



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:13 PM GMT

PDB ID : 3TBL
Title : Structure of Mono-ubiquitinated PCNA: Implications for DNA Polymerase Switching and Okazaki Fragment Maturation
Authors : Zhang, Z.; Lee, M.; Lee, E.; Zhang, S.
Deposited on : 2011-08-07
Resolution : 2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

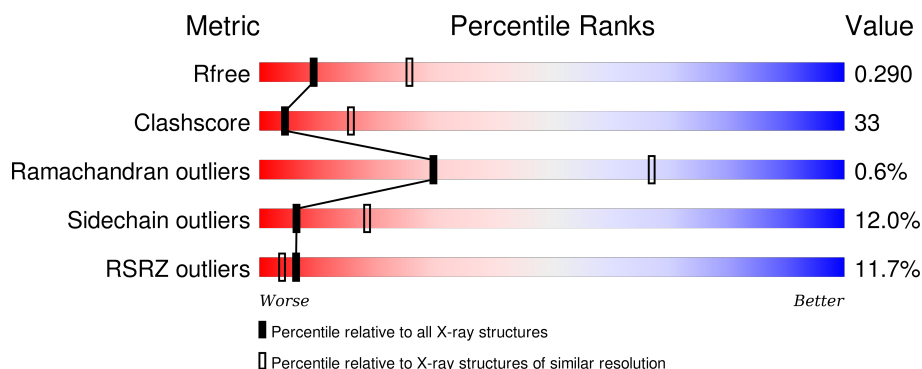
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	261	<div> <div>5%</div> <div> <div>56%</div> <div>36%</div> <div>• •</div> </div> </div>
1	B	261	<div> <div>10%</div> <div> <div>49%</div> <div>41%</div> <div>7%</div> <div>•</div> </div> </div>
1	C	261	<div> <div>6%</div> <div> <div>49%</div> <div>41%</div> <div>7%</div> <div>•</div> </div> </div>
2	D	76	<div> <div>33%</div> <div> <div>32%</div> <div>50%</div> <div>13%</div> <div>5%</div> </div> </div>
2	E	76	<div> <div>33%</div> <div> <div>30%</div> <div>55%</div> <div>8%</div> <div>• 5%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6947 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 Proliferating cell nuclear antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1922	1209	315	382	16			
1	B	251	Total	C	N	O	S	0	0	0
			1931	1214	316	385	16			
1	C	252	Total	C	N	O	S	0	0	0
			1942	1220	317	389	16			

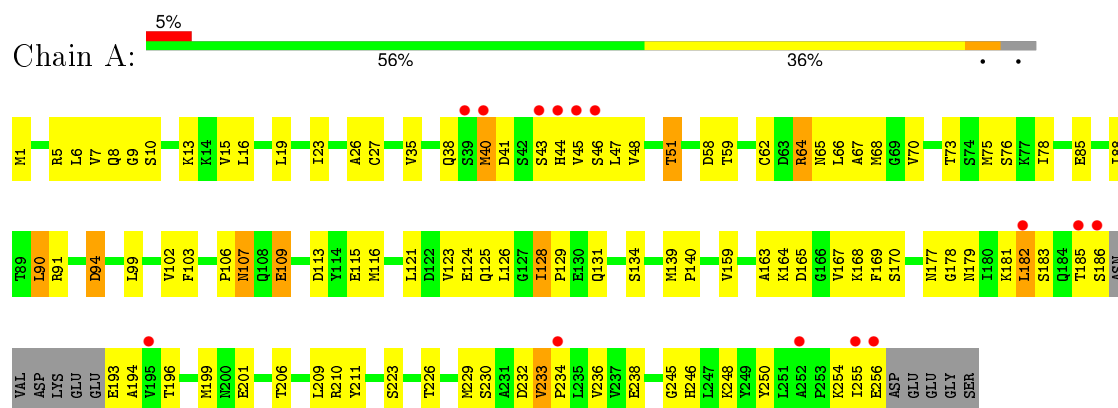
- Molecule 2 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	72	Total	C	N	O	0	0	0
			576	364	100	112			
2	E	72	Total	C	N	O	0	0	0
			576	364	100	112			

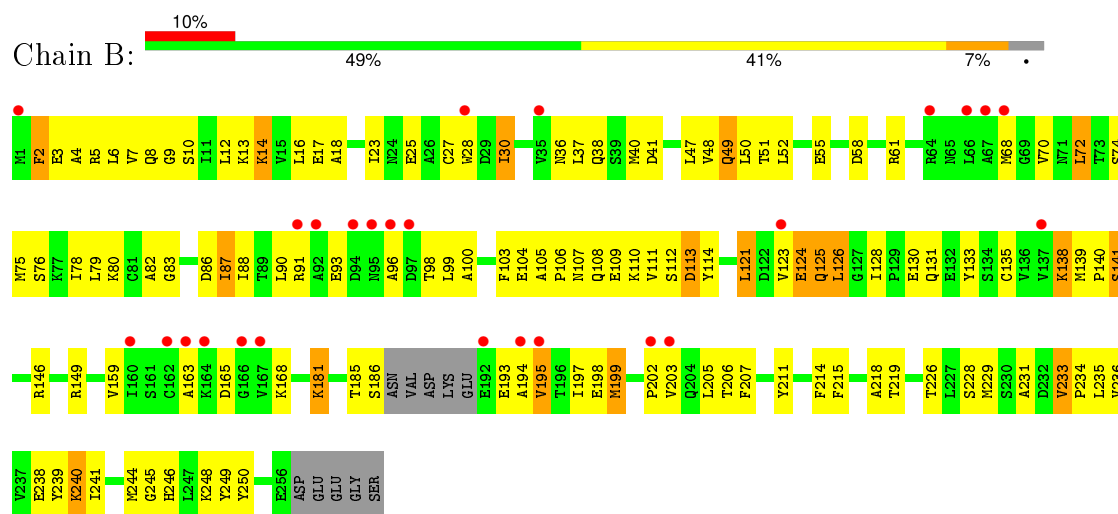
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

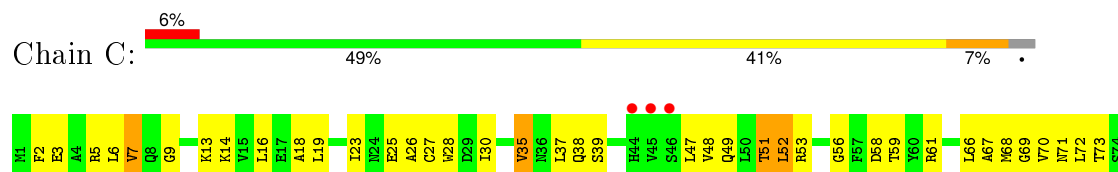
- Molecule 1: Proliferating cell nuclear antigen

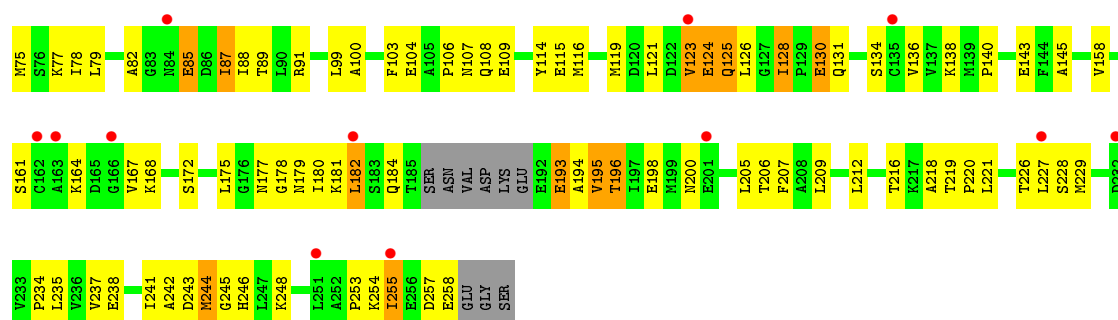


- Molecule 1: Proliferating cell nuclear antigen

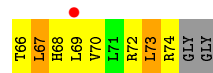
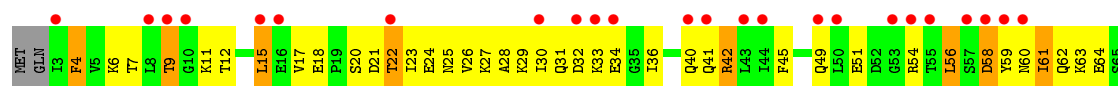


- Molecule 1: Proliferating cell nuclear antigen

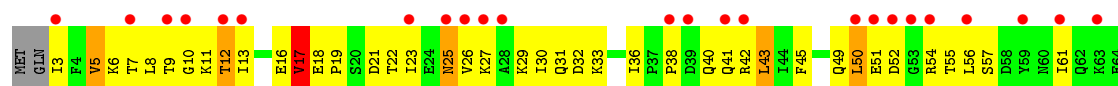




- Molecule 2: Ubiquitin



- Molecule 2: Ubiquitin



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	161.06Å 161.06Å 97.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.60 – 2.90 40.60 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (40.60-2.90) 99.3 (40.60-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.83 (at 2.90Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.222 , 0.293 0.222 , 0.290	Depositor DCC
R_{free} test set	1461 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	83.7	Xtriage
Anisotropy	0.767	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 92.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 28719 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6947	wwPDB-VP
Average B, all atoms (Å ²)	127.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [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	0.29	0/1947	0.54	1/2629 (0.0%)
1	B	0.27	0/1956	0.50	0/2641
1	C	0.28	0/1967	0.51	0/2656
2	D	0.29	0/582	0.56	0/784
2	E	0.27	0/582	0.51	0/784
All	All	0.28	0/7034	0.52	1/9494 (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
2	E	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	90	LEU	CA-CB-CG	5.82	128.68	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	17	VAL	Peptide

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	1922	0	1934	94	0
1	B	1931	0	1940	133	0
1	C	1942	0	1945	114	0
2	D	576	0	603	80	0
2	E	576	0	603	51	0
All	All	6947	0	7025	459	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 33.

All (459) 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:257:ASP:HB2	1:C:258:GLU:HA	1.35	1.04
2:D:59:TYR:CE1	2:D:61:ILE:CG2	2.45	1.00
1:A:9:GLY:HA3	1:A:88:ILE:HD13	1.45	0.98
1:B:23:ILE:HG22	1:B:41:ASP:HA	1.46	0.98
1:B:233:VAL:HG23	1:B:234:PRO:HD2	1.45	0.98
2:E:17:VAL:HG23	2:E:18:GLU:H	1.27	0.97
1:C:255:ILE:HD12	1:C:255:ILE:H	1.29	0.96
2:D:59:TYR:HE1	2:D:61:ILE:CG2	1.77	0.96
1:A:128:ILE:HD12	1:A:128:ILE:H	1.30	0.94
2:D:28:ALA:HA	2:D:31:GLN:OE1	1.70	0.92
2:D:59:TYR:HE1	2:D:61:ILE:HG21	1.33	0.92
1:A:125:GLN:O	1:A:126:LEU:HG	1.69	0.91
2:E:17:VAL:HG21	2:E:29:LYS:NZ	1.85	0.90
2:D:20:SER:N	2:D:56:LEU:HD21	1.86	0.90
1:C:51:THR:O	1:C:245:GLY:HA3	1.71	0.89
1:A:90:LEU:HD12	1:A:99:LEU:HD11	1.55	0.89
1:B:74:SER:HB3	1:C:175:LEU:HD11	1.55	0.88
1:C:5:ARG:HB2	1:C:59:THR:HB	1.54	0.87
1:B:38:GLN:NE2	1:B:126:LEU:H	1.71	0.87
2:D:20:SER:H	2:D:56:LEU:HD11	1.38	0.86
1:B:38:GLN:HE22	1:B:126:LEU:H	1.24	0.86
1:A:185:THR:HA	1:A:186:SER:HB3	1.58	0.84
1:B:185:THR:HA	1:B:186:SER:HB2	1.59	0.84
2:D:15:LEU:HD13	2:D:17:VAL:HG13	1.57	0.84
2:D:61:ILE:O	2:D:61:ILE:HG13	1.76	0.84
1:B:238:GLU:HG2	1:B:240:LYS:NZ	1.93	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:38:GLN:HG2	1:C:49:GLN:HG2	1.61	0.82
2:E:22:THR:HA	2:E:55:THR:HA	1.61	0.82
2:D:59:TYR:CE1	2:D:61:ILE:HG21	2.14	0.82
2:E:17:VAL:HG23	2:E:18:GLU:N	1.94	0.81
1:C:87:ILE:HG23	1:C:104:GLU:HB2	1.62	0.81
1:B:74:SER:HB3	1:C:175:LEU:CD1	2.11	0.81
1:B:23:ILE:HG13	1:B:72:LEU:CD2	2.12	0.80
2:E:5:VAL:HG23	2:E:13:ILE:HG13	1.64	0.79
2:E:16:GLU:O	2:E:17:VAL:HG22	1.82	0.79
2:E:13:ILE:HD12	2:E:33:LYS:HD3	1.65	0.78
2:D:18:GLU:O	2:D:21:ASP:HB2	1.83	0.78
1:C:226:THR:HB	1:C:238:GLU:HB3	1.65	0.78
1:A:1:MET:HA	1:A:64:ARG:HH22	1.47	0.78
1:B:141:SER:HB2	1:B:219:THR:HG23	1.67	0.76
1:C:123:VAL:HG22	1:C:124:GLU:H	1.48	0.76
1:C:134:SER:HA	1:C:200:ASN:OD1	1.84	0.76
2:D:36:ILE:HD13	2:D:41:GLN:HB3	1.68	0.75
1:A:90:LEU:CD1	1:A:99:LEU:HD11	2.16	0.75
1:C:51:THR:OG1	1:C:246:HIS:CE1	2.39	0.75
1:B:138:LYS:HG2	1:B:226:THR:HG22	1.69	0.75
1:B:23:ILE:HG13	1:B:72:LEU:HD23	1.69	0.74
1:C:51:THR:HG1	1:C:246:HIS:CE1	2.04	0.74
1:C:125:GLN:HE21	1:C:125:GLN:HA	1.53	0.74
1:B:16:LEU:HD22	1:B:79:LEU:HD12	1.71	0.73
1:C:26:ALA:HB1	1:C:37:LEU:HD11	1.70	0.72
2:E:43:LEU:HD13	2:E:50:LEU:HB2	1.71	0.72
1:B:185:THR:HB	1:B:186:SER:C	2.09	0.72
1:B:241:ILE:H	1:B:241:ILE:HD12	1.54	0.72
2:D:20:SER:H	2:D:56:LEU:HD21	1.53	0.71
2:D:56:LEU:HA	2:D:59:TYR:CE2	2.24	0.71
1:C:5:ARG:HG2	1:C:89:THR:HG22	1.71	0.71
1:C:257:ASP:CB	1:C:258:GLU:HA	2.15	0.71
1:A:164:LYS:NZ	2:D:72:ARG:HH12	1.88	0.71
1:B:193:GLU:HG2	1:B:194:ALA:N	2.04	0.71
2:E:17:VAL:HG21	2:E:29:LYS:HZ2	1.50	0.71
1:A:47:LEU:HD12	1:A:48:VAL:N	2.06	0.71
2:D:6:LYS:HA	2:D:11:LYS:O	1.91	0.71
1:C:167:VAL:HG12	1:C:182:LEU:HB2	1.71	0.70
1:A:140:PRO:HG3	1:A:193:GLU:HA	1.72	0.70
2:D:51:GLU:HB3	2:D:54:ARG:HD3	1.74	0.70
1:A:126:LEU:HD12	1:A:126:LEU:O	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:85:GLU:H	1:C:85:GLU:CD	1.94	0.70
2:D:6:LYS:HB2	2:D:12:THR:CG2	2.22	0.69
1:A:123:VAL:HG23	1:A:124:GLU:H	1.58	0.69
2:E:7:THR:HG23	2:E:9:THR:H	1.57	0.69
1:B:38:GLN:HE21	1:B:125:GLN:HA	1.57	0.69
1:A:47:LEU:HD12	1:A:48:VAL:H	1.58	0.69
1:C:75:MET:HA	1:C:116:MET:HE1	1.75	0.69
1:C:238:GLU:OE1	1:C:248:LYS:HG2	1.93	0.68
1:B:226:THR:OG1	1:B:238:GLU:HB3	1.94	0.68
1:A:64:ARG:CZ	1:A:94:ASP:HA	2.24	0.68
1:B:47:LEU:HB3	1:B:250:TYR:HB2	1.73	0.68
1:B:93:GLU:H	1:B:96:ALA:HB2	1.60	0.67
1:B:207:PHE:CZ	1:B:235:LEU:HB2	2.30	0.67
1:C:14:LYS:HD3	1:C:220:PRO:HB2	1.77	0.66
1:B:112:SER:HB3	1:C:180:ILE:HD13	1.76	0.66
2:E:17:VAL:HG21	2:E:29:LYS:HZ3	1.59	0.66
2:D:20:SER:H	2:D:56:LEU:CD1	2.08	0.66
2:E:6:LYS:HD3	2:E:12:THR:HG23	1.77	0.66
1:B:233:VAL:HG23	1:B:234:PRO:CD	2.24	0.65
1:B:238:GLU:HG2	1:B:240:LYS:HZ1	1.61	0.65
2:E:23:ILE:HG12	2:E:54:ARG:O	1.95	0.65
1:B:207:PHE:CE1	1:B:235:LEU:HB2	2.31	0.65
1:B:6:LEU:HB3	1:B:88:ILE:HD11	1.77	0.65
1:C:255:ILE:CD1	1:C:255:ILE:H	2.06	0.65
2:E:43:LEU:H	2:E:43:LEU:HD12	1.60	0.65
1:C:193:GLU:OE1	1:C:193:GLU:HA	1.96	0.65
1:A:90:LEU:HD11	1:A:99:LEU:HD21	1.79	0.64
1:B:38:GLN:NE2	1:B:126:LEU:N	2.44	0.64
2:E:19:PRO:HA	2:E:56:LEU:HB2	1.79	0.64
1:C:5:ARG:HG2	1:C:89:THR:CG2	2.26	0.64
1:A:134:SER:H	1:A:230:SER:HB3	1.62	0.64
1:C:123:VAL:HG22	1:C:124:GLU:N	2.13	0.64
2:D:25:ASN:O	2:D:29:LYS:HG3	1.98	0.64
1:B:2:PHE:HA	1:B:61:ARG:O	1.98	0.64
1:B:109:GLU:O	1:B:110:LYS:HB3	1.97	0.64
1:A:168:LYS:HG3	1:A:181:LYS:HD3	1.80	0.63
1:B:239:TYR:C	1:B:240:LYS:HZ3	2.02	0.63
1:B:5:ARG:HE	1:B:87:ILE:HD11	1.63	0.63
2:D:23:ILE:HD12	2:D:23:ILE:H	1.62	0.63
1:B:139:MET:HB2	1:B:140:PRO:HD2	1.81	0.63
1:A:51:THR:O	1:A:245:GLY:HA3	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:53:ARG:HG2	1:C:244:MET:O	1.99	0.62
2:E:23:ILE:HG13	2:E:51:GLU:O	2.00	0.62
1:B:27:CYS:SG	1:B:121:LEU:HD13	2.40	0.62
1:A:47:LEU:HB3	1:A:250:TYR:HB2	1.82	0.62
2:D:56:LEU:O	2:D:59:TYR:O	2.18	0.62
2:D:56:LEU:HA	2:D:59:TYR:CZ	2.35	0.62
1:A:128:ILE:H	1:A:128:ILE:CD1	2.09	0.62
1:B:241:ILE:HD12	1:B:241:ILE:N	2.15	0.62
2:D:45:PHE:HB2	2:D:67:LEU:HD22	1.81	0.62
1:C:136:VAL:CG1	1:C:198:GLU:HB3	2.30	0.61
2:D:42:ARG:HG2	2:D:70:VAL:O	2.00	0.61
1:C:255:ILE:HD12	1:C:255:ILE:N	2.10	0.61
2:E:5:VAL:HG23	2:E:13:ILE:CG1	2.30	0.61
1:B:83:GLY:O	1:B:86:ASP:HB2	2.00	0.61
1:C:18:ALA:HB1	1:C:218:ALA:HB2	1.82	0.61
1:A:9:GLY:CA	1:A:88:ILE:HD13	2.28	0.61
1:B:2:PHE:CG	1:B:30:ILE:HD11	2.36	0.60
1:A:47:LEU:CD1	1:A:126:LEU:HD11	2.31	0.60
2:D:6:LYS:HB2	2:D:12:THR:HG22	1.84	0.60
1:A:1:MET:HE3	1:A:91:ARG:HH11	1.66	0.60
2:E:17:VAL:HG11	2:E:29:LYS:HZ3	1.67	0.60
1:A:178:GLY:HA3	1:C:114:TYR:CD1	2.37	0.60
1:A:128:ILE:N	1:A:128:ILE:HD12	2.10	0.59
1:B:238:GLU:C	1:B:240:LYS:HZ1	2.06	0.59
1:B:10:SER:C	1:B:14:LYS:HZ2	2.05	0.59
1:B:7:VAL:O	1:B:8:GLN:HB3	2.01	0.59
2:D:59:TYR:CE1	2:D:61:ILE:HG22	2.37	0.59
1:B:2:PHE:CD1	1:B:30:ILE:HD11	2.37	0.59
1:C:25:GLU:HG2	1:C:119:MET:HE1	1.83	0.59
2:E:31:GLN:HA	2:E:36:ILE:H	1.68	0.59
1:A:177:ASN:OD1	1:C:115:GLU:HG2	2.03	0.59
1:C:140:PRO:HD3	1:C:194:ALA:O	2.02	0.59
2:D:27:LYS:HB3	2:D:41:GLN:OE1	2.03	0.58
1:A:123:VAL:O	1:A:124:GLU:HG2	2.03	0.58
2:D:20:SER:N	2:D:56:LEU:HD11	2.13	0.58
1:B:135:CYS:SG	1:B:203:VAL:HG23	2.43	0.58
2:D:61:ILE:HD12	2:D:62:GLN:O	2.03	0.58
2:E:23:ILE:HB	2:E:52:ASP:HA	1.86	0.58
1:A:193:GLU:HG3	1:A:194:ALA:N	2.18	0.58
1:C:16:LEU:HD22	1:C:79:LEU:HD13	1.86	0.58
1:A:163:ALA:C	1:A:199:MET:HE3	2.23	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:LYS:HB2	1:B:181:LYS:HG3	1.86	0.58
2:E:6:LYS:HE2	2:E:10:GLY:C	2.24	0.57
1:B:110:LYS:O	1:B:110:LYS:HG3	2.03	0.57
1:B:3:GLU:HG3	1:B:3:GLU:O	2.02	0.57
1:A:27:CYS:SG	1:A:67:ALA:HB1	2.44	0.57
1:B:51:THR:O	1:B:245:GLY:HA3	2.04	0.57
1:A:23:ILE:HG21	1:A:26:ALA:HB2	1.86	0.57
1:B:93:GLU:N	1:B:96:ALA:HB2	2.19	0.57
1:A:107:ASN:HB2	1:A:109:GLU:CD	2.25	0.57
2:D:4:PHE:HB3	2:D:12:THR:HB	1.85	0.57
2:D:28:ALA:CA	2:D:31:GLN:OE1	2.50	0.57
1:A:90:LEU:CD1	1:A:99:LEU:HD21	2.35	0.57
2:E:45:PHE:HB3	2:E:50:LEU:HD11	1.86	0.57
1:C:35:VAL:HG13	1:C:52:LEU:HB2	1.87	0.57
2:D:36:ILE:O	2:D:36:ILE:HD12	2.05	0.56
2:D:72:ARG:NH1	2:D:73:LEU:O	2.38	0.56
1:B:10:SER:O	1:B:13:LYS:HB2	2.05	0.56
1:B:5:ARG:NE	1:B:87:ILE:HD11	2.20	0.56
2:E:26:VAL:HG21	2:E:56:LEU:HD11	1.88	0.56
1:C:85:GLU:HG2	1:C:106:PRO:HG3	1.88	0.56
1:A:123:VAL:HG23	1:A:124:GLU:N	2.19	0.56
1:C:158:VAL:HB	1:C:209:LEU:HD21	1.87	0.56
2:D:6:LYS:HB2	2:D:12:THR:HG23	1.88	0.56
2:D:63:LYS:HG3	2:D:64:GLU:HG2	1.86	0.56
1:A:164:LYS:NZ	2:D:72:ARG:NH1	2.54	0.56
2:D:7:THR:OG1	2:D:9:THR:HG22	2.04	0.56
1:C:106:PRO:C	1:C:108:GLN:H	2.09	0.56
2:E:27:LYS:HA	2:E:41:GLN:NE2	2.21	0.56
1:A:6:LEU:HD21	1:A:8:GLN:O	2.06	0.56
2:D:22:THR:O	2:D:26:VAL:HG23	2.05	0.56
2:D:17:VAL:HG12	2:D:29:LYS:NZ	2.21	0.56
1:A:255:ILE:O	1:A:256:GLU:HB2	2.06	0.55
1:A:47:LEU:HD11	1:A:126:LEU:HD11	1.89	0.55
2:D:20:SER:H	2:D:56:LEU:CD2	2.19	0.55
1:C:99:LEU:O	1:C:115:GLU:HA	2.06	0.55
1:B:163:ALA:O	1:B:197:ILE:HG21	2.07	0.55
1:B:88:ILE:C	1:B:88:ILE:HD12	2.27	0.55
1:B:228:SER:HB2	1:B:236:VAL:HB	1.87	0.55
2:D:9:THR:HG22	2:D:11:LYS:HG2	1.88	0.55
1:C:25:GLU:HG2	1:C:119:MET:CE	2.36	0.55
1:A:6:LEU:CD2	1:A:8:GLN:O	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:VAL:HG13	1:B:72:LEU:HD12	1.88	0.55
2:D:31:GLN:HB3	2:D:36:ILE:O	2.07	0.55
1:C:238:GLU:OE2	1:C:248:LYS:HE3	2.07	0.55
1:B:36:ASN:OD1	1:B:51:THR:HG22	2.06	0.55
2:D:6:LYS:HG3	2:D:11:LYS:C	2.26	0.55
2:E:18:GLU:HG3	2:E:19:PRO:CD	2.37	0.54
1:B:38:GLN:NE2	1:B:125:GLN:HA	2.23	0.54
1:C:7:VAL:HG13	1:C:58:ASP:OD2	2.08	0.54
1:B:86:ASP:HA	1:B:106:PRO:HD3	1.88	0.54
1:A:164:LYS:HZ3	2:D:72:ARG:NH1	2.06	0.54
2:D:24:GLU:H	2:D:24:GLU:CD	2.11	0.54
1:C:3:GLU:CD	1:C:91:ARG:HH21	2.11	0.54
1:A:27:CYS:HA	1:A:68:MET:O	2.08	0.54
1:B:82:ALA:HB2	1:B:103:PHE:CD2	2.43	0.53
1:A:167:VAL:HG13	1:A:182:LEU:HB2	1.90	0.53
1:B:40:MET:SD	1:B:47:LEU:HD13	2.48	0.53
1:A:64:ARG:NH1	1:A:94:ASP:HA	2.24	0.53
1:B:125:GLN:HG3	1:B:126:LEU:N	2.23	0.53
1:C:125:GLN:HE21	1:C:125:GLN:CA	2.15	0.53
1:A:70:VAL:HG23	1:A:116:MET:HE1	1.90	0.53
1:A:38:GLN:HE21	1:A:125:GLN:HA	1.74	0.53
1:B:124:GLU:O	1:B:124:GLU:HG2	2.09	0.53
2:E:19:PRO:HB2	2:E:57:SER:OG	2.09	0.53
2:D:31:GLN:CB	2:D:36:ILE:O	2.57	0.53
1:C:5:ARG:HB2	1:C:59:THR:CB	2.32	0.53
2:D:7:THR:HG22	2:D:69:LEU:HD23	1.91	0.53
1:B:110:LYS:HE3	1:C:143:GLU:OE2	2.09	0.53
1:C:130:GLU:CG	1:C:131:GLN:N	2.71	0.53
2:E:43:LEU:CD1	2:E:50:LEU:HB2	2.38	0.53
2:D:30:ILE:HD12	2:D:41:GLN:HE22	1.75	0.52
1:C:27:CYS:SG	1:C:67:ALA:HB1	2.48	0.52
2:D:6:LYS:HG2	2:D:7:THR:O	2.08	0.52
1:C:234:PRO:HA	1:C:253:PRO:HD3	1.91	0.52
1:A:40:MET:HE2	1:A:46:SER:O	2.08	0.52
1:B:49:GLN:HE22	1:B:51:THR:HG22	1.72	0.52
1:C:6:LEU:O	1:C:87:ILE:HD12	2.10	0.52
1:C:241:ILE:O	1:C:244:MET:HB2	2.10	0.52
1:C:181:LYS:HG2	1:C:182:LEU:H	1.75	0.52
1:C:164:LYS:O	1:C:164:LYS:HG3	2.10	0.52
2:D:42:ARG:NH1	2:D:49:GLN:NE2	2.56	0.52
1:A:64:ARG:NH2	1:A:94:ASP:HA	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:238:GLU:HG3	1:B:248:LYS:HG2	1.91	0.51
2:D:59:TYR:CE1	2:D:61:ILE:HG23	2.44	0.51
1:B:23:ILE:CG2	1:B:41:ASP:HA	2.30	0.51
1:C:13:LYS:HG2	1:C:79:LEU:HB3	1.92	0.51
2:D:6:LYS:NZ	2:D:68:HIS:CE1	2.78	0.51
2:D:54:ARG:NH1	2:D:58:ASP:HB3	2.26	0.51
1:A:85:GLU:HB3	1:A:106:PRO:HG3	1.91	0.51
1:C:106:PRO:O	1:C:107:ASN:CG	2.49	0.51
2:D:21:ASP:H	2:D:56:LEU:CD2	2.24	0.51
1:B:47:LEU:HD11	1:B:126:LEU:HG	1.92	0.51
2:D:15:LEU:C	2:D:15:LEU:HD12	2.31	0.51
1:A:5:ARG:HB3	1:A:59:THR:HB	1.93	0.51
2:E:38:PRO:HA	2:E:41:GLN:HG2	1.93	0.51
1:A:167:VAL:CG1	1:A:182:LEU:HB2	2.41	0.50
1:B:133:TYR:CD2	1:B:228:SER:HB3	2.47	0.50
1:A:139:MET:HG3	1:A:140:PRO:HD2	1.93	0.50
1:A:230:SER:O	1:A:233:VAL:HG12	2.11	0.50
1:B:38:GLN:HA	1:B:48:VAL:O	2.12	0.50
1:A:206:THR:HB	1:A:254:LYS:HB3	1.94	0.50
2:E:42:ARG:HB2	2:E:70:VAL:HG23	1.93	0.50
1:B:231:ALA:O	1:B:233:VAL:HG12	2.11	0.50
1:C:138:LYS:O	1:C:195:VAL:HA	2.11	0.50
1:B:215:PHE:CD1	1:B:249:TYR:CD1	2.99	0.50
1:B:240:LYS:HB3	1:B:240:LYS:NZ	2.26	0.50
1:B:68:MET:HE1	1:B:99:LEU:HD22	1.93	0.50
2:E:72:ARG:O	2:E:73:LEU:HB3	2.12	0.50
1:B:199:MET:HE1	1:B:202:PRO:HA	1.93	0.50
2:E:23:ILE:HD12	2:E:50:LEU:HB3	1.92	0.50
2:D:11:LYS:HG3	2:D:11:LYS:O	2.10	0.50
1:A:255:ILE:O	1:A:256:GLU:CB	2.60	0.50
1:B:105:ALA:C	1:B:107:ASN:N	2.64	0.50
1:C:106:PRO:C	1:C:108:GLN:N	2.66	0.50
1:B:105:ALA:C	1:B:107:ASN:H	2.14	0.50
1:B:146:ARG:HD3	1:B:149:ARG:NH1	2.27	0.50
1:A:78:ILE:HD11	1:A:116:MET:HB3	1.94	0.49
1:C:246:HIS:CE1	1:C:248:LYS:NZ	2.81	0.49
1:B:99:LEU:HD12	1:B:100:ALA:N	2.27	0.49
1:A:236:VAL:HG22	1:A:250:TYR:CD1	2.48	0.49
2:E:27:LYS:HG2	2:E:41:GLN:HE21	1.77	0.49
2:D:15:LEU:O	2:D:15:LEU:HD12	2.12	0.49
2:E:9:THR:OG1	2:E:11:LYS:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:GLN:HE22	1:C:128:ILE:HG22	1.78	0.49
1:A:62:CYS:SG	1:A:64:ARG:O	2.68	0.49
1:C:130:GLU:CG	1:C:131:GLN:H	2.25	0.49
1:B:38:GLN:HB2	1:B:126:LEU:HD22	1.94	0.49
1:A:88:ILE:HG13	1:A:103:PHE:CD1	2.47	0.49
2:D:40:GLN:HA	2:D:72:ARG:HG2	1.95	0.49
1:B:112:SER:CB	1:C:180:ILE:HD13	2.42	0.49
1:B:87:ILE:HG23	1:B:104:GLU:HB2	1.95	0.49
1:B:130:GLU:O	1:B:130:GLU:HG3	2.13	0.49
1:C:71:ASN:OD1	1:C:73:THR:HB	2.12	0.49
1:B:28:TRP:CD1	1:B:37:LEU:HD12	2.49	0.48
1:B:74:SER:O	1:B:78:ILE:HD12	2.13	0.48
1:A:238:GLU:OE2	1:A:248:LYS:HD2	2.13	0.48
1:A:109:GLU:N	1:A:109:GLU:OE1	2.45	0.48
1:A:1:MET:HA	1:A:64:ARG:NH2	2.22	0.48
1:B:246:HIS:CD2	1:B:248:LYS:HZ3	2.31	0.48
1:B:3:GLU:HA	1:B:90:LEU:O	2.14	0.48
1:B:18:ALA:HB2	1:B:218:ALA:HA	1.94	0.48
1:C:28:TRP:HE1	1:C:70:VAL:CG1	2.27	0.48
2:E:61:ILE:HG23	2:E:65:SER:OG	2.13	0.48
2:D:28:ALA:O	2:D:31:GLN:OE1	2.32	0.48
2:D:36:ILE:HD11	2:D:41:GLN:OE1	2.14	0.48
1:B:193:GLU:CG	1:B:194:ALA:N	2.72	0.48
1:B:246:HIS:CD2	1:B:248:LYS:NZ	2.82	0.47
1:A:233:VAL:HG22	1:A:234:PRO:HD2	1.96	0.47
1:C:9:GLY:HA3	1:C:88:ILE:HD12	1.95	0.47
2:D:73:LEU:HG	2:D:74:ARG:N	2.29	0.47
2:E:25:ASN:O	2:E:29:LYS:HG3	2.15	0.47
1:C:178:GLY:C	1:C:179:ASN:OD1	2.53	0.47
1:C:2:PHE:CD1	1:C:30:ILE:HG21	2.49	0.47
2:E:18:GLU:HG3	2:E:19:PRO:N	2.29	0.47
2:D:31:GLN:O	2:D:32:ASP:C	2.51	0.47
1:B:238:GLU:HG2	1:B:240:LYS:HZ2	1.76	0.47
1:C:130:GLU:HG2	1:C:131:GLN:N	2.30	0.47
2:D:34:GLU:OE1	2:D:34:GLU:HA	2.15	0.47
1:B:70:VAL:HG13	1:B:72:LEU:CD1	2.45	0.47
2:D:17:VAL:HG12	2:D:29:LYS:HZ2	1.80	0.47
1:A:10:SER:O	1:A:13:LYS:HB2	2.15	0.47
1:A:246:HIS:ND1	1:A:248:LYS:HD3	2.29	0.47
1:C:49:GLN:HE22	1:C:128:ILE:CG2	2.28	0.47
2:E:23:ILE:N	2:E:54:ARG:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:ILE:CD1	1:A:116:MET:HB3	2.45	0.46
1:A:7:VAL:HG23	1:A:58:ASP:CG	2.35	0.46
1:A:47:LEU:HD13	1:A:126:LEU:HD11	1.95	0.46
1:A:159:VAL:HG12	1:A:206:THR:OG1	2.14	0.46
1:B:88:ILE:HD12	1:B:88:ILE:O	2.15	0.46
1:B:159:VAL:HG22	1:B:206:THR:OG1	2.16	0.46
2:D:9:THR:CG2	2:D:11:LYS:HG2	2.45	0.46
1:C:138:LYS:NZ	1:C:196:THR:HG21	2.30	0.46
1:B:17:GLU:OE2	1:B:80:LYS:HE3	2.16	0.46
2:D:23:ILE:HG22	2:D:27:LYS:HE3	1.98	0.46
1:B:133:TYR:OH	1:B:236:VAL:HG21	2.16	0.46
1:A:102:VAL:HG22	1:A:113:ASP:OD1	2.15	0.46
1:A:185:THR:HA	1:A:186:SER:CB	2.30	0.46
1:B:229:MET:HG2	1:B:235:LEU:CD1	2.46	0.46
2:D:23:ILE:HD12	2:D:23:ILE:N	2.28	0.45
1:A:164:LYS:HZ2	2:D:72:ARG:HH12	1.63	0.45
1:C:99:LEU:HD12	1:C:100:ALA:H	1.81	0.45
1:C:123:VAL:CG2	1:C:124:GLU:H	2.24	0.45
2:E:43:LEU:HD22	2:E:50:LEU:HD23	1.97	0.45
1:B:16:LEU:HD22	1:B:79:LEU:CD1	2.45	0.45
1:C:246:HIS:CE1	1:C:248:LYS:HZ2	2.33	0.45
1:C:5:ARG:CG	1:C:89:THR:HG22	2.44	0.45
1:B:47:LEU:HD21	1:B:126:LEU:HG	1.98	0.45
1:C:125:GLN:NE2	1:C:125:GLN:CA	2.80	0.45
2:E:42:ARG:HH21	2:E:49:GLN:HB2	1.81	0.45
1:B:114:TYR:CD1	1:C:178:GLY:HA3	2.52	0.45
2:D:15:LEU:CD1	2:D:17:VAL:HG13	2.38	0.45
2:E:30:ILE:HB	2:E:41:GLN:HE22	1.81	0.45
1:A:159:VAL:CG2	1:A:170:SER:HB2	2.47	0.45
1:B:131:GLN:NE2	1:B:233:VAL:HG21	2.32	0.45
1:B:49:GLN:HE22	1:B:51:THR:CG2	2.29	0.45
1:B:2:PHE:CE1	1:B:4:ALA:HB2	2.52	0.45
1:C:30:ILE:HB	1:C:66:LEU:HD12	1.99	0.45
1:C:38:GLN:O	1:C:124:GLU:CB	2.65	0.44
1:C:209:LEU:HD23	1:C:212:LEU:HD12	1.99	0.44
1:B:211:TYR:O	1:B:214:PHE:HB2	2.16	0.44
1:C:27:CYS:HA	1:C:68:MET:O	2.17	0.44
2:D:23:ILE:CG2	2:D:27:LYS:HE3	2.47	0.44
1:C:78:ILE:HG13	1:C:116:MET:CE	2.48	0.44
1:B:121:LEU:HD23	1:B:121:LEU:H	1.82	0.44
1:A:16:LEU:HG	1:A:75:MET:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:17:VAL:CG2	2:E:18:GLU:N	2.64	0.44
1:C:207:PHE:CE1	1:C:253:PRO:HB3	2.53	0.44
1:A:45:VAL:HG21	1:A:211:TYR:OH	2.18	0.44
1:C:75:MET:HG3	1:C:116:MET:HE3	1.98	0.44
1:B:7:VAL:HG12	1:B:58:ASP:OD1	2.18	0.44
1:A:199:MET:HE2	1:A:199:MET:HB3	1.77	0.44
1:B:93:GLU:O	1:B:96:ALA:N	2.51	0.44
2:D:24:GLU:N	2:D:24:GLU:CD	2.70	0.44
2:D:20:SER:CA	2:D:56:LEU:HD21	2.48	0.44
1:C:206:THR:HB	1:C:254:LYS:HB3	1.99	0.44
2:D:59:TYR:CD1	2:D:61:ILE:CG2	3.00	0.43
1:B:241:ILE:HG22	1:B:244:MET:HB3	2.00	0.43
1:B:50:LEU:HD21	1:B:52:LEU:HD21	2.00	0.43
1:C:27:CYS:O	1:C:124:GLU:OE2	2.36	0.43
1:C:38:GLN:HA	1:C:48:VAL:O	2.17	0.43
1:B:75:MET:HA	1:B:78:ILE:HD12	2.00	0.43
1:B:240:LYS:N	1:B:240:LYS:HZ3	2.16	0.43
1:C:145:ALA:HA	1:C:216:THR:HG21	1.99	0.43
1:B:241:ILE:H	1:B:241:ILE:CD1	2.27	0.43
2:E:55:THR:OG1	2:E:56:LEU:N	2.51	0.43
2:D:28:ALA:O	2:D:31:GLN:CD	2.56	0.43
1:B:9:GLY:HA3	1:B:88:ILE:HG23	2.01	0.43
1:B:168:LYS:HD2	1:B:181:LYS:NZ	2.33	0.43
1:C:242:ALA:O	1:C:243:ASP:C	2.56	0.43
1:A:70:VAL:HG23	1:A:116:MET:CE	2.48	0.43
1:A:85:GLU:CB	1:A:106:PRO:HG3	2.49	0.43
2:E:40:GLN:HG2	2:E:40:GLN:O	2.19	0.43
1:A:169:PHE:HE2	1:A:182:LEU:HD23	1.83	0.43
1:C:69:GLY:HA2	1:C:121:LEU:HD22	2.01	0.43
1:B:185:THR:HG21	1:B:194:ALA:HA	2.01	0.42
2:E:43:LEU:HA	2:E:68:HIS:O	2.18	0.42
1:A:199:MET:HG3	1:A:199:MET:O	2.19	0.42
1:B:82:ALA:HB2	1:B:103:PHE:CG	2.53	0.42
1:A:70:VAL:HG21	1:A:75:MET:HE2	2.00	0.42
1:C:228:SER:O	1:C:235:LEU:HD12	2.19	0.42
1:B:30:ILE:O	1:B:30:ILE:HG12	2.18	0.42
1:B:91:ARG:O	1:B:99:LEU:HD12	2.18	0.42
1:A:10:SER:HA	1:A:13:LYS:HD3	2.02	0.42
1:A:38:GLN:NE2	1:A:125:GLN:HA	2.34	0.42
2:E:6:LYS:HZ1	2:E:10:GLY:HA2	1.84	0.42
1:C:9:GLY:HA3	1:C:88:ILE:CD1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:125:GLN:HB2	1:C:126:LEU:H	1.72	0.42
1:B:12:LEU:HA	1:B:12:LEU:HD23	1.81	0.42
1:B:28:TRP:NE1	1:B:70:VAL:HG11	2.35	0.42
1:C:51:THR:O	1:C:245:GLY:CA	2.57	0.42
1:C:7:VAL:O	1:C:87:ILE:HA	2.20	0.42
1:B:205:LEU:HD12	1:B:229:MET:CE	2.50	0.42
1:C:219:THR:N	1:C:220:PRO:CD	2.83	0.42
1:B:105:ALA:O	1:B:108:GLN:N	2.52	0.42
1:C:9:GLY:CA	1:C:88:ILE:HD12	2.50	0.42
1:A:99:LEU:O	1:A:115:GLU:HA	2.20	0.42
1:B:50:LEU:HD12	1:B:246:HIS:O	2.19	0.42
1:C:75:MET:HA	1:C:116:MET:CE	2.47	0.42
1:C:255:ILE:N	1:C:255:ILE:CD1	2.79	0.42
1:C:123:VAL:HG21	1:C:125:GLN:OE1	2.19	0.42
1:A:134:SER:HB3	1:A:201:GLU:HB3	2.02	0.42
2:E:29:LYS:O	2:E:32:ASP:HB3	2.20	0.41
1:C:5:ARG:CG	1:C:89:THR:CG2	2.95	0.41
1:C:56:GLY:HA3	1:C:244:MET:HA	2.02	0.41
2:E:18:GLU:HG3	2:E:19:PRO:HD2	2.02	0.41
1:A:193:GLU:CG	1:A:194:ALA:N	2.83	0.41
1:C:85:GLU:CG	1:C:106:PRO:HG3	2.49	0.41
1:A:125:GLN:O	1:A:126:LEU:CG	2.56	0.41
1:B:74:SER:HB3	1:C:175:LEU:HD13	1.96	0.41
1:C:23:ILE:HD13	1:C:39:SER:HB3	2.03	0.41
2:D:11:LYS:CG	2:D:11:LYS:O	2.68	0.41
1:C:168:LYS:HA	1:C:180:ILE:O	2.20	0.41
1:C:82:ALA:HB2	1:C:103:PHE:CE2	2.55	0.41
1:B:72:LEU:CD1	1:B:72:LEU:N	2.82	0.41
1:B:138:LYS:O	1:B:195:VAL:HA	2.21	0.41
1:B:113:ASP:OD1	1:B:114:TYR:N	2.53	0.41
1:B:47:LEU:HD11	1:B:126:LEU:CG	2.50	0.41
1:A:43:SER:HB2	1:A:45:VAL:HG23	2.01	0.41
1:C:19:LEU:HB3	1:C:72:LEU:HD13	2.03	0.41
1:B:229:MET:HG2	1:B:235:LEU:HD13	2.01	0.41
1:B:10:SER:C	1:B:14:LYS:NZ	2.73	0.41
1:A:121:LEU:HA	1:A:121:LEU:HD12	1.87	0.41
1:C:123:VAL:CG2	1:C:124:GLU:N	2.82	0.41
1:B:241:ILE:CG2	1:B:244:MET:HB3	2.50	0.41
1:A:165:ASP:OD1	1:A:165:ASP:N	2.41	0.41
2:D:36:ILE:C	2:D:36:ILE:HD12	2.41	0.41
2:D:6:LYS:HZ2	2:D:68:HIS:CE1	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:LEU:HB3	1:B:88:ILE:CD1	2.48	0.41
1:C:172:SER:CB	1:C:177:ASN:HB3	2.51	0.41
1:C:205:LEU:HD12	1:C:229:MET:HE3	2.03	0.41
2:E:7:THR:HG23	2:E:8:LEU:N	2.36	0.41
1:A:23:ILE:HD13	1:A:41:ASP:HA	2.02	0.41
1:B:36:ASN:OD1	1:B:50:LEU:O	2.39	0.40
2:D:4:PHE:HB2	2:D:66:THR:HA	2.02	0.40
1:C:182:LEU:HD13	1:C:182:LEU:HA	1.59	0.40
1:A:238:GLU:HG3	1:A:248:LYS:HG3	2.04	0.40
2:D:6:LYS:O	2:D:68:HIS:HA	2.21	0.40
1:A:159:VAL:HG23	1:A:159:VAL:O	2.21	0.40
1:C:16:LEU:HD21	1:C:75:MET:HE2	2.02	0.40
1:B:6:LEU:O	1:B:88:ILE:HG13	2.22	0.40
2:E:3:ILE:O	2:E:3:ILE:HG22	2.21	0.40
1:A:15:VAL:O	1:A:19:LEU:HD12	2.22	0.40
1:C:16:LEU:HD11	1:C:75:MET:HE1	2.02	0.40
1:B:203:VAL:HG12	1:B:205:LEU:HG	2.03	0.40
1:A:107:ASN:HB2	1:A:109:GLU:OE2	2.21	0.40
2:D:33:LYS:HG3	2:D:34:GLU:N	2.36	0.40
2:E:21:ASP:O	2:E:56:LEU:HD13	2.22	0.40
2:E:43:LEU:N	2:E:43:LEU:HD12	2.32	0.40
1:B:8:GLN:HG3	1:B:8:GLN:O	2.20	0.40
1:B:100:ALA:HA	1:B:114:TYR:O	2.21	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	246/261 (94%)	223 (91%)	21 (8%)	2 (1%)	24	60
1	B	247/261 (95%)	231 (94%)	16 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	248/261 (95%)	216 (87%)	31 (12%)	1 (0%)	39	74
2	D	70/76 (92%)	65 (93%)	4 (6%)	1 (1%)	14	44
2	E	70/76 (92%)	63 (90%)	6 (9%)	1 (1%)	14	44
All	All	881/935 (94%)	798 (91%)	78 (9%)	5 (1%)	30	67

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	17	VAL
1	A	94	ASP
2	D	58	ASP
1	C	123	VAL
1	A	129	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	218/228 (96%)	194 (89%)	24 (11%)	8	23
1	B	219/228 (96%)	192 (88%)	27 (12%)	6	17
1	C	220/228 (96%)	195 (89%)	25 (11%)	7	21
2	D	66/68 (97%)	56 (85%)	10 (15%)	3	10
2	E	66/68 (97%)	57 (86%)	9 (14%)	5	13
All	All	789/820 (96%)	694 (88%)	95 (12%)	6	18

All (95) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	VAL
1	A	40	MET
1	A	44	HIS
1	A	51	THR
1	A	64	ARG

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Mol	Chain	Res	Type
1	A	65	ASN
1	A	66	LEU
1	A	73	THR
1	A	76	SER
1	A	107	ASN
1	A	109	GLU
1	A	128	ILE
1	A	131	GLN
1	A	179	ASN
1	A	182	LEU
1	A	183	SER
1	A	196	THR
1	A	209	LEU
1	A	210	ARG
1	A	223	SER
1	A	226	THR
1	A	229	MET
1	A	232	ASP
1	A	233	VAL
1	B	2	PHE
1	B	14	LYS
1	B	25	GLU
1	B	30	ILE
1	B	49	GLN
1	B	55	GLU
1	B	72	LEU
1	B	76	SER
1	B	87	ILE
1	B	98	THR
1	B	111	VAL
1	B	113	ASP
1	B	121	LEU
1	B	123	VAL
1	B	124	GLU
1	B	125	GLN
1	B	126	LEU
1	B	128	ILE
1	B	138	LYS
1	B	141	SER
1	B	165	ASP
1	B	181	LYS
1	B	195	VAL

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Mol	Chain	Res	Type
1	B	198	GLU
1	B	199	MET
1	B	233	VAL
1	B	240	LYS
1	C	7	VAL
1	C	35	VAL
1	C	47	LEU
1	C	51	THR
1	C	52	LEU
1	C	61	ARG
1	C	77	LYS
1	C	85	GLU
1	C	87	ILE
1	C	109	GLU
1	C	124	GLU
1	C	125	GLN
1	C	128	ILE
1	C	130	GLU
1	C	161	SER
1	C	182	LEU
1	C	184	GLN
1	C	193	GLU
1	C	195	VAL
1	C	196	THR
1	C	221	LEU
1	C	227	LEU
1	C	237	VAL
1	C	244	MET
1	C	255	ILE
2	D	4	PHE
2	D	9	THR
2	D	15	LEU
2	D	22	THR
2	D	42	ARG
2	D	56	LEU
2	D	60	ASN
2	D	61	ILE
2	D	67	LEU
2	D	73	LEU
2	E	5	VAL
2	E	12	THR
2	E	25	ASN

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Mol	Chain	Res	Type
2	E	43	LEU
2	E	50	LEU
2	E	66	THR
2	E	67	LEU
2	E	69	LEU
2	E	72	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	ASN
1	B	36	ASN
1	B	38	GLN
1	B	49	GLN
1	C	49	GLN
1	C	125	GLN
1	C	246	HIS
2	D	49	GLN
2	D	68	HIS
2	E	41	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](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/261 (95%)	0.31	14 (5%) 28 21	68, 100, 160, 196	0
1	B	251/261 (96%)	0.68	26 (10%) 8 5	80, 121, 195, 248	0
1	C	252/261 (96%)	0.30	15 (5%) 25 18	73, 107, 186, 232	0
2	D	72/76 (94%)	1.50	25 (34%) 0 0	112, 170, 235, 266	0
2	E	72/76 (94%)	1.84	25 (34%) 0 0	133, 178, 222, 235	0
All	All	897/935 (95%)	0.63	105 (11%) 6 4	68, 116, 198, 266	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	95	ASN	7.5
2	E	53	GLY	6.0
2	E	52	ASP	6.0
1	B	194	ALA	5.7
1	B	96	ALA	5.5
1	B	1	MET	5.3
2	E	59	TYR	5.1
1	A	185	THR	5.0
2	E	26	VAL	4.8
1	B	202	PRO	4.7
2	D	41	GLN	4.7
2	E	38	PRO	4.7
1	B	123	VAL	4.7
2	E	51	GLU	4.2
2	E	50	LEU	4.0
2	D	40	GLN	3.9
1	B	28	TRP	3.9
1	A	40	MET	3.8
1	B	68	MET	3.8
1	B	192	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
2	D	49	GLN	3.7
1	A	186	SER	3.7
2	D	59	TYR	3.7
1	B	164	LYS	3.6
1	B	167	VAL	3.6
2	D	60	ASN	3.6
2	D	33	LYS	3.5
2	D	57	SER	3.5
2	E	54	ARG	3.5
2	D	53	GLY	3.4
1	B	97	ASP	3.4
2	D	30	ILE	3.4
1	B	94	ASP	3.3
2	E	61	ILE	3.3
2	D	43	LEU	3.3
1	A	45	VAL	3.3
2	E	56	LEU	3.3
1	A	252	ALA	3.2
1	B	166	GLY	3.2
1	B	66	LEU	3.1
1	B	162	CYS	3.1
2	E	10	GLY	3.1
2	E	41	GLN	3.0
1	B	92	ALA	3.0
1	A	44	HIS	3.0
1	C	45	VAL	3.0
1	A	39	SER	3.0
1	C	44	HIS	3.0
1	B	67	ALA	2.9
1	B	35	VAL	2.9
2	D	54	ARG	2.9
2	E	42	ARG	2.9
1	C	162	CYS	2.8
1	A	46	SER	2.7
2	D	34	GLU	2.7
2	E	67	LEU	2.7
1	B	195	VAL	2.7
2	E	13	ILE	2.7
2	E	27	LYS	2.7
2	E	25	ASN	2.6
2	D	15	LEU	2.6
1	A	255	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	163	ALA	2.6
1	A	182	LEU	2.6
1	C	182	LEU	2.6
2	D	10	GLY	2.6
2	D	32	ASP	2.6
2	D	8	LEU	2.5
2	D	55	THR	2.5
2	E	23	ILE	2.5
1	B	163	ALA	2.5
2	D	9	THR	2.5
1	A	234	PRO	2.5
2	D	3	ILE	2.4
1	C	84	ASN	2.4
1	B	64	ARG	2.4
2	D	69	LEU	2.4
1	A	43	SER	2.4
2	E	9	THR	2.4
1	A	256	GLU	2.4
1	C	255	ILE	2.3
1	B	137	VAL	2.3
2	D	50	LEU	2.3
2	E	3	ILE	2.3
2	E	39	ASP	2.3
1	C	46	SER	2.3
1	B	203	VAL	2.3
1	C	251	LEU	2.3
2	E	63	LYS	2.3
1	C	166	GLY	2.2
1	C	135	CYS	2.2
2	D	58	ASP	2.2
2	D	22	THR	2.2
2	D	16	GLU	2.1
1	A	195	VAL	2.1
1	B	91	ARG	2.1
2	E	7	THR	2.1
2	E	28	ALA	2.1
1	B	160	ILE	2.1
1	C	232	ASP	2.1
2	E	12	THR	2.1
1	C	123	VAL	2.0
1	C	227	LEU	2.0
1	C	201	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
2	D	44	ILE	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 carbohydrates 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.