



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:08 AM UTC

PDB ID : 2FVZ / pdb_00002fvz
Title : Human Inositol Monophosphatase 2
Authors : Ogg, D.; Hallberg, B.M.; Arrowsmith, C.; Berglund, H.; Collins, R.; Edwards, A.; Ehn, M.; Flodin, S.; Graslund, S.; Hammarstrom, M.; Hogbom, M.; Holmberg-Schiavone, L.; Kotenyova, T.; Kursula, P.; Nilsson-Ehle, P.; Nordlund, P.; Nyman, T.; Persson, C.; Sagemark, J.; Stenmark, P.; Sundstrom, M.; Van Den Berg, S.; Weigelt, J.; Thorsell, A.G.; Structural Genomics Consortium (SGC)
Deposited on : 2006-01-31
Resolution : 2.40 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

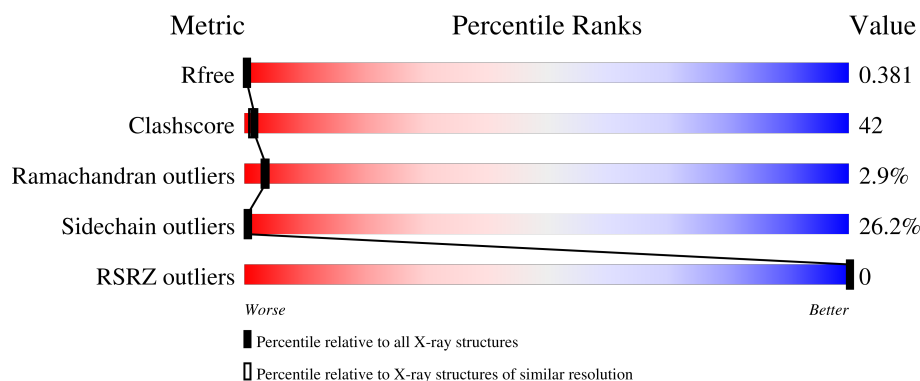
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 $\leq 5\%$. 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	273	
1	B	273	
1	C	273	
1	D	273	

Validation Pipeline (wwPDB-VP) : 2.49

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7516 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.

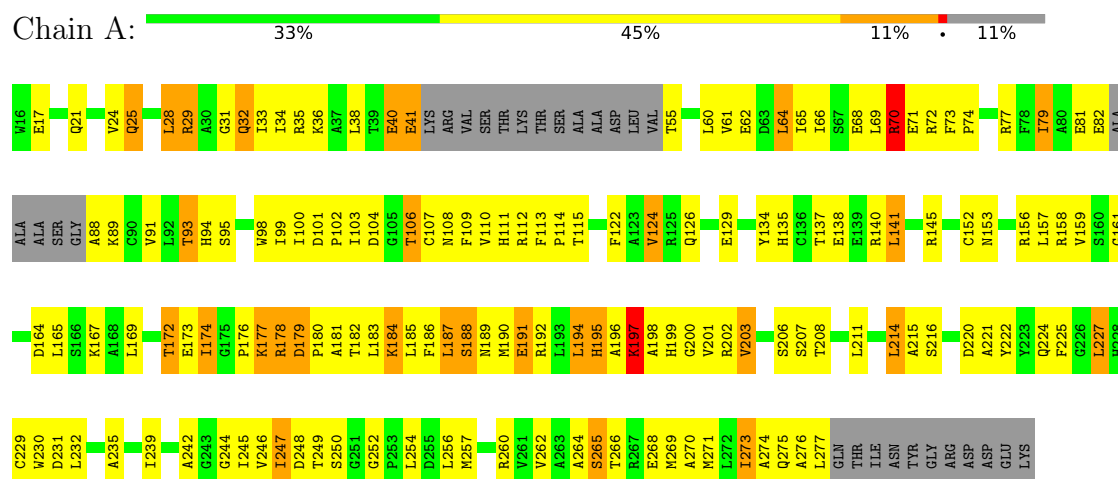
- Molecule 1 is a protein called Inositol monophosphatase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	244	Total	C	N	O	S	0	0	0
			1878	1185	337	344	12			
1	B	244	Total	C	N	O	S	0	0	0
			1878	1185	337	344	12			
1	C	244	Total	C	N	O	S	0	0	0
			1882	1188	338	344	12			
1	D	244	Total	C	N	O	S	0	0	0
			1878	1185	337	344	12			

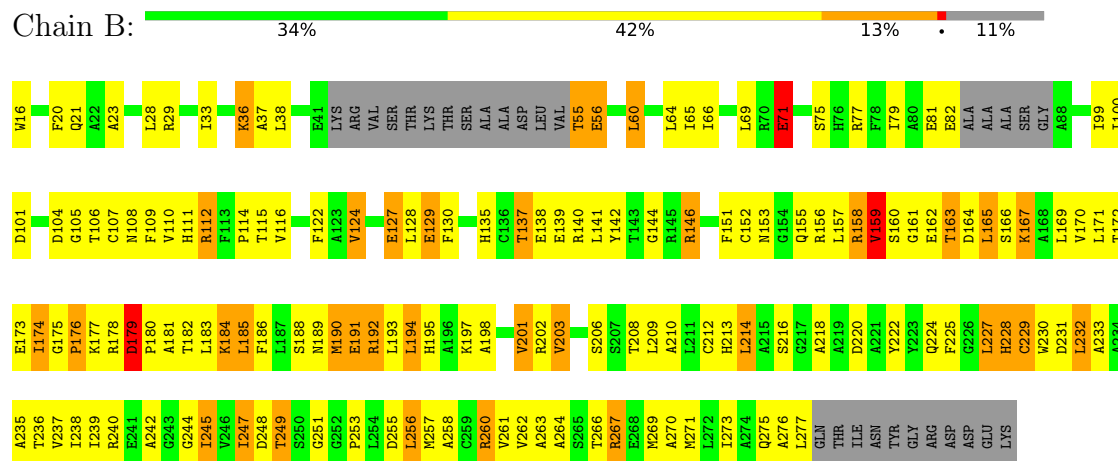
3 Residue-property plots

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.

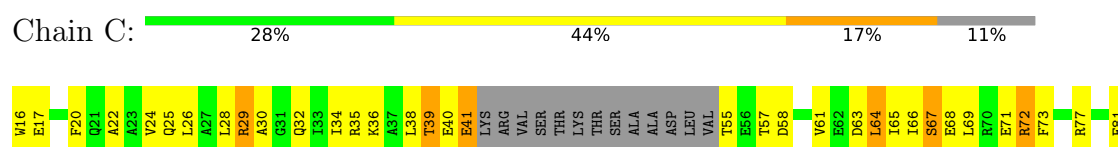
• Molecule 1: Inositol monophosphatase 2

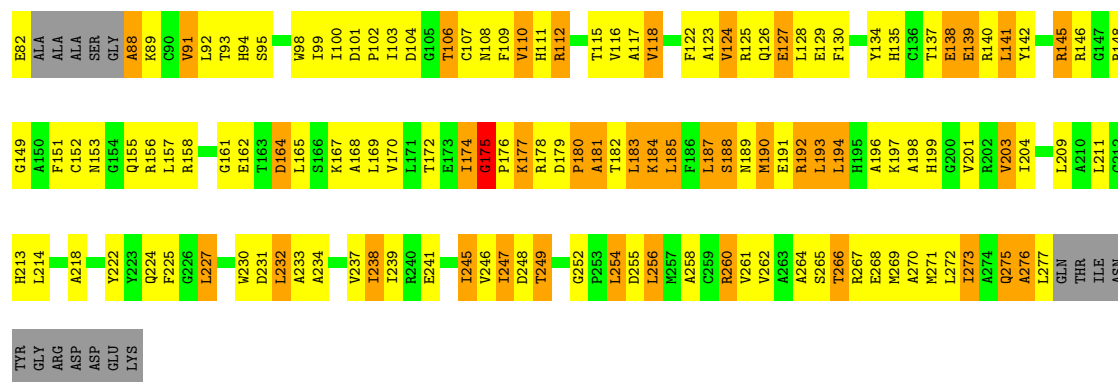


• Molecule 1: Inositol monophosphatase 2

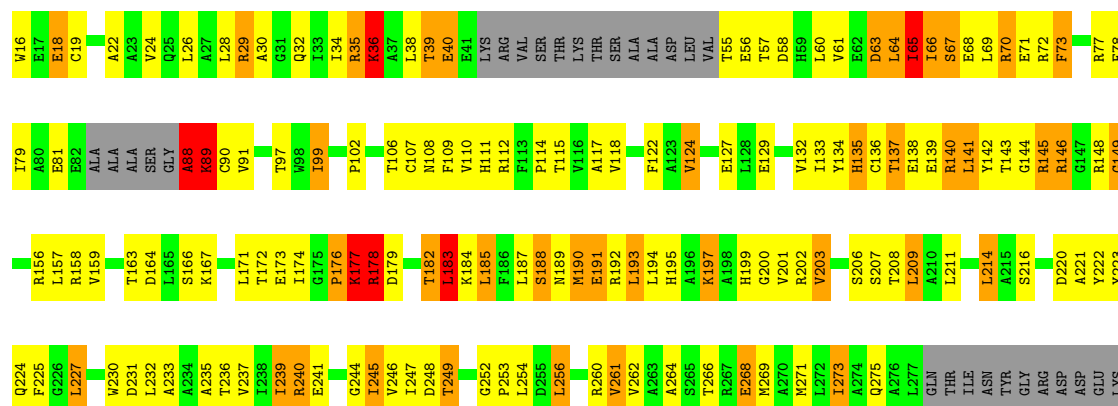


• Molecule 1: Inositol monophosphatase 2





• Molecule 1: Inositol monophosphatase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.03Å 96.95Å 106.97Å 90.00° 90.03° 90.00°	Depositor
Resolution (Å)	10.00 – 2.40 10.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.2 (10.00-2.40) 94.5 (10.00-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.88 (at 2.36Å)	Xtriage
Refinement program	SHELX, SHELXL-97	Depositor
R, R_{free}	0.211 , 0.297 0.209 , 0.381	Depositor DCC
R_{free} test set	34 reflections (0.02%)	wwPDB-VP
Wilson B-factor (Å ²)	26.6	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 50.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.447 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7516	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.19% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.42	0/1911	0.80	0/2587
1	B	0.52	2/1911 (0.1%)	0.87	2/2587 (0.1%)
1	C	0.51	1/1915 (0.1%)	0.81	0/2591
1	D	2.09	4/1911 (0.2%)	1.20	5/2587 (0.2%)
All	All	1.13	7/7648 (0.1%)	0.93	7/10352 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	D	0	3
All	All	0	4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	89	LYS	C-O	76.25	2.20	1.24
1	D	88	ALA	C-N	-41.92	0.74	1.33
1	D	65	ILE	CG1-CD1	12.83	2.01	1.51
1	D	178	ARG	C-N	-11.69	1.09	1.33
1	B	71	GLU	CD-OE2	9.91	1.44	1.25
1	C	175	GLY	N-CA	7.41	1.54	1.44
1	B	71	GLU	CD-OE1	6.36	1.37	1.25

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	89	LYS	O-C-N	-32.10	79.89	122.59
1	D	88	ALA	CA-C-N	16.65	153.34	121.54
1	D	88	ALA	C-N-CA	16.65	153.34	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	88	ALA	O-C-N	-13.61	101.22	123.00
1	D	178	ARG	O-C-N	-13.05	108.00	122.23
1	B	179	ASP	CA-C-N	5.49	126.70	119.84
1	B	179	ASP	C-N-CA	5.49	126.70	119.84

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	88	ALA	Peptide
1	D	178	ARG	Mainchain
1	D	88	ALA	Mainchain
1	D	89	LYS	Mainchain

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	1878	0	1871	151	0
1	B	1878	0	1871	163	0
1	C	1882	0	1882	183	0
1	D	1878	0	1869	163	0
All	All	7516	0	7493	631	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 42.

All (631) 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:D:65:ILE:CD1	1:D:65:ILE:CG1	2.01	1.37
1:D:89:LYS:O	1:D:91:VAL:N	1.69	1.26
1:C:88:ALA:HA	1:C:89:LYS:HB3	1.32	1.11
1:C:88:ALA:HB1	1:C:89:LYS:HG2	1.07	1.06
1:A:74:PRO:HB2	1:C:39:THR:HG21	1.39	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:165:LEU:HB2	1:C:272:LEU:HD13	1.39	1.03
1:C:88:ALA:HB1	1:C:89:LYS:CG	1.94	0.96
1:C:165:LEU:HD12	1:C:272:LEU:HB3	1.47	0.96
1:D:178:ARG:HB3	1:D:183:LEU:CD2	1.95	0.96
1:C:88:ALA:CB	1:C:89:LYS:HG2	1.96	0.94
1:C:161:GLY:H	1:C:265:SER:HB2	1.35	0.90
1:B:159:VAL:HG23	1:B:161:GLY:H	1.32	0.90
1:C:190:MET:HE1	1:C:201:VAL:HG11	1.52	0.88
1:D:26:LEU:HB3	1:D:65:ILE:HD12	1.54	0.88
1:D:190:MET:HE3	1:D:201:VAL:HG21	1.56	0.87
1:C:179:ASP:OD1	1:C:179:ASP:O	1.91	0.87
1:B:267:ARG:O	1:B:271:MET:HG2	1.74	0.86
1:C:102:PRO:O	1:C:118:VAL:HG13	1.77	0.85
1:D:89:LYS:O	1:D:89:LYS:C	2.20	0.85
1:C:224:GLN:HG2	1:C:227:LEU:HB3	1.58	0.85
1:B:271:MET:HE3	1:B:271:MET:HA	1.59	0.84
1:C:88:ALA:HA	1:C:89:LYS:CB	2.07	0.83
1:C:227:LEU:HD11	1:C:232:LEU:HD13	1.59	0.83
1:A:34:ILE:HG23	1:A:109:PHE:HE1	1.44	0.81
1:A:68:GLU:O	1:A:72:ARG:HB2	1.80	0.81
1:B:249:THR:HB	1:B:260:ARG:HD2	1.60	0.81
1:D:178:ARG:HB3	1:D:183:LEU:HD22	1.62	0.81
1:D:134:TYR:HB2	1:D:141:LEU:HD23	1.62	0.81
1:A:211:LEU:HB3	1:A:239:ILE:HD11	1.62	0.81
1:D:190:MET:HE1	1:D:201:VAL:HG11	1.61	0.81
1:C:183:LEU:O	1:C:187:LEU:HD12	1.81	0.80
1:C:38:LEU:HD23	1:C:112:ARG:HD2	1.63	0.79
1:B:159:VAL:HG13	1:B:242:ALA:O	1.83	0.78
1:C:254:LEU:HD21	1:C:256:LEU:HD13	1.64	0.78
1:D:102:PRO:O	1:D:118:VAL:HG22	1.83	0.78
1:D:60:LEU:O	1:D:64:LEU:HB2	1.83	0.78
1:C:63:ASP:O	1:C:67:SER:HB3	1.83	0.78
1:D:26:LEU:HB3	1:D:65:ILE:CD1	2.14	0.78
1:A:244:GLY:O	1:A:245:ILE:HD13	1.84	0.77
1:A:107:CYS:O	1:A:110:VAL:HG22	1.84	0.76
1:C:164:ASP:HB3	1:C:167:LYS:HB2	1.66	0.76
1:B:218:ALA:HA	1:C:111:HIS:O	1.84	0.76
1:D:178:ARG:HB3	1:D:183:LEU:HD21	1.66	0.76
1:C:61:VAL:O	1:C:65:ILE:HG13	1.84	0.75
1:D:61:VAL:HB	1:D:102:PRO:HB3	1.67	0.75
1:A:195:HIS:O	1:A:197:LYS:HE3	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:ALA:O	1:A:239:ILE:HG13	1.86	0.75
1:C:245:ILE:HD13	1:C:267:ARG:HA	1.69	0.75
1:A:246:VAL:HG12	1:A:254:LEU:HD13	1.68	0.75
1:C:130:PHE:HA	1:C:237:VAL:HG11	1.69	0.75
1:A:93:THR:O	1:A:126:GLN:HG3	1.87	0.74
1:D:108:ASN:ND2	1:D:115:THR:HB	2.03	0.74
1:D:63:ASP:O	1:D:67:SER:HB3	1.90	0.72
1:C:64:LEU:HD22	1:C:64:LEU:O	1.89	0.71
1:A:178:ARG:HA	1:A:183:LEU:HD11	1.71	0.71
1:A:17:GLU:O	1:A:21:GLN:HG2	1.89	0.71
1:D:36:LYS:O	1:D:39:THR:HB	1.90	0.71
1:D:18:GLU:OE2	1:D:72:ARG:NH2	2.24	0.70
1:B:20:PHE:O	1:B:23:ALA:HB3	1.92	0.70
1:C:225:PHE:HA	1:C:260:ARG:HB3	1.73	0.70
1:D:232:LEU:HD11	1:D:261:VAL:HG21	1.74	0.70
1:D:179:ASP:OD2	1:D:182:THR:OG1	2.09	0.69
1:D:24:VAL:O	1:D:28:LEU:HG	1.93	0.69
1:A:74:PRO:CB	1:C:39:THR:HG21	2.20	0.69
1:B:165:LEU:O	1:B:198:ALA:HA	1.93	0.69
1:A:62:GLU:OE2	1:A:82:GLU:HB2	1.92	0.69
1:D:61:VAL:O	1:D:65:ILE:HG12	1.92	0.69
1:D:79:ILE:HB	1:D:99:ILE:HG23	1.74	0.69
1:D:232:LEU:HD21	1:D:254:LEU:HD11	1.75	0.69
1:B:174:ILE:HD12	1:B:175:GLY:O	1.92	0.69
1:C:165:LEU:O	1:C:165:LEU:HD23	1.93	0.68
1:A:184:LYS:HD2	1:A:187:LEU:HD12	1.75	0.68
1:D:235:ALA:O	1:D:239:ILE:HG13	1.94	0.68
1:D:166:SER:HA	1:D:197:LYS:O	1.93	0.68
1:C:264:ALA:HB3	1:C:270:ALA:HB2	1.75	0.68
1:A:34:ILE:HG23	1:A:109:PHE:CE1	2.29	0.68
1:B:181:ALA:O	1:B:185:LEU:HB2	1.94	0.68
1:B:159:VAL:HG23	1:B:161:GLY:N	2.07	0.67
1:B:166:SER:HA	1:B:197:LYS:O	1.94	0.67
1:D:248:ASP:HB2	1:D:253:PRO:O	1.93	0.67
1:D:178:ARG:CB	1:D:183:LEU:HD22	2.25	0.67
1:D:182:THR:O	1:D:183:LEU:HD13	1.94	0.67
1:B:114:PRO:HB2	1:B:137:THR:HG21	1.75	0.67
1:D:146:ARG:HA	1:D:241:GLU:OE2	1.94	0.67
1:C:88:ALA:CA	1:C:89:LYS:HB3	2.20	0.67
1:C:180:PRO:HA	1:C:183:LEU:HB2	1.75	0.66
1:C:99:ILE:HG22	1:C:230:TRP:HA	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:161:GLY:N	1:C:265:SER:HB2	2.10	0.66
1:B:170:VAL:O	1:B:201:VAL:HA	1.97	0.65
1:A:198:ALA:O	1:D:178:ARG:NH1	2.29	0.65
1:B:152:CYS:CB	1:B:157:LEU:HD21	2.27	0.65
1:B:192:ARG:O	1:B:195:HIS:HB3	1.96	0.65
1:D:16:TRP:CZ2	1:D:124:VAL:HG11	2.30	0.65
1:C:164:ASP:OD2	1:C:167:LYS:HD3	1.95	0.65
1:D:30:ALA:HB2	1:D:65:ILE:HD11	1.79	0.65
1:D:88:ALA:O	1:D:90:CYS:N	2.30	0.65
1:A:174:ILE:HD11	1:D:202:ARG:HH12	1.62	0.64
1:C:88:ALA:CA	1:C:89:LYS:CB	2.76	0.64
1:C:176:PRO:HD2	1:C:177:LYS:HE2	1.79	0.64
1:C:190:MET:HE2	1:C:194:LEU:HD22	1.79	0.64
1:A:169:LEU:HD11	1:A:202:ARG:HG2	1.79	0.64
1:A:88:ALA:HB2	1:B:21:GLN:OE1	1.97	0.64
1:C:272:LEU:O	1:C:275:GLN:HB2	1.98	0.64
1:A:188:SER:O	1:A:192:ARG:HG3	1.97	0.64
1:D:134:TYR:HA	1:D:140:ARG:O	1.97	0.64
1:C:255:ASP:HB3	1:C:258:ALA:HB2	1.79	0.64
1:D:184:LYS:HA	1:D:187:LEU:HD12	1.79	0.64
1:A:184:LYS:HA	1:A:187:LEU:HD12	1.80	0.64
1:B:186:PHE:O	1:B:190:MET:HB2	1.98	0.64
1:B:214:LEU:HD12	1:B:239:ILE:HD13	1.80	0.64
1:C:81:GLU:HG2	1:C:82:GLU:HG2	1.81	0.63
1:D:108:ASN:HD22	1:D:115:THR:HB	1.61	0.63
1:D:163:THR:HG22	1:D:268:GLU:HB2	1.80	0.63
1:C:36:LYS:O	1:C:39:THR:HB	1.98	0.63
1:D:249:THR:HB	1:D:260:ARG:HG3	1.80	0.63
1:C:172:THR:O	1:C:203:VAL:HB	1.98	0.63
1:D:30:ALA:HB1	1:D:61:VAL:HG13	1.80	0.63
1:D:195:HIS:O	1:D:197:LYS:HE3	1.97	0.63
1:D:188:SER:HB2	1:D:192:ARG:HH11	1.63	0.63
1:C:34:ILE:HD11	1:C:103:ILE:HG12	1.81	0.63
1:A:165:LEU:HA	1:A:269:MET:HE1	1.81	0.62
1:B:38:LEU:HD21	1:B:109:PHE:CD1	2.34	0.62
1:D:66:ILE:HD13	1:D:78:PHE:CD1	2.35	0.62
1:A:71:GLU:CG	1:A:71:GLU:O	2.47	0.62
1:A:135:HIS:CE1	1:A:137:THR:HB	2.35	0.62
1:A:179:ASP:OD1	1:A:182:THR:HG23	2.00	0.62
1:A:61:VAL:HG12	1:A:102:PRO:HB3	1.81	0.62
1:C:164:ASP:O	1:C:269:MET:HE1	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:THR:HG23	1:B:209:LEU:HD12	1.82	0.61
1:C:24:VAL:O	1:C:28:LEU:HG	2.00	0.61
1:D:134:TYR:CE2	1:D:136:CYS:HA	2.36	0.61
1:C:38:LEU:CD2	1:C:112:ARG:HD2	2.30	0.61
1:B:137:THR:HG22	1:B:138:GLU:HG2	1.81	0.61
1:D:34:ILE:HD12	1:D:136:CYS:SG	2.40	0.61
1:B:191:GLU:HG3	1:B:192:ARG:N	2.16	0.60
1:B:191:GLU:O	1:B:195:HIS:HB2	2.01	0.60
1:C:227:LEU:HD23	1:C:260:ARG:HA	1.84	0.60
1:B:152:CYS:HB2	1:B:157:LEU:HD21	1.84	0.60
1:C:72:ARG:HB3	1:C:73:PHE:CD1	2.37	0.60
1:C:88:ALA:CB	1:C:89:LYS:CG	2.69	0.60
1:A:74:PRO:HB2	1:C:39:THR:CG2	2.25	0.60
1:B:71:GLU:OE2	1:B:71:GLU:O	2.20	0.60
1:D:99:ILE:HD12	1:D:233:ALA:HB2	1.83	0.60
1:B:235:ALA:O	1:B:239:ILE:HG13	2.02	0.59
1:D:24:VAL:HG13	1:D:141:LEU:HD11	1.84	0.59
1:A:178:ARG:HD2	1:A:183:LEU:HD11	1.83	0.59
1:C:34:ILE:CD1	1:C:103:ILE:HG12	2.32	0.59
1:C:225:PHE:CE2	1:C:249:THR:HG21	2.37	0.59
1:A:190:MET:CE	1:A:201:VAL:HG11	2.33	0.59
1:B:245:ILE:HD13	1:B:267:ARG:HA	1.84	0.59
1:D:81:GLU:HA	1:D:230:TRP:CH2	2.37	0.59
1:D:236:THR:O	1:D:240:ARG:HG3	2.02	0.59
1:A:249:THR:HG22	1:A:260:ARG:NE	2.17	0.59
1:D:135:HIS:CD2	1:D:138:GLU:HB2	2.37	0.59
1:B:163:THR:HG23	1:B:266:THR:HG21	1.83	0.59
1:C:72:ARG:HB3	1:C:73:PHE:CE1	2.38	0.59
1:D:89:LYS:O	1:D:90:CYS:N	2.36	0.59
1:A:24:VAL:O	1:A:28:LEU:HG	2.03	0.59
1:A:192:ARG:HD2	1:A:277:LEU:HA	1.85	0.59
1:C:40:GLU:O	1:C:41:GLU:OE2	2.21	0.58
1:D:178:ARG:CA	1:D:183:LEU:HD22	2.32	0.58
1:A:71:GLU:O	1:A:71:GLU:CD	2.47	0.58
1:B:108:ASN:ND2	1:B:115:THR:HB	2.18	0.58
1:C:185:LEU:HD22	1:C:189:ASN:ND2	2.18	0.58
1:B:129:GLU:HA	1:B:129:GLU:OE1	2.03	0.58
1:C:189:ASN:HA	1:C:192:ARG:HG3	1.83	0.58
1:C:234:ALA:O	1:C:238:ILE:HG13	2.04	0.58
1:D:122:PHE:CE1	1:D:124:VAL:HG22	2.39	0.58
1:B:99:ILE:HG22	1:B:230:TRP:HA	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:105:GLY:O	1:B:108:ASN:HB2	2.04	0.57
1:C:249:THR:HB	1:C:260:ARG:NE	2.19	0.57
1:D:188:SER:HB2	1:D:192:ARG:NH1	2.19	0.57
1:B:65:ILE:HG21	1:B:100:ILE:HD13	1.85	0.57
1:A:169:LEU:HD12	1:A:200:GLY:O	2.05	0.57
1:B:107:CYS:O	1:B:111:HIS:HD2	1.88	0.57
1:C:164:ASP:CG	1:C:167:LYS:HD3	2.30	0.57
1:B:33:ILE:HG21	1:B:60:LEU:HD12	1.86	0.56
1:B:174:ILE:HD13	1:B:178:ARG:NH1	2.20	0.56
1:B:214:LEU:CD1	1:B:239:ILE:HD13	2.34	0.56
1:C:141:LEU:O	1:C:152:CYS:HA	2.05	0.56
1:C:269:MET:O	1:C:272:LEU:HB2	2.04	0.56
1:D:19:CYS:O	1:D:22:ALA:HB3	2.05	0.56
1:A:174:ILE:HA	1:A:186:PHE:CE2	2.40	0.56
1:C:227:LEU:HD11	1:C:232:LEU:CD1	2.32	0.56
1:C:267:ARG:O	1:C:271:MET:HG2	2.05	0.56
1:C:227:LEU:HD21	1:C:232:LEU:HD21	1.88	0.56
1:C:255:ASP:HB3	1:C:258:ALA:CB	2.36	0.56
1:C:104:ASP:O	1:C:116:VAL:HG13	2.04	0.56
1:B:38:LEU:HA	1:B:112:ARG:NH2	2.21	0.56
1:D:146:ARG:O	1:D:146:ARG:HG3	2.05	0.56
1:D:39:THR:O	1:D:40:GLU:O	2.23	0.56
1:D:57:THR:O	1:D:61:VAL:HG23	2.06	0.56
1:D:132:VAL:HG22	1:D:143:THR:HG22	1.88	0.56
1:A:135:HIS:CE1	1:A:138:GLU:HG2	2.41	0.55
1:C:188:SER:HB2	1:C:192:ARG:HH12	1.71	0.55
1:D:191:GLU:O	1:D:195:HIS:HB2	2.06	0.55
1:C:248:ASP:CG	1:C:260:ARG:HH21	2.14	0.55
1:C:265:SER:O	1:C:266:THR:HG23	2.07	0.55
1:A:157:LEU:HD22	1:A:216:SER:HB2	1.87	0.55
1:B:127:GLU:HG2	1:B:146:ARG:NH2	2.21	0.55
1:C:140:ARG:HA	1:C:153:ASN:HD21	1.71	0.55
1:D:178:ARG:CB	1:D:183:LEU:CD2	2.76	0.55
1:D:208:THR:HG22	1:D:231:ASP:O	2.06	0.55
1:A:108:ASN:ND2	1:A:115:THR:HB	2.21	0.55
1:C:134:TYR:OH	1:C:139:GLU:HB3	2.07	0.55
1:A:169:LEU:HD11	1:A:202:ARG:CG	2.36	0.55
1:B:167:LYS:NZ	1:B:167:LYS:HB3	2.21	0.55
1:B:225:PHE:CE2	1:B:249:THR:HG21	2.42	0.55
1:D:135:HIS:HD2	1:D:140:ARG:NH1	2.05	0.55
1:A:88:ALA:HB2	1:B:21:GLN:NE2	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:TRP:CZ2	1:C:124:VAL:HG11	2.42	0.55
1:D:134:TYR:HB2	1:D:141:LEU:CD2	2.35	0.55
1:B:137:THR:CG2	1:B:138:GLU:HG2	2.36	0.55
1:A:88:ALA:HB2	1:B:21:GLN:CD	2.33	0.55
1:C:254:LEU:HD21	1:C:256:LEU:CD1	2.36	0.55
1:D:188:SER:O	1:D:192:ARG:HD2	2.07	0.54
1:A:264:ALA:HB3	1:A:270:ALA:HB2	1.88	0.54
1:C:24:VAL:HG13	1:C:141:LEU:HD11	1.89	0.54
1:C:170:VAL:HG11	1:C:193:LEU:HD11	1.88	0.54
1:D:26:LEU:CB	1:D:65:ILE:HD12	2.33	0.54
1:D:79:ILE:HG13	1:D:97:THR:CG2	2.38	0.54
1:D:225:PHE:CE2	1:D:249:THR:HG21	2.43	0.54
1:A:81:GLU:HA	1:A:230:TRP:CH2	2.41	0.54
1:A:179:ASP:OD2	1:A:181:ALA:HB3	2.08	0.54
1:A:214:LEU:HD12	1:A:239:ILE:HG23	1.90	0.54
1:C:123:ALA:HB2	1:C:128:LEU:HD23	1.89	0.54
1:A:17:GLU:CD	1:A:145:ARG:HH22	2.15	0.54
1:C:134:TYR:CZ	1:C:139:GLU:HA	2.43	0.54
1:D:157:LEU:HD22	1:D:216:SER:HA	1.89	0.54
1:C:38:LEU:HD23	1:C:112:ARG:CD	2.37	0.54
1:D:65:ILE:CD1	1:D:65:ILE:CB	2.83	0.54
1:B:228:HIS:H	1:B:228:HIS:CD2	2.24	0.54
1:C:273:ILE:O	1:C:276:ALA:HB3	2.08	0.54
1:B:110:VAL:HG23	1:B:111:HIS:CD2	2.43	0.54
1:B:111:HIS:O	1:B:112:ARG:HB2	2.07	0.53
1:B:135:HIS:HB3	1:B:140:ARG:HB2	1.90	0.53
1:A:249:THR:HA	1:A:262:VAL:HG23	1.90	0.53
1:B:164:ASP:OD2	1:B:167:LYS:HD3	2.09	0.53
1:D:61:VAL:CB	1:D:102:PRO:HB3	2.38	0.53
1:A:99:ILE:HG22	1:A:230:TRP:HA	1.90	0.53
1:C:99:ILE:CG2	1:C:230:TRP:HA	2.37	0.53
1:C:192:ARG:HD3	1:C:277:LEU:N	2.23	0.53
1:D:227:LEU:HG	1:D:227:LEU:O	2.08	0.53
1:D:79:ILE:O	1:D:99:ILE:HA	2.09	0.53
1:D:69:LEU:HD22	1:D:73:PHE:HE1	1.73	0.53
1:D:99:ILE:HD12	1:D:233:ALA:CB	2.39	0.53
1:D:159:VAL:HG11	1:D:244:GLY:CA	2.38	0.53
1:D:164:ASP:OD2	1:D:167:LYS:HD2	2.08	0.53
1:A:71:GLU:O	1:A:71:GLU:HG2	2.09	0.53
1:B:192:ARG:NH2	1:B:277:LEU:HA	2.24	0.53
1:A:25:GLN:HA	1:A:28:LEU:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:ALA:HB2	1:B:21:GLN:HE22	1.74	0.53
1:B:104:ASP:O	1:B:116:VAL:HG13	2.09	0.53
1:D:26:LEU:HD13	1:D:65:ILE:HG23	1.90	0.53
1:B:114:PRO:O	1:B:135:HIS:HE1	1.91	0.53
1:A:69:LEU:HD22	1:A:98:TRP:CZ2	2.44	0.52
1:A:190:MET:HE2	1:A:194:LEU:HD22	1.91	0.52
1:B:99:ILE:CG2	1:B:230:TRP:HA	2.39	0.52
1:A:32:GLN:HG2	1:A:33:ILE:N	2.22	0.52
1:B:16:TRP:CZ2	1:B:124:VAL:HG11	2.44	0.52
1:B:210:ALA:O	1:B:213:HIS:HB2	2.09	0.52
1:C:108:ASN:ND2	1:C:115:THR:HB	2.25	0.52
1:D:163:THR:HG21	1:D:268:GLU:OE1	2.09	0.52
1:A:183:LEU:O	1:A:187:LEU:HG	2.10	0.52
1:B:81:GLU:O	1:B:82:GLU:HG3	2.09	0.52
1:B:247:ILE:CD1	1:B:251:GLY:HA2	2.39	0.52
1:D:67:SER:O	1:D:70:ARG:HB2	2.09	0.52
1:B:138:GLU:OE2	1:C:138:GLU:OE2	2.27	0.52
1:D:171:LEU:CD1	1:D:202:ARG:HB2	2.40	0.52
1:D:236:THR:HG23	1:D:246:VAL:HG11	1.91	0.52
1:A:25:GLN:O	1:A:28:LEU:HD12	2.10	0.52
1:B:115:THR:CG2	1:B:209:LEU:HD12	2.39	0.52
1:B:267:ARG:O	1:B:271:MET:CG	2.54	0.52
1:C:189:ASN:HA	1:C:192:ARG:HD2	1.91	0.52
1:D:171:LEU:HG	1:D:202:ARG:HB2	1.91	0.52
1:D:184:LYS:HD2	1:D:184:LYS:O	2.10	0.52
1:A:184:LYS:O	1:A:188:SER:OG	2.25	0.52
1:B:169:LEU:HB2	1:C:111:HIS:ND1	2.25	0.52
1:C:249:THR:HB	1:C:260:ARG:HD2	1.93	0.52
1:D:79:ILE:HG13	1:D:97:THR:HG21	1.93	0.51
1:A:79:ILE:O	1:A:79:ILE:HG22	2.10	0.51
1:B:192:ARG:CZ	1:B:277:LEU:HA	2.39	0.51
1:C:168:ALA:HB2	1:C:269:MET:CE	2.40	0.51
1:D:148:ARG:O	1:D:149:GLY:O	2.28	0.51
1:D:91:VAL:HG12	1:D:91:VAL:O	2.10	0.51
1:B:111:HIS:CE1	1:C:169:LEU:HB2	2.45	0.51
1:C:168:ALA:HB2	1:C:269:MET:HE1	1.92	0.51
1:A:91:VAL:HG12	1:A:91:VAL:O	2.11	0.51
1:C:145:ARG:HB2	1:C:148:ARG:HB2	1.91	0.51
1:C:190:MET:HE3	1:C:201:VAL:HG21	1.92	0.51
1:A:40:GLU:C	1:A:112:ARG:HH21	2.19	0.51
1:B:101:ASP:OD2	1:B:231:ASP:OD1	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:91:VAL:HG12	1:C:91:VAL:O	2.10	0.51
1:A:29:ARG:HG2	1:A:64:LEU:HD11	1.92	0.51
1:B:248:ASP:HB2	1:B:253:PRO:O	2.11	0.51
1:C:254:LEU:HD12	1:C:261:VAL:HG23	1.92	0.51
1:D:185:LEU:HD22	1:D:189:ASN:ND2	2.25	0.51
1:B:37:ALA:O	1:B:112:ARG:NH2	2.44	0.51
1:A:101:ASP:OD2	1:A:231:ASP:OD1	2.29	0.51
1:A:179:ASP:OD2	1:A:181:ALA:N	2.44	0.51
1:B:152:CYS:HB3	1:B:157:LEU:HD21	1.92	0.51
1:C:138:GLU:HB2	1:C:140:ARG:HG3	1.93	0.51
1:D:32:GLN:O	1:D:36:LYS:HB2	2.11	0.51
1:D:149:GLY:C	1:D:241:GLU:HB3	2.36	0.51
1:B:175:GLY:O	1:B:176:PRO:O	2.29	0.51
1:C:174:ILE:O	1:C:175:GLY:O	2.29	0.51
1:B:162:GLU:HG3	1:B:269:MET:CE	2.40	0.50
1:B:190:MET:O	1:B:190:MET:HE2	2.11	0.50
1:D:28:LEU:HD21	1:D:141:LEU:HG	1.93	0.50
1:D:122:PHE:HE1	1:D:124:VAL:HG22	1.76	0.50
1:A:111:HIS:HE1	1:D:220:ASP:OD2	1.95	0.50
1:B:163:THR:HG22	1:B:266:THR:OG1	2.11	0.50
1:C:81:GLU:HB2	1:C:230:TRP:CZ2	2.46	0.50
1:C:170:VAL:HG21	1:C:193:LEU:CD1	2.42	0.50
1:D:163:THR:HG22	1:D:266:THR:OG1	2.12	0.50
1:B:173:GLU:HA	1:B:173:GLU:OE1	2.11	0.50
1:A:273:ILE:O	1:A:276:ALA:O	2.30	0.50
1:C:101:ASP:OD2	1:C:231:ASP:OD1	2.30	0.50
1:D:222:TYR:OH	1:D:224:GLN:NE2	2.45	0.50
1:B:206:SER:HB3	1:B:209:LEU:HB2	1.93	0.50
1:D:115:THR:HG23	1:D:209:LEU:HD12	1.94	0.50
1:A:248:ASP:OD1	1:A:250:SER:OG	2.27	0.50
1:D:22:ALA:O	1:D:26:LEU:HG	2.12	0.50
1:A:224:GLN:NE2	1:A:227:LEU:HD13	2.27	0.49
1:A:66:ILE:O	1:A:70:ARG:HG3	2.13	0.49
1:A:190:MET:HE1	1:A:201:VAL:HG11	1.94	0.49
1:A:211:LEU:HD21	1:A:222:TYR:CD1	2.47	0.49
1:B:247:ILE:HD12	1:B:248:ASP:O	2.12	0.49
1:C:211:LEU:HD22	1:C:239:ILE:HD11	1.94	0.49
1:A:165:LEU:CA	1:A:269:MET:HE1	2.42	0.49
1:A:190:MET:HE3	1:A:201:VAL:HG21	1.94	0.49
1:D:163:THR:HG23	1:D:266:THR:HG21	1.93	0.49
1:A:190:MET:HE2	1:A:194:LEU:CD2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:24:VAL:HG13	1:D:141:LEU:CD1	2.42	0.49
1:A:104:ASP:OD2	1:A:208:THR:HG23	2.12	0.49
1:C:111:HIS:O	1:C:112:ARG:HB2	2.11	0.49
1:A:188:SER:HB2	1:A:192:ARG:NH1	2.27	0.49
1:C:179:ASP:OD1	1:C:182:THR:N	2.37	0.49
1:D:111:HIS:O	1:D:112:ARG:HB2	2.12	0.49
1:A:191:GLU:OE2	1:A:195:HIS:ND1	2.46	0.49
1:D:29:ARG:HG2	1:D:64:LEU:HD11	1.95	0.49
1:A:269:MET:O	1:A:273:ILE:HD12	2.13	0.49
1:C:81:GLU:O	1:C:81:GLU:HG3	2.13	0.49
1:C:135:HIS:CD2	1:C:138:GLU:HG3	2.48	0.49
1:D:149:GLY:HA3	1:D:156:ARG:NH2	2.28	0.49
1:A:24:VAL:HG13	1:A:141:LEU:HD11	1.94	0.48
1:A:177:LYS:O	1:A:178:ARG:HD3	2.12	0.48
1:D:30:ALA:CB	1:D:61:VAL:HG13	2.42	0.48
1:D:179:ASP:OD2	1:D:179:ASP:O	2.31	0.48
1:D:249:THR:HA	1:D:262:VAL:HG23	1.95	0.48
1:A:179:ASP:O	1:A:183:LEU:HD13	2.12	0.48
1:B:214:LEU:HD11	1:B:264:ALA:N	2.28	0.48
1:C:269:MET:O	1:C:272:LEU:N	2.46	0.48
1:D:184:LYS:O	1:D:188:SER:OG	2.30	0.48
1:A:165:LEU:N	1:A:269:MET:HE1	2.28	0.48
1:D:26:LEU:HD13	1:D:65:ILE:CG2	2.43	0.48
1:B:146:ARG:O	1:B:146:ARG:HG2	2.12	0.48
1:D:183:LEU:HD12	1:D:183:LEU:HA	1.70	0.48
1:C:29:ARG:NH2	1:C:68:GLU:OE2	2.47	0.48
1:C:258:ALA:O	1:C:260:ARG:HG2	2.13	0.48
1:D:134:TYR:OH	1:D:139:GLU:HG2	2.13	0.48
1:A:65:ILE:HG21	1:A:100:ILE:HD13	1.96	0.48
1:A:108:ASN:O	1:A:113:PHE:N	2.47	0.48
1:A:161:GLY:H	1:A:265:SER:HB2	1.77	0.48
1:B:38:LEU:HA	1:B:112:ARG:CZ	2.44	0.48
1:B:232:LEU:O	1:B:232:LEU:HG	2.11	0.48
1:C:34:ILE:HG23	1:C:109:PHE:HE1	1.77	0.48
1:B:130:PHE:HB2	1:B:144:GLY:O	2.14	0.48
1:A:275:GLN:O	1:A:277:LEU:O	2.32	0.48
1:B:202:ARG:HH12	1:C:174:ILE:HD11	1.79	0.48
1:C:249:THR:HB	1:C:260:ARG:CD	2.44	0.48
1:C:145:ARG:HH11	1:C:145:ARG:HG3	1.79	0.48
1:D:89:LYS:O	1:D:90:CYS:C	2.50	0.48
1:D:185:LEU:HD22	1:D:189:ASN:HD21	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:ILE:HB	1:A:252:GLY:O	2.14	0.47
1:B:107:CYS:O	1:B:110:VAL:HG22	2.14	0.47
1:A:192:ARG:HD2	1:A:277:LEU:CA	2.44	0.47
1:B:191:GLU:HA	1:B:194:LEU:HD12	1.95	0.47
1:D:144:GLY:O	1:D:237:VAL:HG11	2.13	0.47
1:D:224:GLN:HB3	1:D:227:LEU:HD22	1.96	0.47
1:B:174:ILE:HD12	1:B:175:GLY:N	2.28	0.47
1:B:185:LEU:HD22	1:B:189:ASN:ND2	2.29	0.47
1:C:17:GLU:OE2	1:C:145:ARG:NH2	2.47	0.47
1:C:117:ALA:HB2	1:C:209:LEU:HD11	1.96	0.47
1:B:142:TYR:HB3	1:B:238:ILE:HD13	1.97	0.47
1:B:142:TYR:CE1	1:B:212:CYS:HB3	2.49	0.47
1:B:163:THR:CA	1:B:269:MET:HE2	2.45	0.47
1:C:170:VAL:HG11	1:C:193:LEU:CD1	2.43	0.47
1:A:188:SER:HB2	1:A:192:ARG:HH12	1.79	0.47
1:C:162:GLU:OE1	1:C:164:ASP:HB2	2.14	0.47
1:C:190:MET:CE	1:C:201:VAL:HG21	2.45	0.47
1:A:165:LEU:CD2	1:A:196:ALA:HB1	2.45	0.47
1:D:190:MET:CE	1:D:201:VAL:HG11	2.39	0.47
1:A:172:THR:OG1	1:A:173:GLU:N	2.48	0.47
1:B:162:GLU:O	1:B:266:THR:OG1	2.28	0.47
1:B:188:SER:O	1:B:191:GLU:N	2.45	0.47
1:B:236:THR:O	1:B:240:ARG:HG3	2.15	0.47
1:A:114:PRO:HB2	1:A:137:THR:HG21	1.95	0.47
1:B:208:THR:HG22	1:B:231:ASP:O	2.15	0.47
1:A:185:LEU:CD2	1:A:189:ASN:HD21	2.26	0.46
1:C:164:ASP:CB	1:C:167:LYS:HD3	2.45	0.46
1:D:149:GLY:HA3	1:D:156:ARG:CZ	2.45	0.46
1:A:185:LEU:O	1:A:188:SER:OG	2.33	0.46
1:B:159:VAL:HG11	1:B:244:GLY:N	2.29	0.46
1:B:192:ARG:NE	1:B:277:LEU:HA	2.30	0.46
1:B:256:LEU:HD12	1:B:256:LEU:HA	1.80	0.46
1:B:167:LYS:NZ	1:B:167:LYS:CB	2.76	0.46
1:B:174:ILE:HD13	1:B:178:ARG:CZ	2.45	0.46
1:C:179:ASP:OD1	1:C:179:ASP:C	2.58	0.46
1:C:189:ASN:CA	1:C:192:ARG:HG3	2.46	0.46
1:A:122:PHE:CE1	1:A:124:VAL:HG22	2.50	0.46
1:A:138:GLU:HG3	1:A:140:ARG:NH2	2.31	0.46
1:C:179:ASP:OD1	1:C:182:THR:HG23	2.16	0.46
1:A:140:ARG:HA	1:A:153:ASN:HD21	1.80	0.46
1:B:157:LEU:O	1:B:158:ARG:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:LEU:O	1:B:165:LEU:HD12	2.16	0.46
1:A:29:ARG:NH2	1:A:64:LEU:HD21	2.30	0.46
1:A:161:GLY:HA2	1:A:266:THR:HG23	1.96	0.46
1:D:32:GLN:HA	1:D:35:ARG:NH2	2.31	0.46
1:D:135:HIS:N	1:D:140:ARG:O	2.49	0.46
1:D:247:ILE:HB	1:D:252:GLY:O	2.16	0.46
1:A:111:HIS:CE1	1:D:220:ASP:OD2	2.69	0.46
1:B:179:ASP:O	1:B:181:ALA:N	2.48	0.46
1:C:247:ILE:HB	1:C:252:GLY:O	2.16	0.46
1:D:211:LEU:HD21	1:D:222:TYR:CD1	2.51	0.46
1:A:184:LYS:HZ2	1:A:187:LEU:HB2	1.81	0.46
1:B:179:ASP:N	1:B:182:THR:OG1	2.49	0.46
1:B:267:ARG:C	1:B:271:MET:HG2	2.41	0.46
1:C:190:MET:HE2	1:C:194:LEU:CD2	2.46	0.46
1:A:225:PHE:CE2	1:A:249:THR:HG21	2.51	0.46
1:B:79:ILE:HD12	1:B:99:ILE:HG12	1.98	0.46
1:B:151:PHE:CE2	1:B:156:ARG:HD3	2.51	0.46
1:D:178:ARG:C	1:D:183:LEU:HD22	2.40	0.46
1:A:79:ILE:N	1:A:98:TRP:O	2.49	0.45
1:A:174:ILE:HD13	1:D:200:GLY:HA2	1.98	0.45
1:B:169:LEU:HB2	1:C:111:HIS:CE1	2.51	0.45
1:B:179:ASP:O	1:B:182:THR:N	2.49	0.45
1:C:122:PHE:O	1:C:129:GLU:HB3	2.16	0.45
1:C:213:HIS:O	1:C:218:ALA:N	2.49	0.45
1:A:227:LEU:HD23	1:A:227:LEU:O	2.15	0.45
1:B:115:THR:HG22	1:B:115:THR:O	2.14	0.45
1:C:41:GLU:OE2	1:C:41:GLU:HA	2.17	0.45
1:C:185:LEU:HD22	1:C:189:ASN:HD21	1.80	0.45
1:A:38:LEU:HD23	1:A:38:LEU:HA	1.79	0.45
1:A:81:GLU:HG2	1:A:82:GLU:OE2	2.16	0.45
1:C:57:THR:O	1:C:61:VAL:HG23	2.17	0.45
1:C:93:THR:O	1:C:126:GLN:HA	2.16	0.45
1:B:194:LEU:HD21	1:B:201:VAL:HG11	1.97	0.45
1:B:222:TYR:OH	1:B:224:GLN:NE2	2.49	0.45
1:D:214:LEU:HD12	1:D:239:ILE:HD13	1.97	0.45
1:A:222:TYR:OH	1:A:224:GLN:NE2	2.50	0.45
1:B:65:ILE:HG22	1:B:69:LEU:HD12	1.97	0.45
1:B:202:ARG:HG2	1:B:202:ARG:HH11	1.82	0.45
1:C:189:ASN:O	1:C:192:ARG:HG3	2.17	0.45
1:D:66:ILE:O	1:D:70:ARG:HB2	2.17	0.45
1:D:141:LEU:HD23	1:D:141:LEU:HA	1.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:176:PRO:HB2	1:B:177:LYS:H	1.55	0.45
1:C:179:ASP:O	1:C:181:ALA:N	2.50	0.45
1:A:190:MET:O	1:A:194:LEU:HB2	2.16	0.45
1:B:127:GLU:HG2	1:B:146:ARG:CZ	2.47	0.45
1:B:178:ARG:NH2	1:C:199:HIS:O	2.50	0.45
1:C:123:ALA:HB1	1:C:127:GLU:O	2.17	0.45
1:D:135:HIS:NE2	1:D:138:GLU:HG2	2.30	0.45
1:A:138:GLU:HB2	1:A:140:ARG:HG3	1.99	0.44
1:A:199:HIS:CE1	1:D:111:HIS:HE2	2.35	0.44
1:B:160:SER:OG	1:B:220:ASP:OD1	2.30	0.44
1:B:184:LYS:HE2	1:B:188:SER:HB2	1.98	0.44
1:B:140:ARG:HA	1:B:153:ASN:ND2	2.32	0.44
1:C:273:ILE:O	1:C:276:ALA:N	2.50	0.44
1:A:110:VAL:HG23	1:A:111:HIS:CD2	2.53	0.44
1:C:146:ARG:HG3	1:C:146:ARG:HH11	1.83	0.44
1:C:254:LEU:CD2	1:C:256:LEU:HD13	2.42	0.44
1:D:158:ARG:HB2	1:D:158:ARG:CZ	2.48	0.44
1:B:128:LEU:O	1:B:146:ARG:NH1	2.50	0.44
1:B:172:THR:OG1	1:B:173:GLU:N	2.50	0.44
1:C:110:VAL:HG22	1:C:111:HIS:CD2	2.52	0.44
1:C:246:VAL:HG12	1:C:254:LEU:HD13	1.98	0.44
1:D:38:LEU:HG	1:D:109:PHE:CE1	2.53	0.44
1:D:107:CYS:O	1:D:111:HIS:HD2	2.00	0.44
1:C:142:TYR:CD1	1:C:152:CYS:HB2	2.53	0.44
1:D:193:LEU:HD23	1:D:223:TYR:CE1	2.52	0.44
1:D:249:THR:HB	1:D:260:ARG:CG	2.46	0.44
1:B:179:ASP:OD1	1:B:182:THR:HG23	2.18	0.44
1:B:276:ALA:O	1:B:277:LEU:CB	2.65	0.44
1:C:222:TYR:OH	1:C:224:GLN:NE2	2.50	0.44
1:C:227:LEU:HD21	1:C:232:LEU:CD2	2.48	0.44
1:C:261:VAL:HG22	1:C:262:VAL:N	2.33	0.44
1:A:41:GLU:OE2	1:A:41:GLU:O	2.35	0.44
1:C:269:MET:HE2	1:C:269:MET:HB2	1.87	0.44
1:B:163:THR:N	1:B:269:MET:HE2	2.33	0.44
1:B:245:ILE:HD11	1:B:270:ALA:HB3	2.00	0.44
1:C:188:SER:HB2	1:C:192:ARG:NH1	2.33	0.44
1:D:172:THR:OG1	1:D:173:GLU:N	2.50	0.44
1:D:63:ASP:OD1	1:D:64:LEU:N	2.50	0.44
1:D:66:ILE:HA	1:D:78:PHE:CE1	2.53	0.44
1:D:269:MET:HG3	1:D:273:ILE:CD1	2.47	0.44
1:A:38:LEU:O	1:A:112:ARG:NE	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:94:HIS:CE1	1:C:126:GLN:OE1	2.70	0.43
1:C:152:CYS:HB3	1:C:157:LEU:HD21	2.00	0.43
1:C:276:ALA:O	1:C:277:LEU:CB	2.66	0.43
1:A:81:GLU:HG2	1:A:82:GLU:CD	2.43	0.43
1:B:255:ASP:HB3	1:B:258:ALA:CB	2.48	0.43
1:C:178:ARG:HD3	1:C:178:ARG:HA	1.66	0.43
1:A:190:MET:HE3	1:A:201:VAL:HG11	2.00	0.43
1:A:249:THR:O	1:A:274:ALA:HB1	2.18	0.43
1:B:255:ASP:HB3	1:B:258:ALA:HB3	2.00	0.43
1:C:179:ASP:CG	1:C:182:THR:HG23	2.43	0.43
1:A:177:LYS:C	1:A:178:ARG:HD3	2.43	0.43
1:A:203:VAL:O	1:A:203:VAL:HG22	2.19	0.43
1:B:140:ARG:HA	1:B:153:ASN:HD21	1.84	0.43
1:B:164:ASP:O	1:B:167:LYS:N	2.50	0.43
1:C:184:LYS:HD2	1:C:184:LYS:HA	1.55	0.43
1:C:245:ILE:CD1	1:C:267:ARG:HA	2.45	0.43
1:A:191:GLU:O	1:A:195:HIS:HB2	2.19	0.43
1:A:203:VAL:HG13	1:D:203:VAL:HG13	1.99	0.43
1:B:99:ILE:HG21	1:B:233:ALA:HB2	1.99	0.43
1:B:271:MET:HA	1:B:271:MET:CE	2.41	0.43
1:C:35:ARG:O	1:C:38:LEU:N	2.52	0.43
1:C:174:ILE:H	1:C:174:ILE:HG13	1.67	0.43
1:C:180:PRO:HA	1:C:183:LEU:HD23	2.00	0.43
1:D:137:THR:HG22	1:D:138:GLU:OE1	2.19	0.43
1:A:164:ASP:C	1:A:269:MET:HE1	2.44	0.43
1:A:196:ALA:O	1:A:197:LYS:HB2	2.19	0.43
1:B:228:HIS:HB2	1:B:230:TRP:CE2	2.53	0.43
1:C:124:VAL:N	1:C:127:GLU:O	2.50	0.43
1:C:225:PHE:CZ	1:C:249:THR:HG21	2.54	0.43
1:D:133:ILE:O	1:D:142:TYR:N	2.49	0.43
1:B:55:THR:HG22	1:B:56:GLU:N	2.34	0.43
1:C:149:GLY:C	1:C:241:GLU:HB3	2.44	0.43
1:A:106:THR:HG22	1:A:107:CYS:N	2.34	0.43
1:B:218:ALA:O	1:C:111:HIS:HB3	2.18	0.43
1:C:65:ILE:HG22	1:C:69:LEU:HD12	2.01	0.43
1:C:106:THR:HG22	1:C:107:CYS:N	2.33	0.43
1:C:148:ARG:NH1	1:C:148:ARG:HG2	2.34	0.43
1:A:38:LEU:HD21	1:A:109:PHE:CD1	2.54	0.43
1:A:248:ASP:OD2	1:A:260:ARG:NE	2.48	0.43
1:B:179:ASP:C	1:B:182:THR:HG1	2.20	0.43
1:A:173:GLU:OE2	1:A:206:SER:N	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:257:MET:HE1	1:B:28:LEU:CD1	2.48	0.42
1:B:264:ALA:HB3	1:B:270:ALA:HB2	2.00	0.42
1:D:159:VAL:HG11	1:D:244:GLY:HA3	2.00	0.42
1:C:148:ARG:HG2	1:C:148:ARG:HH11	1.84	0.42
1:A:129:GLU:OE1	1:A:129:GLU:HA	2.19	0.42
1:B:111:HIS:ND1	1:C:169:LEU:HB2	2.35	0.42
1:C:20:PHE:O	1:C:24:VAL:HG23	2.19	0.42
1:D:61:VAL:CG1	1:D:102:PRO:HB3	2.49	0.42
1:A:140:ARG:HB3	1:A:152:CYS:SG	2.59	0.42
1:A:156:ARG:HG3	1:A:157:LEU:N	2.33	0.42
1:A:165:LEU:HD12	1:A:269:MET:SD	2.60	0.42
1:A:220:ASP:O	1:A:221:ALA:HB2	2.19	0.42
1:A:229:CYS:HB2	1:A:256:LEU:HG	2.01	0.42
1:B:214:LEU:HD23	1:B:214:LEU:HA	1.83	0.42
1:D:26:LEU:CD1	1:D:69:LEU:HD21	2.49	0.42
1:A:31:GLY:HA3	1:A:134:TYR:CD2	2.54	0.42
1:C:22:ALA:O	1:C:26:LEU:HD12	2.20	0.42
1:B:115:THR:HG22	1:B:206:SER:HB2	2.01	0.42
1:B:224:GLN:NE2	1:B:227:LEU:HB2	2.33	0.42
1:C:151:PHE:CD2	1:C:156:ARG:HA	2.55	0.42
1:D:38:LEU:HD23	1:D:38:LEU:HA	1.86	0.42
1:D:64:LEU:HD22	1:D:64:LEU:HA	1.93	0.42
1:D:145:ARG:O	1:D:148:ARG:N	2.50	0.42
1:A:108:ASN:HD22	1:A:115:THR:HB	1.84	0.42
1:A:197:LYS:HA	1:A:197:LYS:HD3	1.85	0.42
1:B:140:ARG:HD2	1:B:142:TYR:CE2	2.55	0.42
1:B:159:VAL:HG23	1:B:160:SER:N	2.34	0.42
1:C:192:ARG:HD3	1:C:276:ALA:C	2.44	0.42
1:B:151:PHE:CZ	1:B:156:ARG:HD3	2.54	0.42
1:B:186:PHE:O	1:B:190:MET:N	2.48	0.42
1:B:202:ARG:NH1	1:C:174:ILE:HD11	2.35	0.42
1:C:35:ARG:HH12	1:C:139:GLU:CD	2.25	0.42
1:D:129:GLU:OE2	1:D:146:ARG:HG2	2.20	0.42
1:A:268:GLU:OE2	1:A:268:GLU:N	2.50	0.42
1:B:135:HIS:HD2	1:B:140:ARG:NH1	2.18	0.42
1:C:81:GLU:HA	1:C:230:TRP:CH2	2.55	0.42
1:D:206:SER:HB3	1:D:209:LEU:HB2	2.01	0.42
1:A:38:LEU:HD23	1:A:109:PHE:CZ	2.55	0.42
1:A:65:ILE:HG22	1:A:69:LEU:HD12	2.01	0.42
1:A:215:ALA:O	1:A:242:ALA:HB1	2.20	0.42
1:A:224:GLN:HE21	1:A:227:LEU:HD13	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:THR:O	1:B:203:VAL:HB	2.20	0.42
1:C:89:LYS:HE2	1:C:91:VAL:HG21	2.02	0.42
1:C:193:LEU:O	1:C:198:ALA:HB2	2.20	0.42
1:D:117:ALA:HB2	1:D:209:LEU:HD21	2.02	0.42
1:D:135:HIS:HB3	1:D:140:ARG:HG3	2.02	0.42
1:A:182:THR:O	1:A:185:LEU:HB3	2.20	0.41
1:C:26:LEU:CD2	1:C:64:LEU:HD13	2.50	0.41
1:A:187:LEU:CD2	1:D:191:GLU:HA	2.51	0.41
1:B:185:LEU:HA	1:B:185:LEU:HD23	1.76	0.41
1:B:261:VAL:HG22	1:B:262:VAL:N	2.35	0.41
1:D:256:LEU:HD12	1:D:256:LEU:HA	1.84	0.41
1:B:167:LYS:HB2	1:B:167:LYS:HE3	1.78	0.41
1:C:30:ALA:HB1	1:C:61:VAL:CG1	2.49	0.41
1:A:179:ASP:OD1	1:A:182:THR:CG2	2.68	0.41
1:B:194:LEU:H	1:B:194:LEU:HG	1.67	0.41
1:C:138:GLU:HG3	1:C:140:ARG:NH2	2.35	0.41
1:D:187:LEU:O	1:D:191:GLU:HB3	2.21	0.41
1:A:202:ARG:HA	1:D:203:VAL:HG22	2.03	0.41
1:A:249:THR:HG22	1:A:260:ARG:CZ	2.50	0.41
1:B:135:HIS:HD2	1:B:140:ARG:HH12	1.68	0.41
1:B:164:ASP:OD2	1:B:167:LYS:HG3	2.20	0.41
1:B:214:LEU:HD12	1:B:263:ALA:HB1	2.02	0.41
1:C:28:LEU:HG	1:C:28:LEU:H	1.69	0.41
1:D:176:PRO:HB2	1:D:177:LYS:H	1.60	0.41
1:A:180:PRO:O	1:A:184:LYS:HB2	2.20	0.41
1:B:115:THR:HG22	1:B:206:SER:CB	2.51	0.41
1:C:69:LEU:HD22	1:C:98:TRP:CE2	2.55	0.41
1:B:158:ARG:HE	1:B:158:ARG:HB2	1.64	0.41
1:C:20:PHE:CZ	1:C:145:ARG:HD3	2.55	0.41
1:B:166:SER:C	1:B:167:LYS:HG3	2.46	0.41
1:C:92:LEU:O	1:C:126:GLN:NE2	2.53	0.41
1:D:189:ASN:HB3	1:D:223:TYR:CE2	2.56	0.41
1:B:249:THR:CB	1:B:260:ARG:HD2	2.42	0.41
1:D:236:THR:CG2	1:D:246:VAL:HG11	2.51	0.41
1:B:267:ARG:CZ	1:B:267:ARG:HB2	2.49	0.40
1:C:124:VAL:CG2	1:C:129:GLU:HB2	2.51	0.40
1:C:124:VAL:HG22	1:C:129:GLU:HB2	2.02	0.40
1:C:177:LYS:H	1:C:177:LYS:HG2	1.38	0.40
1:C:196:ALA:O	1:C:197:LYS:HB2	2.20	0.40
1:D:114:PRO:HB2	1:D:137:THR:HG21	2.02	0.40
1:A:94:HIS:HB2	1:B:139:GLU:OE2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:GLU:HG3	1:A:140:ARG:CZ	2.51	0.40
1:A:257:MET:HE1	1:B:28:LEU:HD11	2.02	0.40
1:B:170:VAL:C	1:B:171:LEU:HD12	2.46	0.40
1:D:117:ALA:HB2	1:D:209:LEU:CD2	2.52	0.40
1:D:245:ILE:O	1:D:245:ILE:HG13	2.12	0.40
1:B:122:PHE:O	1:B:129:GLU:N	2.49	0.40
1:C:89:LYS:HD2	1:C:91:VAL:HG23	2.02	0.40
1:D:26:LEU:HD11	1:D:69:LEU:HD21	2.03	0.40
1:D:32:GLN:OE1	1:D:36:LYS:NZ	2.49	0.40
1:C:161:GLY:HA2	1:C:266:THR:HG23	2.04	0.40
1:D:221:ALA:HA	1:D:264:ALA:HA	2.04	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	238/273 (87%)	210 (88%)	20 (8%)	8 (3%)	3	2
1	B	238/273 (87%)	208 (87%)	23 (10%)	7 (3%)	3	3
1	C	238/273 (87%)	208 (87%)	25 (10%)	5 (2%)	5	7
1	D	238/273 (87%)	206 (87%)	24 (10%)	8 (3%)	3	2
All	All	952/1092 (87%)	832 (87%)	92 (10%)	28 (3%)	3	3

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	176	PRO
1	B	229	CYS
1	C	175	GLY
1	D	40	GLU

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Mol	Chain	Res	Type
1	D	89	LYS
1	A	159	VAL
1	B	36	LYS
1	C	181	ALA
1	D	36	LYS
1	D	135	HIS
1	D	149	GLY
1	D	176	PRO
1	D	183	LEU
1	A	70	ARG
1	A	89	LYS
1	B	146	ARG
1	C	276	ALA
1	D	177	LYS
1	A	40	GLU
1	A	93	THR
1	A	176	PRO
1	A	197	LYS
1	B	159	VAL
1	C	233	ALA
1	B	180	PRO
1	B	237	VAL
1	A	79	ILE
1	C	180	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	195/219 (89%)	154 (79%)	41 (21%)	1	1
1	B	195/219 (89%)	145 (74%)	50 (26%)	0	0
1	C	196/219 (90%)	137 (70%)	59 (30%)	0	0
1	D	195/219 (89%)	140 (72%)	55 (28%)	0	0
All	All	781/876 (89%)	576 (74%)	205 (26%)	0	0

All (205) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	28	LEU
1	A	29	ARG
1	A	32	GLN
1	A	35	ARG
1	A	36	LYS
1	A	41	GLU
1	A	55	THR
1	A	60	LEU
1	A	64	LEU
1	A	70	ARG
1	A	73	PHE
1	A	77	ARG
1	A	95	SER
1	A	103	ILE
1	A	106	THR
1	A	124	VAL
1	A	141	LEU
1	A	158	ARG
1	A	167	LYS
1	A	172	THR
1	A	174	ILE
1	A	177	LYS
1	A	178	ARG
1	A	179	ASP
1	A	184	LYS
1	A	187	LEU
1	A	188	SER
1	A	191	GLU
1	A	194	LEU
1	A	195	HIS
1	A	197	LYS
1	A	203	VAL
1	A	207	SER
1	A	214	LEU
1	A	227	LEU
1	A	232	LEU
1	A	247	ILE
1	A	265	SER
1	A	271	MET
1	A	273	ILE
1	B	29	ARG

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Mol	Chain	Res	Type
1	B	36	LYS
1	B	55	THR
1	B	56	GLU
1	B	60	LEU
1	B	64	LEU
1	B	66	ILE
1	B	71	GLU
1	B	75	SER
1	B	77	ARG
1	B	106	THR
1	B	112	ARG
1	B	124	VAL
1	B	127	GLU
1	B	129	GLU
1	B	137	THR
1	B	141	LEU
1	B	155	GLN
1	B	158	ARG
1	B	159	VAL
1	B	163	THR
1	B	165	LEU
1	B	167	LYS
1	B	174	ILE
1	B	179	ASP
1	B	183	LEU
1	B	184	LYS
1	B	185	LEU
1	B	190	MET
1	B	191	GLU
1	B	192	ARG
1	B	193	LEU
1	B	194	LEU
1	B	201	VAL
1	B	203	VAL
1	B	214	LEU
1	B	216	SER
1	B	227	LEU
1	B	228	HIS
1	B	229	CYS
1	B	232	LEU
1	B	245	ILE
1	B	247	ILE

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Mol	Chain	Res	Type
1	B	249	THR
1	B	256	LEU
1	B	257	MET
1	B	260	ARG
1	B	267	ARG
1	B	273	ILE
1	B	275	GLN
1	C	25	GLN
1	C	29	ARG
1	C	32	GLN
1	C	39	THR
1	C	41	GLU
1	C	55	THR
1	C	58	ASP
1	C	64	LEU
1	C	66	ILE
1	C	67	SER
1	C	71	GLU
1	C	72	ARG
1	C	77	ARG
1	C	91	VAL
1	C	95	SER
1	C	100	ILE
1	C	106	THR
1	C	110	VAL
1	C	112	ARG
1	C	118	VAL
1	C	124	VAL
1	C	125	ARG
1	C	127	GLU
1	C	137	THR
1	C	138	GLU
1	C	139	GLU
1	C	141	LEU
1	C	145	ARG
1	C	155	GLN
1	C	158	ARG
1	C	164	ASP
1	C	174	ILE
1	C	177	LYS
1	C	183	LEU
1	C	184	LYS

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Mol	Chain	Res	Type
1	C	185	LEU
1	C	187	LEU
1	C	188	SER
1	C	190	MET
1	C	191	GLU
1	C	192	ARG
1	C	193	LEU
1	C	194	LEU
1	C	203	VAL
1	C	204	ILE
1	C	214	LEU
1	C	227	LEU
1	C	232	LEU
1	C	238	ILE
1	C	245	ILE
1	C	247	ILE
1	C	249	THR
1	C	254	LEU
1	C	256	LEU
1	C	260	ARG
1	C	266	THR
1	C	268	GLU
1	C	273	ILE
1	C	275	GLN
1	D	18	GLU
1	D	29	ARG
1	D	35	ARG
1	D	36	LYS
1	D	39	THR
1	D	55	THR
1	D	56	GLU
1	D	58	ASP
1	D	63	ASP
1	D	64	LEU
1	D	65	ILE
1	D	66	ILE
1	D	67	SER
1	D	68	GLU
1	D	70	ARG
1	D	71	GLU
1	D	73	PHE
1	D	77	ARG

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Mol	Chain	Res	Type
1	D	99	ILE
1	D	106	THR
1	D	110	VAL
1	D	124	VAL
1	D	127	GLU
1	D	137	THR
1	D	140	ARG
1	D	141	LEU
1	D	145	ARG
1	D	146	ARG
1	D	174	ILE
1	D	177	LYS
1	D	182	THR
1	D	183	LEU
1	D	185	LEU
1	D	188	SER
1	D	190	MET
1	D	191	GLU
1	D	193	LEU
1	D	194	LEU
1	D	197	LYS
1	D	199	HIS
1	D	203	VAL
1	D	207	SER
1	D	209	LEU
1	D	214	LEU
1	D	227	LEU
1	D	239	ILE
1	D	240	ARG
1	D	245	ILE
1	D	249	THR
1	D	256	LEU
1	D	261	VAL
1	D	268	GLU
1	D	271	MET
1	D	273	ILE
1	D	275	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	HIS

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Mol	Chain	Res	Type
1	A	94	HIS
1	A	135	HIS
1	A	153	ASN
1	A	189	ASN
1	A	224	GLN
1	B	94	HIS
1	B	135	HIS
1	B	153	ASN
1	B	199	HIS
1	B	224	GLN
1	B	228	HIS
1	B	275	GLN
1	C	25	GLN
1	C	32	GLN
1	C	59	HIS
1	C	94	HIS
1	C	111	HIS
1	C	135	HIS
1	C	153	ASN
1	C	199	HIS
1	C	224	GLN
1	D	21	GLN
1	D	94	HIS
1	D	135	HIS
1	D	224	GLN
1	D	228	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	178:ARG	C	179:ASP	N	1.09
1	D	88:ALA	C	89:LYS	N	0.75

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	244/273 (89%)	-1.37	0 100 100	22, 46, 90, 118	0
1	B	244/273 (89%)	-1.34	0 100 100	25, 49, 98, 138	0
1	C	244/273 (89%)	-1.26	0 100 100	23, 52, 94, 124	0
1	D	244/273 (89%)	-1.22	0 100 100	22, 56, 109, 139	0
All	All	976/1092 (89%)	-1.30	0 100 100	22, 51, 100, 139	0

There are no RSRZ outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.