LEU:HD12	1.72	0.72
1:D:145:VAL:HG23	1:D:156:GLY:HA2	1.71	0.71
1:D:133:PHE:HB3	1:D:145:VAL:CG1	2.20	0.71
1:C:131:GLU:HB3	1:C:147:TRP:CZ3	2.24	0.71
1:D:205:LEU:HA	1:D:208:LEU:HD12	1.70	0.71
1:B:174:GLU:HA	1:B:217:LEU:CD1	2.20	0.71
1:B:102:THR:HA	1:B:142:ASP:OD1	1.91	0.71
1:B:53:ALA:O	1:B:57:GLU:HB3	1.91	0.70
1:C:157:GLY:C	1:C:196:SER:HB2	2.12	0.70
1:C:161:LYS:HB3	1:C:164:GLY:O	1.89	0.70
1:C:54:LYS:CD	1:C:58:LYS:HD2	2.20	0.70
1:B:199:GLU:OE2	1:D:199:GLU:HA	1.92	0.70
1:D:37:VAL:HG13	1:D:46:LEU:HD23	1.74	0.70
1:D:72:GLY:HA2	1:D:95:PRO:O	1.91	0.70
1:D:140:THR:HA	1:D:170:ASP:O	1.92	0.69
1:C:160:ILE:HG12	1:C:193:VAL:HG11	1.74	0.69
1:B:83:THR:HG21	1:B:106:LEU:HD21	1.73	0.69
1:B:88:TRP:O	1:B:91:SER:HB3	1.92	0.69
1:C:149:PRO:O	1:C:152:LYS:HE2	1.92	0.69
1:D:145:VAL:HG21	1:D:154:LEU:HD11	1.74	0.69
1:B:147:TRP:O	1:B:149:PRO:HD3	1.93	0.69
1:B:33:LYS:HG3	1:B:81:GLU:HB3	1.75	0.69
1:D:140:THR:HG22	1:D:142:ASP:H	1.57	0.69
1:C:145:VAL:CG2	1:C:156:GLY:HA2	2.19	0.69
1:D:37:VAL:HG21	1:D:59:LEU:HD11	1.76	0.68
1:D:193:VAL:O	1:D:195:PRO:HD3	1.94	0.68
1:D:131:GLU:HB3	1:D:147:TRP:HB3	1.74	0.68
1:D:33:LYS:HG3	1:D:81:GLU:HB3	1.75	0.68
1:A:126:VAL:HG21	1:A:130:ILE:HD13	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:158:CYS:N	1:C:196:SER:HB2	2.08	0.68
1:D:147:TRP:CH2	1:D:152:LYS:HA	2.29	0.68
1:A:111:LYS:HA	1:A:111:LYS:HE2	1.75	0.68
1:C:202:ASP:O	1:C:204:SER:N	2.27	0.68
1:C:104:GLU:CD	1:D:88:TRP:HE1	1.97	0.68
1:C:124:TRP:HB3	1:C:126:VAL:O	1.94	0.68
1:A:161:LYS:HB3	1:A:164:GLY:O	1.94	0.67
1:D:54:LYS:O	1:D:58:LYS:HG3	1.93	0.67
1:B:102:THR:HG22	1:B:142:ASP:OD1	1.95	0.67
1:C:38:VAL:HG11	1:C:130:ILE:HD11	1.75	0.67
1:A:43:GLU:HG2	1:A:69:LYS:HG3	1.75	0.67
1:A:214:VAL:CG2	1:A:215:LYS:N	2.58	0.67
1:D:147:TRP:O	1:D:149:PRO:HD3	1.95	0.67
1:A:125:LEU:HD23	1:A:130:ILE:HG21	1.77	0.67
1:A:62:TRP:O	1:A:66:ARG:HG3	1.95	0.67
1:C:78:PHE:HA	1:C:83:THR:HG21	1.78	0.66
1:A:151:ARG:HA	1:A:151:ARG:HE	1.59	0.66
1:D:210:LEU:O	1:D:214:VAL:HG13	1.95	0.66
1:D:16:VAL:HG11	1:D:153:ILE:HD12	1.77	0.66
1:D:141:PRO:HD3	1:D:170:ASP:O	1.94	0.66
1:C:60:VAL:HG13	1:C:70:ILE:HG13	1.76	0.66
1:D:26:ASN:O	1:D:28:TRP:N	2.29	0.66
1:A:210:LEU:O	1:A:214:VAL:HG13	1.95	0.66
1:C:151:ARG:HA	1:C:151:ARG:NE	2.09	0.66
1:D:102:THR:HA	1:D:142:ASP:OD1	1.96	0.66
1:D:140:THR:CG2	1:D:142:ASP:OD2	2.44	0.65
1:C:160:ILE:HG22	1:C:160:ILE:O	1.96	0.65
1:C:45:TYR:OH	1:C:71:LYS:HD3	1.95	0.65
1:A:60:VAL:HG13	1:A:70:ILE:CD1	2.25	0.65
1:C:38:VAL:HG23	1:C:47:ILE:HD11	1.79	0.65
1:B:38:VAL:HG22	1:B:148:LEU:HD11	1.77	0.65
1:C:164:GLY:CA	1:C:212:GLN:HE22	2.09	0.65
1:A:140:THR:HA	1:A:170:ASP:O	1.97	0.64
1:A:193:VAL:O	1:A:195:PRO:HD3	1.97	0.64
1:B:153:ILE:HG12	1:B:192:LEU:HB2	1.79	0.64
1:A:124:TRP:CZ3	1:A:131:GLU:HB2	2.32	0.64
1:A:19:HIS:CE1	1:A:35:GLY:HA3	2.33	0.64
1:B:214:VAL:HG23	1:B:215:LYS:N	2.12	0.64
1:B:193:VAL:O	1:B:195:PRO:HD3	1.97	0.64
1:D:127:LYS:N	1:D:127:LYS:HD2	2.11	0.64
1:B:104:GLU:OE1	1:B:108:LYS:HD2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:153:ILE:HG12	1:C:192:LEU:HB2	1.80	0.64
1:D:56:THR:O	1:D:60:VAL:HG23	1.99	0.63
1:B:37:VAL:HG21	1:B:59:LEU:HD11	1.81	0.63
1:A:104:GLU:O	1:A:108:LYS:HB2	1.98	0.62
1:A:199:GLU:OE2	1:C:199:GLU:HA	1.99	0.62
1:B:177:PRO:HG2	1:B:217:LEU:HD22	1.80	0.62
1:B:166:GLY:HA2	1:D:28:TRP:CH2	2.34	0.62
1:B:54:LYS:O	1:B:58:LYS:HG3	1.99	0.62
1:B:83:THR:O	1:B:86:ILE:HG13	1.99	0.62
1:D:143:ASN:OD1	1:D:159:PHE:HD2	1.83	0.62
1:B:39:LEU:HD13	1:B:68:TYR:CE1	2.34	0.62
1:B:98:ALA:HB1	1:B:102:THR:OG1	1.99	0.61
1:A:151:ARG:NE	1:A:151:ARG:HA	2.16	0.61
1:D:17:TYR:O	1:D:36:LEU:HA	2.01	0.61
1:A:47:ILE:O	1:A:48:ASP:HB2	2.01	0.61
1:B:162:PRO:C	1:B:212:GLN:HE22	2.03	0.61
1:B:165:LEU:HD21	1:B:213:ALA:HA	1.82	0.61
1:D:33:LYS:HB2	1:D:51:PHE:CZ	2.35	0.61
1:D:89:LEU:HD23	1:D:94:ILE:HD12	1.82	0.60
1:A:193:VAL:HB	1:A:205:LEU:HD12	1.83	0.60
1:A:165:LEU:HD11	1:A:216:GLY:HA3	1.84	0.60
1:C:145:VAL:HG23	1:C:155:PHE:O	2.02	0.60
1:B:18:VAL:HG22	1:B:36:LEU:CD2	2.31	0.60
1:A:145:VAL:HG21	1:A:154:LEU:HD21	1.81	0.60
1:B:44:ALA:HB3	1:B:70:ILE:HD13	1.84	0.60
1:B:102:THR:O	1:B:106:LEU:HG	2.01	0.60
1:B:214:VAL:CG2	1:B:215:LYS:N	2.65	0.60
1:A:145:VAL:HG23	1:A:155:PHE:O	2.01	0.60
1:B:66:ARG:HB2	1:B:68:TYR:HD2	1.67	0.60
1:B:56:THR:OG1	1:B:85:GLY:HA3	2.02	0.60
1:D:33:LYS:HZ3	1:D:155:PHE:HZ	1.50	0.59
1:B:160:ILE:HG22	1:B:162:PRO:HD3	1.84	0.59
1:D:140:THR:HG22	1:D:142:ASP:OD2	2.02	0.59
1:B:26:ASN:O	1:B:27:GLY:C	2.40	0.59
1:C:71:LYS:O	1:C:95:PRO:HD2	2.01	0.59
1:C:147:TRP:CZ3	1:C:149:PRO:HD3	2.38	0.59
1:B:129:LYS:O	1:B:149:PRO:HD2	2.03	0.59
1:D:18:VAL:HG22	1:D:36:LEU:CD2	2.32	0.59
1:B:87:GLU:HG3	1:B:112:VAL:HG21	1.85	0.59
1:B:166:GLY:HA2	1:D:28:TRP:HZ3	1.61	0.58
1:B:191:LYS:O	1:B:192:LEU:HD23	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:131:GLU:HB3	1:C:147:TRP:CE3	2.38	0.58
1:D:157:GLY:O	1:D:196:SER:HB2	2.03	0.58
1:A:145:VAL:CG2	1:A:156:GLY:HA2	2.31	0.58
1:B:177:PRO:HG2	1:B:217:LEU:CD2	2.34	0.58
1:C:102:THR:HG22	1:C:142:ASP:OD1	2.03	0.58
1:C:102:THR:HG22	1:C:142:ASP:CG	2.24	0.58
1:C:218:ASN:O	1:C:219:GLU:HG3	2.03	0.58
1:C:131:GLU:CB	1:C:147:TRP:CZ3	2.87	0.58
1:B:140:THR:HA	1:B:170:ASP:O	2.04	0.58
1:D:133:PHE:HB3	1:D:145:VAL:HG12	1.84	0.57
1:A:46:LEU:HD22	1:A:59:LEU:HD21	1.84	0.57
1:A:145:VAL:HG11	1:A:183:LEU:HD11	1.86	0.57
1:D:33:LYS:NZ	1:D:155:PHE:HZ	2.02	0.57
1:C:47:ILE:HD12	1:C:47:ILE:N	2.18	0.57
1:C:145:VAL:CG2	1:C:155:PHE:O	2.52	0.57
1:C:147:TRP:O	1:C:147:TRP:CE3	2.58	0.57
1:D:162:PRO:HG2	1:D:205:LEU:HD22	1.87	0.57
1:A:73:SER:HB3	1:A:89:LEU:HD13	1.87	0.57
1:A:81:GLU:OE1	3:A:401:ACY:H1	2.05	0.57
1:B:161:LYS:HB3	1:B:164:GLY:O	2.03	0.57
1:D:48:ASP:OD2	1:D:82:SER:OG	2.22	0.57
1:B:126:VAL:HG21	1:B:130:ILE:HD13	1.86	0.57
1:B:124:TRP:CZ3	1:B:131:GLU:HB2	2.40	0.57
1:A:214:VAL:HG22	1:A:215:LYS:N	2.20	0.57
1:D:43:GLU:OE2	1:D:71:LYS:HD3	2.05	0.57
1:A:54:LYS:HE3	1:A:58:LYS:HD2	1.86	0.57
1:B:135:PRO:HG3	1:B:183:LEU:HD13	1.86	0.57
1:A:129:LYS:HE3	1:A:150:GLU:OE1	2.04	0.56
1:C:160:ILE:HD11	1:C:206:LEU:HD23	1.87	0.56
1:C:164:GLY:CA	1:C:212:GLN:NE2	2.68	0.56
1:D:18:VAL:HG22	1:D:36:LEU:HD21	1.87	0.56
1:B:66:ARG:HB2	1:B:68:TYR:CD2	2.40	0.56
1:B:143:ASN:ND2	1:B:143:ASN:O	2.37	0.56
1:D:140:THR:HG21	1:D:142:ASP:OD2	2.05	0.56
1:C:74:ILE:HD13	1:C:75:SER:N	2.20	0.56
1:D:26:ASN:O	1:D:27:GLY:C	2.44	0.56
1:C:164:GLY:N	1:C:212:GLN:NE2	2.44	0.56
1:B:130:ILE:HG23	1:B:146:VAL:CG1	2.35	0.56
1:A:88:TRP:CH2	1:A:92:ARG:HG3	2.40	0.56
1:B:79:HIS:O	1:B:83:THR:HG23	2.06	0.56
1:B:39:LEU:HD22	1:B:68:TYR:CD1	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:33:LYS:CG	1:D:81:GLU:HB3	2.36	0.55
1:A:125:LEU:HB3	1:A:130:ILE:CG2	2.36	0.55
1:D:126:VAL:CG2	1:D:130:ILE:HD13	2.37	0.55
1:D:16:VAL:HG11	1:D:153:ILE:CD1	2.36	0.55
1:D:214:VAL:CG2	1:D:215:LYS:N	2.69	0.55
1:B:43:GLU:CD	1:B:71:LYS:HE3	2.26	0.55
1:C:16:VAL:CG2	1:C:36:LEU:HD22	2.36	0.55
1:C:54:LYS:HE2	1:C:58:LYS:NZ	2.21	0.55
1:C:51:PHE:HA	1:C:84:GLY:HA3	1.88	0.55
1:B:22:PHE:CE2	1:B:32:PRO:HB3	2.41	0.55
1:B:158:CYS:N	1:B:196:SER:HB2	2.21	0.55
1:C:104:GLU:O	1:C:108:LYS:HB2	2.06	0.55
1:A:130:ILE:HG22	1:A:130:ILE:O	2.06	0.55
1:B:177:PRO:HG3	1:B:213:ALA:O	2.07	0.55
1:A:20:THR:HG23	1:A:34:HIS:HD2	1.70	0.55
1:B:25:VAL:HG21	1:B:31:VAL:CG2	2.37	0.55
1:B:74:ILE:HA	1:B:97:TYR:O	2.07	0.55
1:D:102:THR:HG22	1:D:142:ASP:CG	2.27	0.54
1:A:12:LEU:HD13	1:A:18:VAL:HG21	1.89	0.54
1:A:18:VAL:HA	1:A:36:LEU:HD23	1.89	0.54
1:C:191:LYS:O	1:C:192:LEU:HD23	2.07	0.54
1:C:137:PRO:HB2	1:C:175:ALA:HB3	1.90	0.54
1:A:102:THR:HA	1:A:142:ASP:OD1	2.07	0.54
1:A:99:SER:OG	1:A:102:THR:HG23	2.07	0.54
1:B:145:VAL:HG21	1:B:183:LEU:HD11	1.89	0.54
1:B:193:VAL:HB	1:B:205:LEU:HD12	1.89	0.54
1:C:13:ASP:HB2	1:C:153:ILE:HD11	1.89	0.54
1:B:159:PHE:CD1	1:B:159:PHE:C	2.81	0.54
1:D:134:TYR:HA	1:D:144:VAL:HG12	1.89	0.54
1:D:140:THR:HG23	1:D:141:PRO:CD	2.37	0.54
1:C:141:PRO:CB	1:D:91:SER:HB2	2.38	0.54
1:D:63:PHE:HB2	1:D:70:ILE:HD11	1.89	0.54
1:A:141:PRO:HD3	1:A:170:ASP:O	2.08	0.54
1:A:145:VAL:HG23	1:A:156:GLY:CA	2.36	0.54
1:D:139:HIS:CD2	1:D:158:CYS:HB2	2.43	0.53
1:A:63:PHE:O	1:A:68:TYR:HB2	2.09	0.53
1:C:141:PRO:HB3	1:D:91:SER:HB2	1.90	0.53
1:C:121:VAL:HG13	1:C:122:ASN:N	2.24	0.53
1:D:152:LYS:CB	1:D:191:LYS:HG3	2.39	0.53
1:C:118:PHE:HB2	1:C:123:TYR:CD2	2.44	0.53
1:C:177:PRO:HG3	1:C:213:ALA:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:THR:O	1:A:105:LEU:HB2	2.08	0.53
1:B:199:GLU:OE2	1:D:34:HIS:HE1	1.91	0.53
1:D:7:LEU:HD12	1:D:55:ASP:HB3	1.91	0.53
1:A:43:GLU:HG2	1:A:71:LYS:HD3	1.91	0.53
1:B:160:ILE:C	1:B:162:PRO:HD3	2.28	0.53
1:B:147:TRP:CD1	1:B:149:PRO:HG3	2.44	0.53
1:D:129:LYS:O	1:D:149:PRO:HD2	2.09	0.52
1:A:140:THR:HG22	1:A:142:ASP:H	1.73	0.52
1:A:56:THR:O	1:A:60:VAL:HG23	2.10	0.52
1:D:102:THR:HG22	1:D:142:ASP:OD1	2.09	0.52
1:D:145:VAL:HG23	1:D:155:PHE:O	2.10	0.52
1:B:60:VAL:HG13	1:B:70:ILE:HG13	1.91	0.52
1:D:182:LEU:O	1:D:185:SER:HB2	2.08	0.52
1:A:76:SER:O	1:A:144:VAL:HG22	2.08	0.52
1:A:24:GLU:C	1:A:26:ASN:H	2.12	0.52
1:A:89:LEU:HB3	1:A:94:ILE:HB	1.92	0.52
1:B:33:LYS:HE3	1:B:81:GLU:O	2.10	0.52
1:B:25:VAL:HG21	1:B:31:VAL:HG22	1.91	0.52
1:A:13:ASP:HB3	1:A:16:VAL:CG1	2.40	0.52
1:A:23:GLU:HB2	1:A:51:PHE:CD1	2.44	0.52
1:A:126:VAL:CG2	1:A:130:ILE:HD13	2.39	0.52
1:B:19:HIS:CE1	1:B:35:GLY:HA3	2.45	0.52
1:C:89:LEU:HD23	1:C:94:ILE:HD12	1.91	0.52
1:A:143:ASN:ND2	1:A:143:ASN:O	2.43	0.51
1:D:36:LEU:HD12	1:D:155:PHE:HB2	1.91	0.51
1:A:12:LEU:HB2	1:A:18:VAL:CG2	2.38	0.51
1:A:34:HIS:HE1	1:C:199:GLU:OE2	1.93	0.51
1:C:38:VAL:CG1	1:C:130:ILE:HD11	2.39	0.51
1:B:147:TRP:CH2	1:B:152:LYS:HA	2.45	0.51
1:C:28:TRP:O	1:C:28:TRP:CE3	2.62	0.51
1:D:40:VAL:HG21	1:D:45:TYR:CE1	2.45	0.51
1:A:47:ILE:HA	1:A:74:ILE:HG23	1.90	0.51
1:C:56:THR:OG1	1:C:85:GLY:HA3	2.09	0.51
1:B:97:TYR:CG	1:B:125:LEU:HD11	2.46	0.51
1:A:37:VAL:HG21	1:A:59:LEU:HD11	1.92	0.51
1:B:40:VAL:CG1	1:B:41:ASN:N	2.59	0.51
1:B:62:TRP:CZ2	1:B:66:ARG:NH1	2.79	0.51
1:A:103:ASN:OD1	1:A:113:GLN:HB3	2.11	0.51
1:A:46:LEU:HD22	1:A:59:LEU:CD2	2.41	0.51
1:B:139:HIS:CD2	1:B:158:CYS:HB2	2.45	0.51
1:C:33:LYS:HE3	1:C:81:GLU:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:VAL:O	1:B:30:VAL:HG12	2.10	0.51
1:C:18:VAL:HA	1:C:35:GLY:O	2.11	0.51
1:B:4:LEU:N	1:B:4:LEU:HD12	2.25	0.51
1:C:65:GLU:C	1:C:67:GLY:H	2.13	0.51
1:D:165:LEU:HD21	1:D:213:ALA:HA	1.93	0.51
1:A:18:VAL:HG22	1:A:36:LEU:CD2	2.41	0.51
1:D:152:LYS:HB3	1:D:191:LYS:HG3	1.92	0.51
1:C:159:PHE:O	1:C:176:TRP:HZ2	1.94	0.51
1:B:140:THR:HG22	1:B:141:PRO:CD	2.41	0.51
1:A:54:LYS:CE	1:A:58:LYS:HD2	2.40	0.51
1:D:176:TRP:HB3	1:D:177:PRO:HD3	1.92	0.50
1:D:76:SER:HA	1:D:144:VAL:HG23	1.92	0.50
1:B:102:THR:HG22	1:B:142:ASP:CG	2.30	0.50
1:C:33:LYS:HD3	1:C:34:HIS:N	2.26	0.50
1:A:140:THR:CG2	1:A:142:ASP:OD2	2.59	0.50
1:B:36:LEU:HD12	1:B:155:PHE:HB2	1.93	0.50
1:B:176:TRP:N	1:B:177:PRO:CD	2.75	0.50
1:A:214:VAL:HG22	1:A:215:LYS:H	1.74	0.50
1:B:216:GLY:C	1:B:218:ASN:N	2.64	0.50
1:A:81:GLU:OE1	3:A:401:ACY:CH3	2.59	0.50
1:C:160:ILE:O	1:C:160:ILE:CG2	2.60	0.50
1:A:207:LYS:O	1:A:210:LEU:HB3	2.11	0.50
1:C:143:ASN:O	1:C:143:ASN:ND2	2.44	0.50
1:A:65:GLU:HG3	1:A:65:GLU:O	2.11	0.50
1:C:36:LEU:HD12	1:C:155:PHE:HB2	1.94	0.50
1:D:173:ILE:HG22	1:D:174:GLU:OE2	2.11	0.50
1:C:163:TYR:N	1:C:163:TYR:CD2	2.77	0.50
1:B:127:LYS:NZ	1:B:127:LYS:H	2.09	0.49
1:C:60:VAL:HG21	1:C:88:TRP:HZ3	1.76	0.49
1:B:96:THR:O	1:B:114:ALA:HB1	2.13	0.49
1:D:33:LYS:HE3	1:D:81:GLU:O	2.12	0.49
1:B:99:SER:HB3	1:B:102:THR:HG23	1.94	0.49
1:D:59:LEU:O	1:D:63:PHE:HD1	1.95	0.49
1:A:39:LEU:O	1:A:40:VAL:C	2.49	0.49
1:C:147:TRP:HE3	1:C:147:TRP:O	1.95	0.49
1:B:23:GLU:HG3	1:B:24:GLU:N	2.22	0.49
1:C:160:ILE:HG12	1:C:193:VAL:CG1	2.39	0.49
1:A:81:GLU:OE1	3:A:401:ACY:OXT	2.29	0.49
1:C:5:PRO:HB2	1:C:22:PHE:CD1	2.47	0.49
1:D:74:ILE:HD13	1:D:74:ILE:C	2.32	0.49
1:D:160:ILE:HG22	1:D:162:PRO:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:PHE:O	1:B:83:THR:HG21	2.12	0.49
1:A:140:THR:HG23	1:A:141:PRO:HD2	1.94	0.49
1:C:127:LYS:CE	1:C:127:LYS:HA	2.40	0.49
1:D:133:PHE:CE2	1:D:135:PRO:HA	2.47	0.49
1:D:196:SER:HB3	1:D:197:HIS:CD2	2.47	0.49
1:A:5:PRO:HB2	1:A:22:PHE:CG	2.47	0.49
1:B:13:ASP:OD1	1:B:14:GLU:HG2	2.13	0.49
1:B:147:TRP:C	1:B:149:PRO:HD3	2.33	0.49
1:D:173:ILE:HG23	1:D:217:LEU:HD13	1.94	0.49
1:D:78:PHE:CD1	1:D:105:LEU:HD13	2.47	0.49
1:C:140:THR:HA	1:C:170:ASP:O	2.13	0.48
1:C:202:ASP:C	1:C:204:SER:H	2.15	0.48
1:A:151:ARG:CA	1:A:151:ARG:HE	2.25	0.48
1:C:214:VAL:HG23	1:C:215:LYS:N	2.27	0.48
1:B:47:ILE:HG23	1:B:146:VAL:HG21	1.95	0.48
1:D:14:GLU:HB2	1:D:151:ARG:HD2	1.94	0.48
1:D:127:LYS:H	1:D:127:LYS:CD	2.26	0.48
1:A:176:TRP:HB3	1:A:177:PRO:HD3	1.95	0.48
1:D:60:VAL:O	1:D:64:VAL:HG23	2.13	0.48
1:A:156:GLY:HA3	1:A:160:ILE:CG1	2.43	0.48
1:D:88:TRP:CH2	1:D:92:ARG:HG3	2.48	0.48
1:D:179:SER:O	1:D:182:LEU:N	2.47	0.48
1:B:167:ASN:HD22	3:B:402:ACY:C	2.26	0.48
1:A:160:ILE:C	1:A:162:PRO:HD3	2.32	0.48
1:A:18:VAL:HG22	1:A:36:LEU:HD21	1.96	0.48
1:A:199:GLU:OE2	1:C:34:HIS:HE1	1.96	0.48
1:C:38:VAL:HG23	1:C:47:ILE:CD1	2.42	0.48
1:D:70:ILE:CG2	1:D:94:ILE:HG21	2.44	0.48
1:B:124:TRP:CE2	1:B:131:GLU:HG3	2.48	0.48
1:A:8:LYS:O	1:A:9:ILE:HD13	2.14	0.48
1:B:90:ASN:N	1:B:90:ASN:HD22	2.11	0.48
1:C:129:LYS:O	1:C:149:PRO:HD2	2.12	0.48
1:C:54:LYS:HE2	1:C:58:LYS:HZ3	1.79	0.48
1:C:126:VAL:HG13	1:C:127:LYS:N	2.29	0.48
1:C:214:VAL:CG2	1:C:215:LYS:N	2.76	0.48
1:D:98:ALA:HB1	1:D:102:THR:OG1	2.13	0.48
1:B:60:VAL:HG12	1:B:61:THR:N	2.27	0.48
1:B:141:PRO:HD3	1:B:170:ASP:O	2.13	0.48
1:A:147:TRP:O	1:A:149:PRO:HD3	2.14	0.48
1:B:173:ILE:HG23	1:B:217:LEU:HA	1.96	0.48
1:C:195:PRO:HG2	1:C:199:GLU:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:121:VAL:CG1	1:C:122:ASN:N	2.77	0.48
1:D:15:GLY:O	1:D:39:LEU:N	2.31	0.48
1:B:159:PHE:O	1:B:176:TRP:HZ2	1.96	0.48
1:A:208:LEU:HD22	1:C:5:PRO:HG3	1.96	0.48
1:D:101:LEU:CD2	1:D:101:LEU:H	2.26	0.48
1:D:70:ILE:HG22	1:D:94:ILE:CG2	2.43	0.48
1:D:143:ASN:N	1:D:143:ASN:HD22	2.10	0.48
1:B:12:LEU:HB2	1:B:18:VAL:HG23	1.96	0.47
1:B:60:VAL:HG21	1:B:88:TRP:HZ3	1.78	0.47
1:B:52:THR:HG22	1:B:54:LYS:H	1.79	0.47
1:D:162:PRO:CG	1:D:205:LEU:HD22	2.44	0.47
1:C:126:VAL:CG1	1:C:127:LYS:N	2.78	0.47
1:B:127:LYS:CD	1:B:127:LYS:H	2.26	0.47
1:D:25:VAL:HG22	1:D:31:VAL:HG22	1.95	0.47
1:C:139:HIS:CD2	1:C:158:CYS:HB2	2.49	0.47
1:C:33:LYS:NZ	1:C:48:ASP:OD2	2.33	0.47
1:B:22:PHE:CD1	1:B:22:PHE:N	2.82	0.47
1:A:13:ASP:OD1	1:A:14:GLU:N	2.40	0.47
1:D:47:ILE:O	1:D:48:ASP:O	2.33	0.47
1:C:78:PHE:HE1	1:C:140:THR:HG23	1.79	0.47
1:B:105:LEU:O	1:B:109:ASP:HB2	2.14	0.47
1:C:62:TRP:CZ2	1:C:66:ARG:CZ	2.98	0.47
1:A:74:ILE:HD12	1:A:97:TYR:O	2.15	0.47
1:A:130:ILE:HD12	1:A:130:ILE:N	2.30	0.47
1:C:140:THR:CG2	1:C:142:ASP:OD2	2.63	0.47
1:B:34:HIS:CE1	1:B:198:SER:O	2.68	0.47
1:B:20:THR:HG23	1:B:34:HIS:CD2	2.50	0.47
1:C:191:LYS:NZ	1:C:191:LYS:HB2	2.30	0.47
1:A:37:VAL:HG22	1:A:46:LEU:HD23	1.95	0.47
1:D:38:VAL:HG23	1:D:47:ILE:HD13	1.97	0.47
1:A:61:THR:O	1:A:65:GLU:HB3	2.15	0.47
1:C:23:GLU:HB2	1:C:51:PHE:CE1	2.50	0.47
1:D:70:ILE:HG22	1:D:94:ILE:HG21	1.97	0.47
1:D:103:ASN:OD1	1:D:113:GLN:HB3	2.15	0.47
1:B:36:LEU:HD21	1:B:194:VAL:HG11	1.97	0.47
1:A:74:ILE:HB	1:A:125:LEU:CD2	2.44	0.47
1:D:127:LYS:N	1:D:127:LYS:CD	2.77	0.47
1:C:151:ARG:O	1:C:191:LYS:NZ	2.44	0.46
1:D:130:ILE:HD12	1:D:130:ILE:N	2.29	0.46
1:D:211:GLU:O	1:D:214:VAL:HG22	2.14	0.46
1:D:87:GLU:O	1:D:90:ASN:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:ALA:HB1	1:A:102:THR:OG1	2.15	0.46
1:A:187:TYR:O	1:A:206:LEU:HD11	2.15	0.46
1:B:13:ASP:OD1	1:B:14:GLU:N	2.36	0.46
1:C:17:TYR:O	1:C:36:LEU:HA	2.15	0.46
1:D:57:GLU:HG3	1:D:58:LYS:N	2.30	0.46
1:B:174:GLU:H	1:B:174:GLU:CD	2.18	0.46
1:A:33:LYS:HB2	1:A:51:PHE:CZ	2.50	0.46
1:B:134:TYR:CZ	1:B:136:GLY:HA2	2.51	0.46
1:C:124:TRP:CZ3	1:C:131:GLU:HB2	2.51	0.46
1:D:195:PRO:HG3	1:D:205:LEU:HD13	1.96	0.46
1:A:147:TRP:HH2	1:A:190:ALA:HA	1.81	0.46
1:A:38:VAL:HG23	1:A:47:ILE:HD13	1.97	0.46
1:D:127:LYS:H	1:D:127:LYS:HD2	1.81	0.46
1:B:214:VAL:CG2	1:B:215:LYS:H	2.28	0.46
1:D:124:TRP:CH2	1:D:131:GLU:HB2	2.51	0.46
1:B:216:GLY:C	1:B:218:ASN:H	2.18	0.46
1:D:101:LEU:CD2	1:D:101:LEU:N	2.79	0.46
1:D:78:PHE:CE1	1:D:105:LEU:HD13	2.51	0.46
1:D:101:LEU:HD23	1:D:101:LEU:H	1.81	0.46
1:A:155:PHE:HA	1:A:194:VAL:HB	1.97	0.46
1:D:13:ASP:OD1	1:D:14:GLU:N	2.38	0.45
1:C:88:TRP:CZ2	1:C:92:ARG:HD3	2.51	0.45
1:B:54:LYS:HD3	1:B:58:LYS:HD2	1.98	0.45
1:B:5:PRO:HB2	1:B:22:PHE:CD1	2.51	0.45
1:C:117:SER:O	1:C:118:PHE:HB3	2.16	0.45
1:C:65:GLU:C	1:C:67:GLY:N	2.68	0.45
1:B:47:ILE:O	1:B:48:ASP:HB2	2.16	0.45
1:C:140:THR:HG21	1:C:142:ASP:OD2	2.16	0.45
1:B:31:VAL:HA	1:B:32:PRO:HD3	1.72	0.45
1:C:173:ILE:HD11	1:C:217:LEU:N	2.32	0.45
1:D:46:LEU:O	1:D:73:SER:HA	2.16	0.45
1:D:155:PHE:CZ	1:D:157:GLY:HA2	2.52	0.45
1:A:76:SER:HA	1:A:144:VAL:HG23	1.98	0.45
1:C:46:LEU:O	1:C:73:SER:HA	2.17	0.45
1:C:58:LYS:O	1:C:62:TRP:HB2	2.16	0.45
1:D:126:VAL:HG21	1:D:130:ILE:HD13	1.98	0.45
1:D:129:LYS:C	1:D:130:ILE:HD12	2.36	0.45
1:D:133:PHE:CE1	1:D:186:LYS:HG2	2.52	0.45
1:D:18:VAL:HA	1:D:36:LEU:HD23	1.98	0.45
1:B:165:LEU:HB2	1:B:168:LEU:HD21	1.99	0.45
1:B:173:ILE:HG22	1:B:174:GLU:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:33:LYS:HG3	1:C:81:GLU:HB3	1.99	0.45
1:A:8:LYS:O	1:A:19:HIS:HA	2.17	0.45
1:C:89:LEU:CD2	1:C:94:ILE:HD12	2.46	0.45
1:C:28:TRP:HA	1:C:28:TRP:CE3	2.50	0.45
1:C:39:LEU:HD22	1:C:68:TYR:CD1	2.52	0.45
1:D:74:ILE:HA	1:D:97:TYR:O	2.16	0.45
1:C:33:LYS:NZ	1:C:48:ASP:HB3	2.32	0.45
1:B:9:ILE:HG21	1:B:62:TRP:CZ3	2.52	0.45
1:C:176:TRP:N	1:C:177:PRO:CD	2.80	0.45
1:C:13:ASP:OD1	1:C:151:ARG:HD3	2.16	0.45
1:B:163:TYR:N	1:B:163:TYR:CD2	2.83	0.45
1:D:31:VAL:HA	1:D:32:PRO:HD3	1.71	0.45
1:C:28:TRP:HA	1:C:28:TRP:HE3	1.81	0.45
1:A:132:VAL:HG12	1:A:133:PHE:N	2.32	0.45
1:A:27:GLY:O	1:A:28:TRP:HB3	2.16	0.45
1:A:88:TRP:CZ3	1:A:92:ARG:HG3	2.52	0.45
1:A:140:THR:HG22	1:A:142:ASP:OD2	2.17	0.45
1:C:88:TRP:CZ3	1:C:92:ARG:HG3	2.52	0.45
1:A:124:TRP:CE3	1:A:127:LYS:O	2.70	0.45
1:A:202:ASP:O	1:A:204:SER:N	2.50	0.45
1:C:107:LYS:HB2	1:C:113:GLN:CD	2.36	0.45
1:A:142:ASP:OD2	1:A:143:ASN:N	2.50	0.44
1:B:139:HIS:HE1	1:B:167:ASN:HD21	1.65	0.44
1:C:38:VAL:CG2	1:C:47:ILE:HD11	2.46	0.44
1:A:43:GLU:HB3	1:A:71:LYS:CG	2.41	0.44
1:B:162:PRO:C	1:B:163:TYR:CD2	2.90	0.44
1:B:176:TRP:O	1:B:176:TRP:HD1	2.00	0.44
1:A:39:LEU:HD21	1:A:63:PHE:CD2	2.51	0.44
1:B:155:PHE:CZ	1:B:157:GLY:HA2	2.52	0.44
1:D:154:LEU:CD1	1:D:187:TYR:CD1	3.00	0.44
1:D:207:LYS:HG2	1:D:211:GLU:OE2	2.16	0.44
1:D:177:PRO:HB3	1:D:214:VAL:HG12	1.99	0.44
1:B:104:GLU:O	1:B:108:LYS:HB2	2.18	0.44
1:C:152:LYS:HD2	1:C:191:LYS:HE3	2.00	0.44
1:D:158:CYS:N	1:D:196:SER:HB2	2.33	0.44
1:D:16:VAL:HG22	1:D:36:LEU:HD22	2.00	0.44
1:D:124:TRP:CZ3	1:D:131:GLU:HB2	2.52	0.44
1:C:62:TRP:O	1:C:66:ARG:HG2	2.18	0.44
1:B:145:VAL:HB	1:B:155:PHE:O	2.17	0.44
1:D:56:THR:OG1	1:D:85:GLY:HA3	2.17	0.44
1:C:125:LEU:HD23	1:C:130:ILE:HG21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:ASN:OD1	1:A:41:ASN:N	2.50	0.44
1:D:83:THR:HB	1:D:86:ILE:HD12	2.00	0.44
1:D:33:LYS:NZ	1:D:48:ASP:OD2	2.20	0.44
1:D:80:SER:O	1:D:82:SER:N	2.51	0.44
1:A:54:LYS:O	1:A:58:LYS:HG3	2.18	0.44
1:C:66:ARG:HB2	1:C:68:TYR:HD2	1.83	0.44
1:B:36:LEU:CD1	1:B:155:PHE:HB2	2.47	0.44
1:A:187:TYR:O	1:A:206:LEU:CD1	2.65	0.44
1:C:25:VAL:O	1:C:27:GLY:N	2.51	0.44
1:C:40:VAL:HB	1:C:43:GLU:O	2.17	0.44
1:A:125:LEU:HB3	1:A:130:ILE:HG22	1.99	0.44
1:D:19:HIS:CE1	1:D:36:LEU:N	2.86	0.43
1:D:106:LEU:O	1:D:110:GLY:N	2.50	0.43
1:C:145:VAL:HG11	1:C:183:LEU:HD11	1.99	0.43
1:A:60:VAL:HG21	1:A:88:TRP:HZ3	1.82	0.43
1:A:129:LYS:O	1:A:149:PRO:HD2	2.18	0.43
1:C:47:ILE:O	1:C:48:ASP:O	2.36	0.43
1:B:140:THR:HG22	1:B:141:PRO:N	2.33	0.43
1:B:125:LEU:HA	1:B:125:LEU:HD12	1.85	0.43
1:C:173:ILE:O	1:C:177:PRO:HD3	2.18	0.43
1:C:139:HIS:CD2	1:C:158:CYS:CB	3.02	0.43
1:B:152:LYS:HB2	1:B:191:LYS:HG3	1.99	0.43
1:A:173:ILE:HG13	1:A:217:LEU:HD13	2.00	0.43
1:C:126:VAL:HG12	1:C:129:LYS:H	1.82	0.43
1:A:107:LYS:HB2	1:A:113:GLN:CD	2.39	0.43
1:C:162:PRO:HB2	1:C:163:TYR:CE2	2.53	0.43
1:A:60:VAL:HG22	1:A:70:ILE:HD13	2.00	0.43
1:A:160:ILE:CD1	1:A:206:LEU:HD23	2.49	0.43
1:D:179:SER:O	1:D:180:ALA:C	2.57	0.43
1:A:166:GLY:HA2	1:C:28:TRP:HE1	1.83	0.43
1:D:168:LEU:O	1:D:169:GLY:C	2.56	0.43
1:C:152:LYS:CB	1:C:191:LYS:HE3	2.37	0.43
1:C:81:GLU:OE2	1:C:197:HIS:CE1	2.71	0.43
1:A:75:SER:OG	1:A:82:SER:O	2.24	0.43
1:D:161:LYS:CB	1:D:165:LEU:HA	2.49	0.43
1:B:101:LEU:O	1:B:102:THR:C	2.57	0.43
1:B:140:THR:HG22	1:B:141:PRO:HD2	1.99	0.43
1:C:152:LYS:HB2	1:C:191:LYS:CE	2.35	0.43
1:A:46:LEU:O	1:A:73:SER:HA	2.18	0.43
1:D:89:LEU:CD2	1:D:94:ILE:HD12	2.46	0.43
1:B:131:GLU:HB3	1:B:147:TRP:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:151:ARG:O	1:D:191:LYS:HE3	2.19	0.43
1:C:56:THR:O	1:C:60:VAL:HG23	2.18	0.43
1:B:16:VAL:O	1:B:16:VAL:HG22	2.18	0.43
1:B:40:VAL:CG1	1:B:41:ASN:H	1.96	0.43
1:B:145:VAL:HG12	1:B:156:GLY:HA2	2.00	0.43
1:B:9:ILE:HD11	1:B:59:LEU:HD13	2.01	0.43
1:B:100:GLU:HG3	1:B:117:SER:OG	2.18	0.43
1:B:81:GLU:OE1	1:B:158:CYS:SG	2.76	0.43
1:D:81:GLU:OE1	3:D:404:ACY:C	2.67	0.43
1:B:163:TYR:CE1	1:D:32:PRO:HG3	2.54	0.43
1:D:118:PHE:HB2	1:D:123:TYR:CD2	2.54	0.42
1:C:18:VAL:HG22	1:C:36:LEU:CD2	2.49	0.42
1:C:191:LYS:HZ2	1:C:191:LYS:CB	2.32	0.42
1:C:191:LYS:HB2	1:C:191:LYS:HZ2	1.83	0.42
1:A:88:TRP:O	1:A:91:SER:N	2.52	0.42
1:D:78:PHE:HB2	1:D:106:LEU:HD23	2.01	0.42
1:A:27:GLY:O	1:A:31:VAL:HG12	2.20	0.42
1:D:214:VAL:HG23	1:D:215:LYS:N	2.33	0.42
1:A:31:VAL:HA	1:A:32:PRO:HD3	1.82	0.42
1:B:25:VAL:CG2	1:B:31:VAL:HG22	2.48	0.42
1:C:126:VAL:HG11	1:C:129:LYS:HB2	2.00	0.42
1:C:74:ILE:HG12	1:C:97:TYR:HB2	2.01	0.42
1:A:159:PHE:O	1:A:176:TRP:HZ2	2.02	0.42
1:D:19:HIS:NE2	1:D:35:GLY:HA3	2.34	0.42
1:D:33:LYS:HB2	1:D:51:PHE:CE1	2.55	0.42
1:A:39:LEU:O	1:A:40:VAL:O	2.37	0.42
1:B:176:TRP:HB3	1:B:177:PRO:HD3	2.00	0.42
1:C:33:LYS:HZ2	1:C:48:ASP:HB3	1.85	0.42
1:A:161:LYS:NZ	3:A:401:ACY:O	2.52	0.42
1:B:212:GLN:O	1:B:213:ALA:C	2.58	0.42
1:C:158:CYS:SG	1:C:196:SER:OG	2.71	0.42
1:D:152:LYS:HB2	1:D:191:LYS:HE3	2.01	0.42
1:B:38:VAL:HG21	1:B:148:LEU:HD21	2.01	0.42
1:A:39:LEU:HD21	1:A:63:PHE:CE2	2.54	0.42
1:C:118:PHE:C	1:C:118:PHE:CD1	2.92	0.42
1:D:7:LEU:C	1:D:7:LEU:HD23	2.40	0.42
1:B:103:ASN:HB3	1:B:113:GLN:OE1	2.19	0.42
1:C:54:LYS:CE	1:C:58:LYS:HD2	2.50	0.42
1:C:20:THR:OG1	1:C:34:HIS:HD2	2.02	0.42
1:C:173:ILE:HG23	1:C:174:GLU:CD	2.40	0.42
1:C:22:PHE:N	1:C:22:PHE:CD1	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:LEU:HB2	1:C:73:SER:CB	2.50	0.42
1:D:71:LYS:HG3	1:D:71:LYS:O	2.20	0.42
1:C:137:PRO:HB3	1:C:172:ASN:CB	2.50	0.42
1:A:135:PRO:HA	1:A:182:LEU:HD23	2.01	0.42
1:C:40:VAL:O	1:C:41:ASN:C	2.58	0.41
1:B:207:LYS:O	1:B:210:LEU:HB3	2.20	0.41
1:C:105:LEU:HD12	1:C:142:ASP:OD1	2.20	0.41
1:D:214:VAL:O	1:D:217:LEU:N	2.52	0.41
1:A:51:PHE:CD1	1:A:51:PHE:N	2.86	0.41
1:C:168:LEU:HA	1:C:171:ALA:HB3	2.02	0.41
1:C:131:GLU:CB	1:C:147:TRP:HZ3	2.30	0.41
1:A:145:VAL:CG2	1:A:154:LEU:HD11	2.50	0.41
1:B:152:LYS:CB	1:B:191:LYS:HG3	2.50	0.41
1:C:148:LEU:O	1:C:152:LYS:N	2.53	0.41
1:B:159:PHE:HD1	1:B:159:PHE:C	2.23	0.41
1:D:99:SER:OG	1:D:102:THR:HG23	2.21	0.41
1:B:60:VAL:O	1:B:64:VAL:HG23	2.20	0.41
1:D:150:GLU:HG2	1:D:150:GLU:H	1.46	0.41
1:A:139:HIS:CD2	1:A:158:CYS:HB3	2.55	0.41
1:C:48:ASP:OD2	1:C:82:SER:OG	2.37	0.41
1:C:97:TYR:N	1:C:97:TYR:CD1	2.87	0.41
1:C:137:PRO:HB2	1:C:175:ALA:CB	2.50	0.41
1:D:145:VAL:CG2	1:D:155:PHE:O	2.67	0.41
1:A:129:LYS:C	1:A:130:ILE:HD12	2.40	0.41
1:B:124:TRP:CH2	1:B:131:GLU:HB2	2.56	0.41
1:D:152:LYS:HD2	1:D:152:LYS:N	2.35	0.41
1:A:81:GLU:OE1	3:A:401:ACY:C	2.69	0.41
1:C:137:PRO:HG3	1:D:91:SER:HA	2.02	0.41
1:C:5:PRO:HB2	1:C:22:PHE:CG	2.56	0.41
1:D:33:LYS:HD3	1:D:34:HIS:N	2.36	0.41
1:A:147:TRP:CE3	1:A:154:LEU:HB2	2.55	0.41
1:C:105:LEU:HD12	1:C:142:ASP:CG	2.41	0.41
1:A:22:PHE:HB3	1:A:30:VAL:CG1	2.50	0.41
1:A:49:THR:OG1	1:A:85:GLY:N	2.47	0.41
1:C:145:VAL:HG22	1:C:155:PHE:O	2.21	0.41
1:C:33:LYS:C	1:C:33:LYS:HD3	2.41	0.41
1:B:19:HIS:CD2	1:B:59:LEU:HD21	2.55	0.41
1:D:106:LEU:O	1:D:107:LYS:C	2.59	0.41
1:C:147:TRP:CE3	1:C:149:PRO:HD3	2.55	0.41
1:D:133:PHE:HE2	1:D:135:PRO:HA	1.83	0.41
1:D:48:ASP:CG	1:D:82:SER:HG	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:PHE:CD1	1:C:105:LEU:HD13	2.55	0.41
1:B:62:TRP:HE3	1:B:63:PHE:CD1	2.38	0.41
1:A:27:GLY:C	1:A:29:GLY:N	2.71	0.41
1:A:57:GLU:C	1:A:57:GLU:CD	2.79	0.41
1:D:145:VAL:HG21	1:D:154:LEU:CD1	2.48	0.41
1:B:162:PRO:HB2	1:B:163:TYR:CE2	2.56	0.41
1:C:51:PHE:CD2	1:C:81:GLU:HA	2.56	0.41
1:B:55:ASP:O	1:B:58:LYS:N	2.53	0.41
1:A:22:PHE:CD1	1:A:22:PHE:N	2.88	0.41
1:C:133:PHE:HB2	1:C:187:TYR:OH	2.21	0.41
1:C:20:THR:HG23	1:C:34:HIS:CD2	2.56	0.41
1:C:86:ILE:O	1:C:87:GLU:C	2.58	0.41
1:A:89:LEU:HD23	1:A:94:ILE:HG13	2.03	0.40
1:D:158:CYS:O	1:D:161:LYS:HE2	2.21	0.40
1:B:53:ALA:O	1:B:57:GLU:N	2.48	0.40
1:C:33:LYS:HE2	1:C:196:SER:OG	2.21	0.40
1:A:30:VAL:O	1:C:163:TYR:HB3	2.22	0.40
1:D:193:VAL:CB	1:D:205:LEU:HD12	2.47	0.40
1:A:56:THR:HG21	1:A:89:LEU:HG	2.03	0.40
1:B:127:LYS:HZ2	1:B:127:LYS:H	1.69	0.40
1:B:205:LEU:HD23	1:B:208:LEU:HD12	2.03	0.40
1:B:55:ASP:O	1:B:56:THR:C	2.60	0.40
1:C:11:LYS:HA	1:C:17:TYR:CD2	2.56	0.40
1:C:37:VAL:HA	1:C:45:TYR:O	2.22	0.40
1:B:12:LEU:HD12	1:B:12:LEU:HA	1.87	0.40
1:B:157:GLY:O	1:B:196:SER:N	2.55	0.40
1:A:190:ALA:O	1:A:203:ALA:HB2	2.22	0.40
1:B:149:PRO:O	1:B:150:GLU:C	2.59	0.40
1:D:129:LYS:HD3	1:D:150:GLU:OE1	2.21	0.40
1:C:159:PHE:C	1:C:159:PHE:CD1	2.94	0.40
1:D:8:LYS:CB	1:D:8:LYS:NZ	2.85	0.40
1:D:140:THR:CG2	1:D:141:PRO:N	2.85	0.40
1:B:13:ASP:HB3	1:B:16:VAL:HG13	2.02	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	215/228 (94%)	186 (86%)	21 (10%)	8 (4%)	4	23
1	B	214/228 (94%)	179 (84%)	27 (13%)	8 (4%)	4	23
1	C	215/228 (94%)	180 (84%)	27 (13%)	8 (4%)	4	23
1	D	215/228 (94%)	184 (86%)	23 (11%)	8 (4%)	4	23
All	All	859/912 (94%)	729 (85%)	98 (11%)	32 (4%)	4	23

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	127	LYS
1	C	26	ASN
1	C	41	ASN
1	C	203	ALA
1	A	127	LYS
1	B	40	VAL
1	C	48	ASP
1	D	14	GLU
1	D	27	GLY
1	D	81	GLU
1	D	127	LYS
1	A	40	VAL
1	A	203	ALA
1	B	27	GLY
1	B	48	ASP
1	B	84	GLY
1	B	203	ALA
1	C	14	GLU
1	C	109	ASP
1	D	26	ASN
1	D	48	ASP
1	D	165	LEU

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Mol	Chain	Res	Type
1	A	219	GLU
1	D	169	GLY
1	C	5	PRO
1	A	195	PRO
1	B	216	GLY
1	A	25	VAL
1	A	95	PRO
1	A	138	GLY
1	C	27	GLY
1	B	149	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	186/196 (95%)	173 (93%)	13 (7%)	19	55
1	B	185/196 (94%)	169 (91%)	16 (9%)	13	44
1	C	186/196 (95%)	169 (91%)	17 (9%)	12	41
1	D	186/196 (95%)	175 (94%)	11 (6%)	24	63
All	All	743/784 (95%)	686 (92%)	57 (8%)	16	50

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASP
1	A	14	GLU
1	A	31	VAL
1	A	49	THR
1	A	51	PHE
1	A	52	THR
1	A	57	GLU
1	A	109	ASP
1	A	143	ASN
1	A	144	VAL
1	A	199	GLU

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Mol	Chain	Res	Type
1	A	214	VAL
1	A	219	GLU
1	B	6	ASP
1	B	16	VAL
1	B	23	GLU
1	B	41	ASN
1	B	57	GLU
1	B	65	GLU
1	B	66	ARG
1	B	74	ILE
1	B	99	SER
1	B	121	VAL
1	B	143	ASN
1	B	150	GLU
1	B	159	PHE
1	B	167	ASN
1	B	173	ILE
1	B	212	GLN
1	C	11	LYS
1	C	16	VAL
1	C	28	TRP
1	C	51	PHE
1	C	52	THR
1	C	54	LYS
1	C	71	LYS
1	C	74	ILE
1	C	108	LYS
1	C	127	LYS
1	C	143	ASN
1	C	147	TRP
1	C	151	ARG
1	C	152	LYS
1	C	160	ILE
1	C	167	ASN
1	C	198	SER
1	D	6	ASP
1	D	41	ASN
1	D	57	GLU
1	D	64	VAL
1	D	74	ILE
1	D	101	LEU
1	D	127	LYS

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Mol	Chain	Res	Type
1	D	143	ASN
1	D	152	LYS
1	D	154	LEU
1	D	196	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	90	ASN
1	A	116	ASN
1	B	34	HIS
1	B	90	ASN
1	B	116	ASN
1	B	122	ASN
1	B	212	GLN
1	C	34	HIS
1	C	90	ASN
1	C	116	ASN
1	C	212	GLN
1	C	218	ASN
1	D	34	HIS
1	D	90	ASN
1	D	143	ASN
1	D	212	GLN

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 (i)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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	$\#\|Z\| > 2$
3	ACY	A	401	2	1,3,3	3.35	1 (100%)	0,3,3	0.00	-
3	ACY	B	402	2	1,3,3	3.43	1 (100%)	0,3,3	0.00	-
3	ACY	C	403	2	1,3,3	3.38	1 (100%)	0,3,3	0.00	-
3	ACY	D	404	2	1,3,3	3.41	1 (100%)	0,3,3	0.00	-

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
3	ACY	A	401	2	-	0/0/0/0	0/0/0/0
3	ACY	B	402	2	-	0/0/0/0	0/0/0/0
3	ACY	C	403	2	-	0/0/0/0	0/0/0/0
3	ACY	D	404	2	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	ACY	CH3-C	3.35	1.53	1.48
3	C	403	ACY	CH3-C	3.38	1.53	1.48
3	D	404	ACY	CH3-C	3.41	1.53	1.48
3	B	402	ACY	CH3-C	3.43	1.53	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	ACY	5	0
3	B	402	ACY	1	0
3	D	404	ACY	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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

6.4 Ligands

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

6.5 Other polymers

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