



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 3, 2017 – 12:06 AM EDT

PDB ID : 1U6J
Title : The Structure of native coenzyme F420-dependent methylenetetrahydromethanopterin dehydrogenase at 2.4Å resolution
Authors : Warkentin, E.; Hagemeier, C.H.; Shima, S.; Thauer, R.K.; Ermler, U.
Deposited on : unknown
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

<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
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

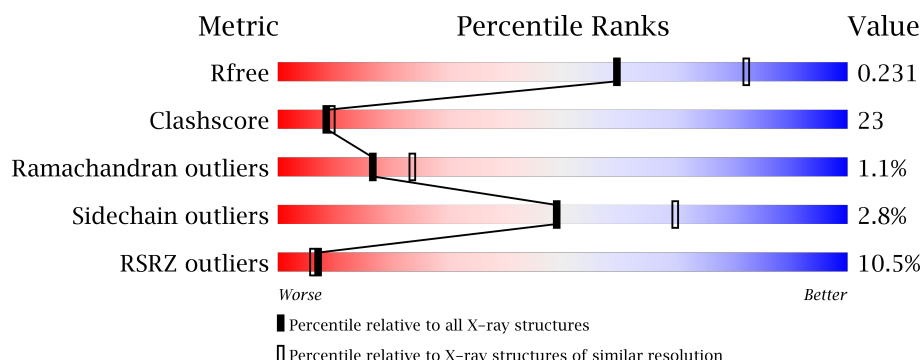
1 Overall quality at a glance

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}	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (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 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	283	<div> <div>68%</div> <div>30%</div> <div>.</div> </div>
1	B	283	<div> <div>72%</div> <div>28%</div> <div>.</div> </div>
1	C	283	<div> <div>11%</div> <div>49%</div> <div>48%</div> <div>.</div> </div>
1	D	283	<div> <div>8%</div> <div>59%</div> <div>40%</div> <div>.</div> </div>
1	E	283	<div> <div>6%</div> <div>51%</div> <div>47%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	283	<div><div></div><div>20%59%40%</div><div></div></div>
1	G	283	<div><div></div><div>67%31%</div><div></div></div>
1	H	283	<div><div></div><div>3%71%28%</div><div></div></div>
1	I	283	<div><div></div><div>18%51%46%</div><div></div></div>
1	J	283	<div><div></div><div>6%58%41%</div><div></div></div>
1	K	283	<div><div></div><div>23%51%47%</div><div></div></div>
1	L	283	<div><div></div><div>30%36%58%6%</div><div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 26753 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 F420-dependent methylenetetrahydromethanopterin dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	B	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	C	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	D	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	E	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	F	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	G	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	H	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	I	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	J	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	K	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			
1	L	282	Total	C	N	O	S	0	0	0
			2182	1369	357	437	19			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP P94951
B	1	MET	-	INITIATING METHIONINE	UNP P94951
C	1	MET	-	INITIATING METHIONINE	UNP P94951
D	1	MET	-	INITIATING METHIONINE	UNP P94951

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1	MET	-	INITIATING METHIONINE	UNP P94951
F	1	MET	-	INITIATING METHIONINE	UNP P94951
G	1	MET	-	INITIATING METHIONINE	UNP P94951
H	1	MET	-	INITIATING METHIONINE	UNP P94951
I	1	MET	-	INITIATING METHIONINE	UNP P94951
J	1	MET	-	INITIATING METHIONINE	UNP P94951
K	1	MET	-	INITIATING METHIONINE	UNP P94951
L	1	MET	-	INITIATING METHIONINE	UNP P94951

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	H	2	Total Mg 2 2	0	0
2	G	2	Total Mg 2 2	0	0
2	B	2	Total Mg 2 2	0	0
2	A	2	Total Mg 2 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	69	Total O 69 69	0	0
3	B	82	Total O 82 82	0	0
3	C	34	Total O 34 34	0	0
3	D	35	Total O 35 35	0	0
3	E	30	Total O 30 30	0	0
3	F	33	Total O 33 33	0	0
3	G	71	Total O 71 71	0	0
3	H	84	Total O 84 84	0	0
3	I	25	Total O 25 25	0	0

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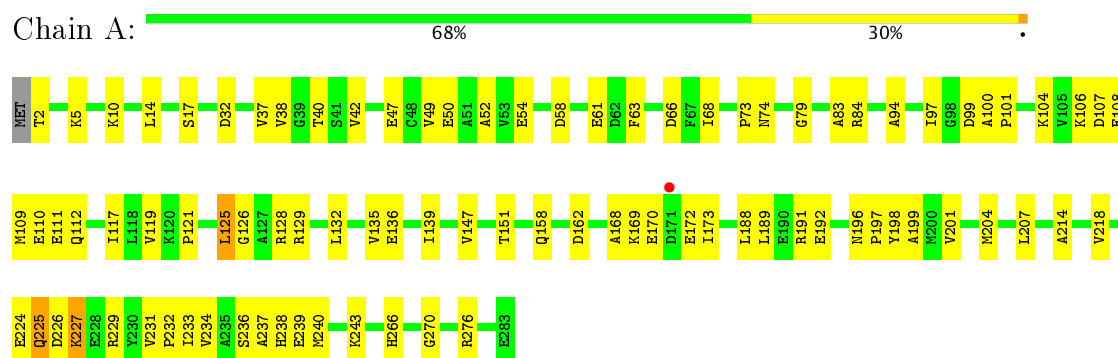
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	39	Total	O	0	0
			39	39		
3	K	25	Total	O	0	0
			25	25		
3	L	34	Total	O	0	0
			34	34		

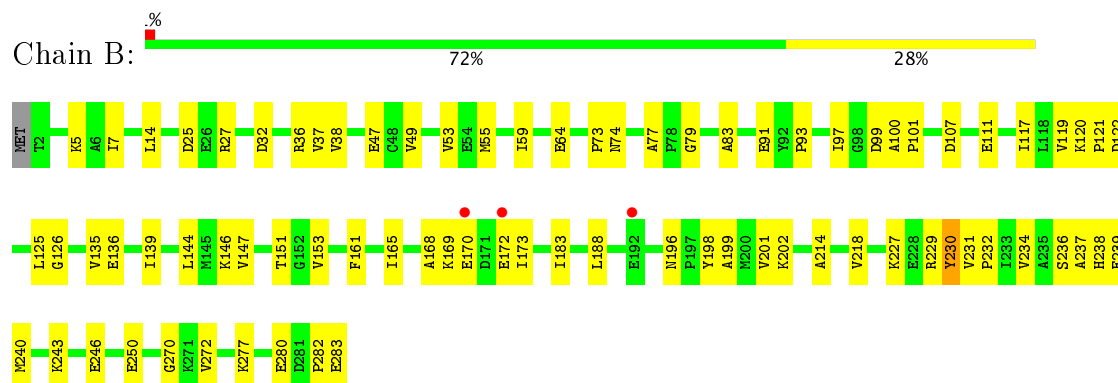
3 Residue-property plots [i](#)

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

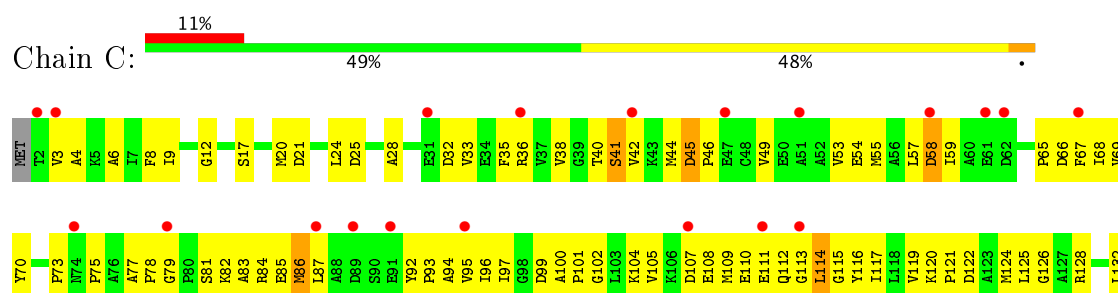
- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase

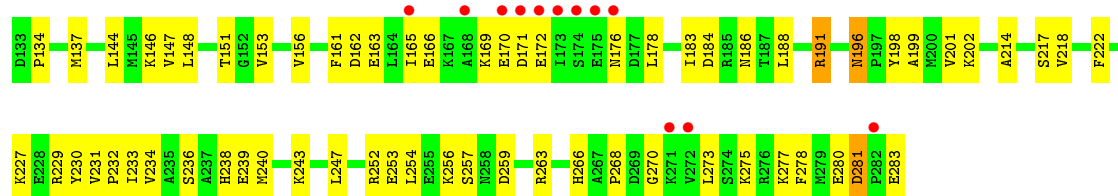


- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase

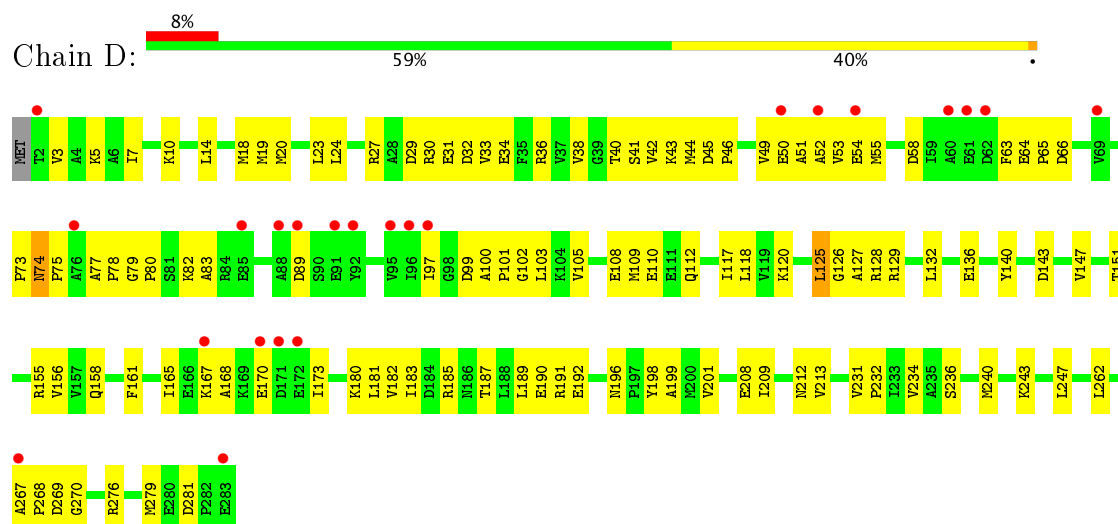


- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase

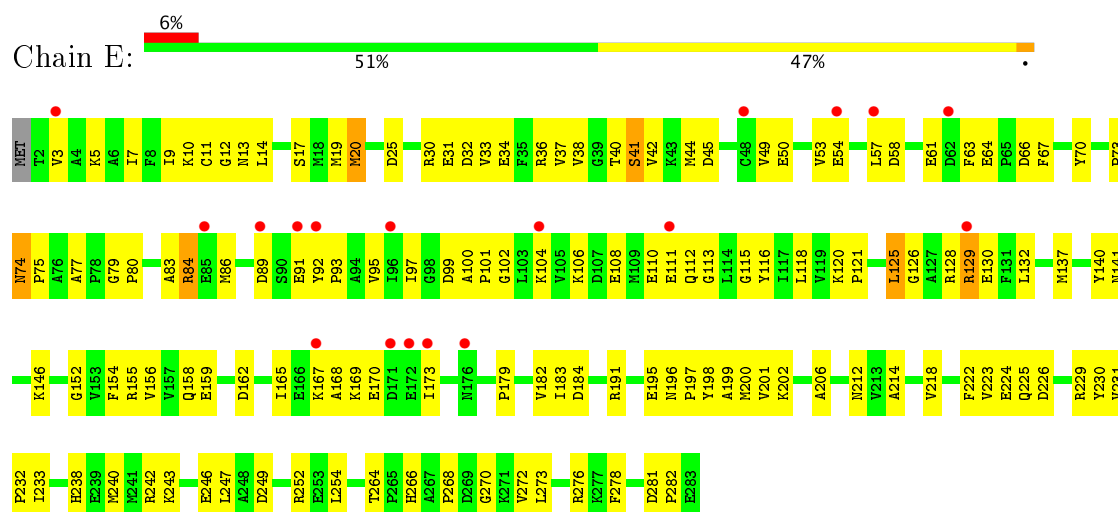




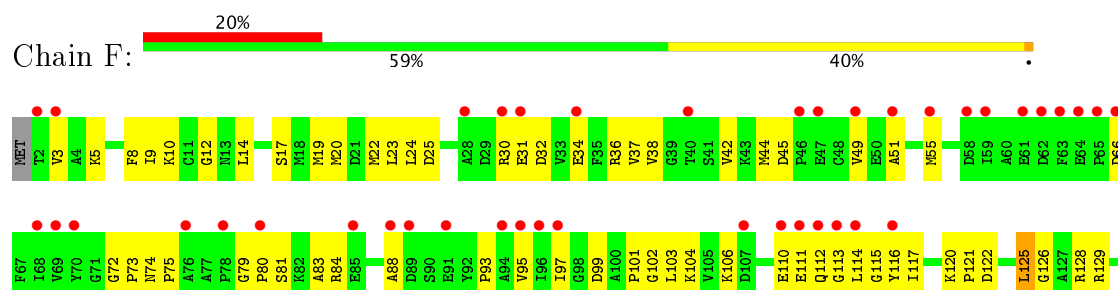
• Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase

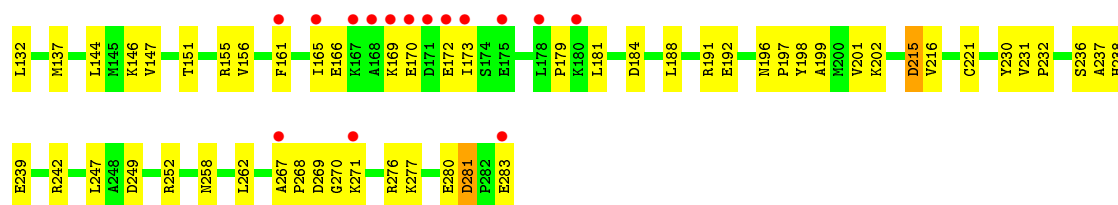


• Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase



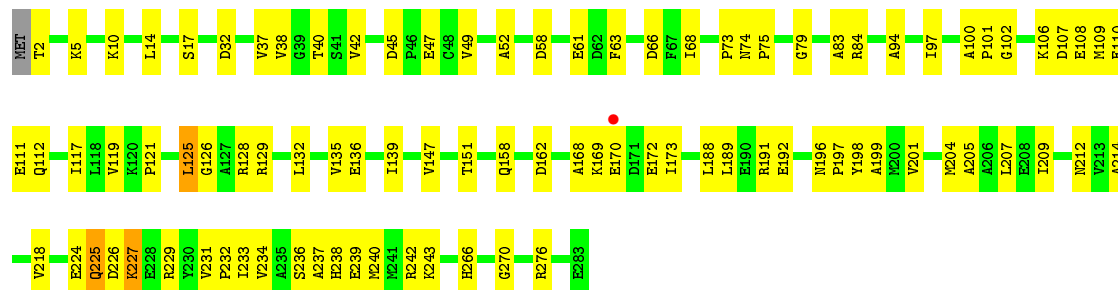
• Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase





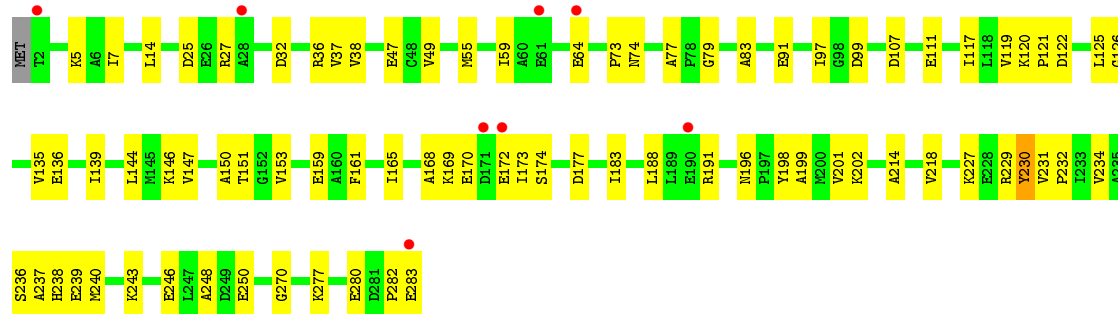
• Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase

Chain G: 67% 31%



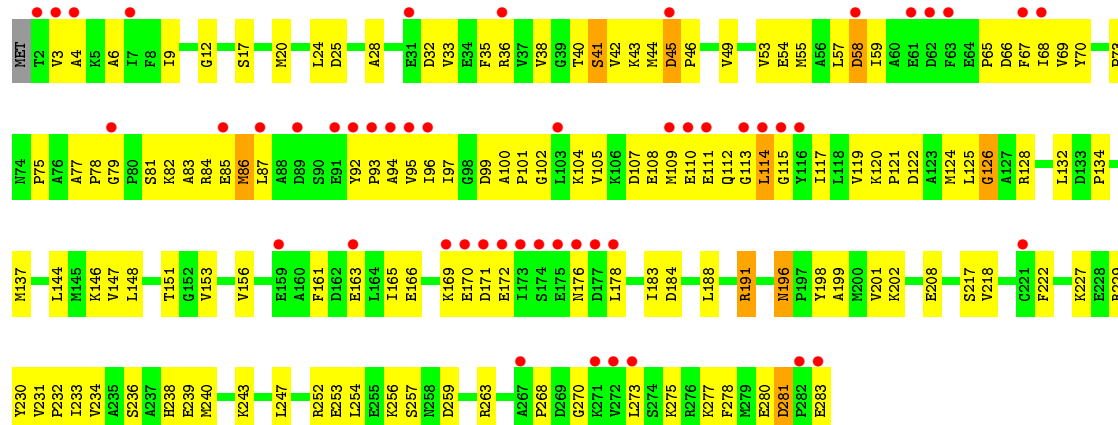
• Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase

Chain H: 3% 71% 28%

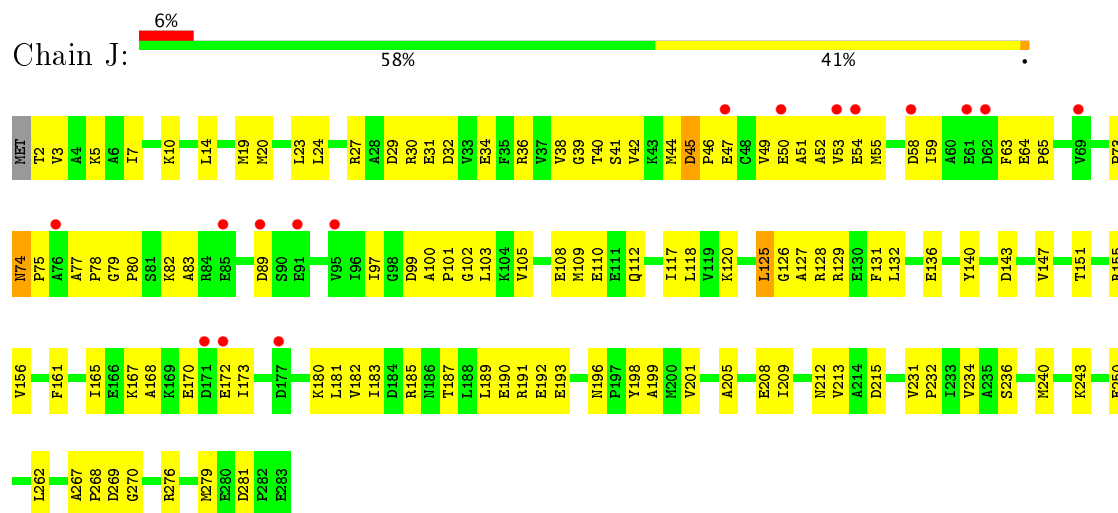


• Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase

Chain I: 18% 51% 46%



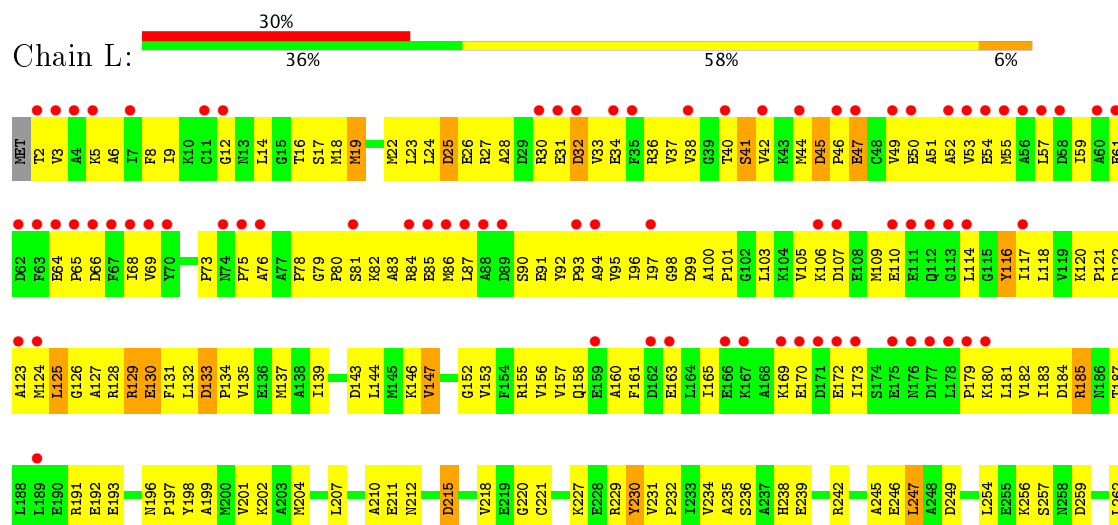
• Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase

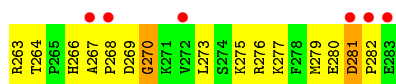


• Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase



• Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	150.90Å 118.90Å 219.20Å 90.00° 90.01° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40 19.93 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.0 (20.00-2.40) 97.5 (19.93-2.40)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.71 (at 2.41Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.175 , 0.235 0.176 , 0.231	Depositor DCC
R_{free} test set	7031 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.875	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.487 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	26753	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 89.73 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 3.0503e-08. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.38	0/2215	0.62	0/2989
1	B	0.39	0/2215	0.61	0/2989
1	C	0.34	0/2215	0.58	0/2989
1	D	0.35	0/2215	0.59	0/2989
1	E	0.34	0/2215	0.57	0/2989
1	F	0.36	0/2215	0.61	0/2989
1	G	0.39	0/2215	0.61	0/2989
1	H	0.38	0/2215	0.61	0/2989
1	I	0.34	0/2215	0.58	0/2989
1	J	0.35	0/2215	0.59	0/2989
1	K	0.34	0/2215	0.57	0/2989
1	L	0.34	0/2215	0.61	0/2989
All	All	0.36	0/26580	0.60	0/35868

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2182	0	2157	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2182	0	2157	62	0
1	C	2182	0	2157	127	0
1	D	2182	0	2157	106	0
1	E	2182	0	2157	125	0
1	F	2182	0	2157	103	0
1	G	2182	0	2157	73	0
1	H	2182	0	2157	63	0
1	I	2182	0	2157	130	0
1	J	2182	0	2157	116	0
1	K	2182	0	2157	142	0
1	L	2182	0	2157	196	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
3	A	69	0	0	1	0
3	B	82	0	0	5	0
3	C	34	0	0	5	0
3	D	35	0	0	4	0
3	E	30	0	0	2	0
3	F	33	0	0	3	0
3	G	71	0	0	4	0
3	H	84	0	0	3	0
3	I	25	0	0	2	0
3	J	39	0	0	3	0
3	K	25	0	0	4	0
3	L	34	0	0	1	0
All	All	26753	0	25884	1195	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 23.

All (1195) 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:G:225:GLN:HA	1:G:225:GLN:HE21	1.20	1.02
1:A:225:GLN:HE21	1:A:225:GLN:HA	1.21	0.98
1:I:124:MET:HE2	1:I:217:SER:HB3	1.49	0.95
1:C:124:MET:HE2	1:C:217:SER:HB3	1.49	0.92
1:E:38:VAL:HG12	1:F:38:VAL:HG12	1.51	0.90
1:E:129:ARG:NH1	1:F:268:PRO:HD3	1.87	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:129:ARG:HH12	1:L:268:PRO:HB3	1.37	0.88
1:D:156:VAL:HG22	1:D:191:ARG:HH11	1.38	0.88
1:L:25:ASP:OD1	1:L:30:ARG:HB3	1.75	0.86
1:J:156:VAL:HG22	1:J:191:ARG:HH11	1.39	0.86
1:L:30:ARG:HG3	1:L:270:GLY:HA2	1.57	0.86
1:C:231:VAL:HB	1:C:232:PRO:HD3	1.58	0.84
1:I:231:VAL:HB	1:I:232:PRO:HD3	1.61	0.81
1:L:126:GLY:H	1:L:238:HIS:HE1	1.28	0.80
1:K:126:GLY:H	1:K:238:HIS:HE1	1.29	0.79
1:L:24:LEU:HA	1:L:266:HIS:HE1	1.46	0.79
1:I:81:SER:HA	1:I:84:ARG:HE	1.47	0.79
1:L:132:LEU:HD11	1:L:137:MET:HA	1.65	0.78
1:D:156:VAL:HG22	1:D:191:ARG:NH1	1.98	0.78
1:L:277:LYS:HB2	1:L:280:GLU:HB2	1.66	0.77
1:H:196:ASN:HD21	1:H:198:TYR:HB2	1.46	0.77
1:D:156:VAL:CG2	1:D:191:ARG:HH11	1.97	0.77
1:E:126:GLY:H	1:E:238:HIS:HE1	1.30	0.77
1:K:74:ASN:HD22	1:K:77:ALA:HB2	1.50	0.76
1:L:128:ARG:HE	1:L:221:CYS:HA	1.51	0.76
1:D:231:VAL:HB	1:D:232:PRO:HD3	1.68	0.76
1:B:91:GLU:HG2	3:B:8246:HOH:O	1.85	0.76
1:J:156:VAL:HG22	1:J:191:ARG:NH1	2.01	0.76
1:J:231:VAL:HB	1:J:232:PRO:HD3	1.67	0.75
1:C:81:SER:HA	1:C:84:ARG:HE	1.50	0.75
1:J:156:VAL:CG2	1:J:191:ARG:HH11	1.98	0.75
1:B:196:ASN:HD21	1:B:198:TYR:HB2	1.50	0.74
1:L:196:ASN:ND2	1:L:198:TYR:H	1.85	0.74
1:L:26:GLU:HG2	1:L:27:ARG:H	1.52	0.74
1:E:74:ASN:HD22	1:E:77:ALA:HB2	1.52	0.74
1:L:130:GLU:H	1:L:130:GLU:CD	1.87	0.74
1:A:126:GLY:H	1:A:238:HIS:HE1	1.36	0.73
1:H:107:ASP:O	1:H:111:GLU:HG3	1.88	0.73
1:L:14:LEU:HD13	1:L:73:PRO:HB3	1.68	0.73
1:F:81:SER:HA	1:F:84:ARG:HE	1.52	0.73
1:B:107:ASP:O	1:B:111:GLU:HG3	1.89	0.73
1:F:49:VAL:CG1	1:F:83:ALA:HB2	2.19	0.73
1:K:129:ARG:NH1	1:L:268:PRO:HB3	2.03	0.73
1:A:231:VAL:HB	1:A:232:PRO:HD3	1.70	0.72
1:F:128:ARG:HE	1:F:221:CYS:HA	1.54	0.72
1:L:83:ALA:O	1:L:87:LEU:HG	1.89	0.72
1:I:126:GLY:HA3	1:I:234:VAL:HB	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:196:ASN:HD22	1:D:199:ALA:H	1.37	0.71
1:B:170:GLU:O	1:B:172:GLU:HG3	1.91	0.71
1:C:126:GLY:HA3	1:C:234:VAL:HB	1.72	0.71
1:G:126:GLY:H	1:G:238:HIS:HE1	1.36	0.71
1:G:231:VAL:HB	1:G:232:PRO:HD3	1.70	0.71
1:D:99:ASP:CG	1:D:101:PRO:HD2	2.10	0.71
1:G:225:GLN:HA	1:G:225:GLN:NE2	2.02	0.71
1:L:116:TYR:HE2	1:L:180:LYS:HA	1.55	0.71
1:B:99:ASP:HB2	3:B:8091:HOH:O	1.90	0.71
1:G:107:ASP:O	1:G:111:GLU:HG3	1.91	0.71
1:G:196:ASN:HD21	1:G:198:TYR:HB2	1.56	0.70
1:L:267:ALA:HB1	1:L:268:PRO:HD2	1.71	0.70
1:J:99:ASP:CG	1:J:101:PRO:HD2	2.12	0.70
1:L:84:ARG:HH21	1:L:109:MET:HG2	1.56	0.70
1:A:196:ASN:HD21	1:A:198:TYR:HB2	1.57	0.70
1:D:196:ASN:HD21	1:D:198:TYR:HB2	1.54	0.70
1:E:42:VAL:HG21	1:F:25:ASP:O	1.92	0.70
1:I:24:LEU:HD21	1:I:161:PHE:HB2	1.72	0.70
1:L:5:LYS:HG2	1:L:34:GLU:HB3	1.73	0.70
1:A:32:ASP:HB2	1:A:169:LYS:HE2	1.74	0.70
1:F:97:ILE:HD11	1:F:161:PHE:CZ	2.26	0.70
1:F:242:ARG:HD2	3:F:8160:HOH:O	1.92	0.70
1:E:196:ASN:HD22	1:E:199:ALA:H	1.40	0.69
1:H:196:ASN:HD22	1:H:199:ALA:H	1.40	0.69
1:A:107:ASP:O	1:A:111:GLU:HG3	1.92	0.69
1:F:106:LYS:O	1:F:110:GLU:HG3	1.93	0.69
1:I:55:MET:HE3	1:J:36:ARG:HD2	1.74	0.69
1:K:127:ALA:HB1	1:L:27:ARG:HG2	1.74	0.69
1:K:196:ASN:HD22	1:K:199:ALA:H	1.40	0.69
1:A:225:GLN:NE2	1:A:225:GLN:HA	2.03	0.69
1:C:24:LEU:HD21	1:C:161:PHE:HB2	1.73	0.69
1:J:196:ASN:HD21	1:J:198:TYR:HB2	1.58	0.69
1:K:129:ARG:NH2	1:L:268:PRO:HD3	2.08	0.69
1:L:116:TYR:O	1:L:116:TYR:HD2	1.76	0.69
1:F:156:VAL:HA	1:F:191:ARG:HH21	1.58	0.68
1:H:246:GLU:O	1:H:250:GLU:HG3	1.93	0.68
1:E:128:ARG:O	1:E:130:GLU:N	2.27	0.68
1:H:170:GLU:O	1:H:172:GLU:HG3	1.93	0.68
1:K:128:ARG:O	1:K:130:GLU:N	2.26	0.68
1:B:196:ASN:HD22	1:B:199:ALA:H	1.42	0.67
1:J:44:MET:SD	1:J:73:PRO:HG2	2.34	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:126:GLY:H	1:F:238:HIS:HE1	1.42	0.67
1:J:196:ASN:HD22	1:J:199:ALA:H	1.43	0.67
1:D:74:ASN:ND2	1:D:77:ALA:HB2	2.09	0.67
1:J:243:LYS:HG3	1:K:247:LEU:HG	1.77	0.67
1:G:32:ASP:HB2	1:G:169:LYS:HE2	1.76	0.67
1:L:49:VAL:CG1	1:L:83:ALA:HB2	2.24	0.67
1:J:143:ASP:O	1:J:147:VAL:HG23	1.95	0.67
1:L:95:VAL:HG13	1:L:179:PRO:HG3	1.75	0.67
1:J:196:ASN:ND2	1:J:198:TYR:H	1.92	0.67
1:J:187:THR:O	1:J:190:GLU:HG2	1.95	0.67
1:J:74:ASN:ND2	1:J:77:ALA:HB2	2.09	0.67
1:D:143:ASP:O	1:D:147:VAL:HG23	1.95	0.66
1:L:93:PRO:HG2	1:L:173:ILE:HB	1.76	0.66
1:B:126:GLY:H	1:B:238:HIS:HE1	1.43	0.66
1:L:76:ALA:HB2	1:L:105:VAL:HG22	1.77	0.66
1:H:168:ALA:HB2	1:H:173:ILE:HD11	1.76	0.66
1:F:156:VAL:HA	1:F:191:ARG:NH2	2.11	0.66
1:F:3:VAL:HG22	1:F:32:ASP:HA	1.77	0.66
1:L:155:ARG:HG2	1:L:191:ARG:HH12	1.59	0.66
1:H:126:GLY:H	1:H:238:HIS:HE1	1.41	0.66
1:H:227:LYS:HA	1:H:230:TYR:CZ	2.31	0.66
1:L:117:ILE:HD13	1:L:181:LEU:HB2	1.78	0.66
1:L:196:ASN:HD21	1:L:198:TYR:HB2	1.61	0.66
1:L:9:ILE:CG2	1:L:52:ALA:HB1	2.26	0.66
1:J:46:PRO:HA	1:J:79:GLY:HA2	1.78	0.65
1:L:61:GLU:O	1:L:64:GLU:HG3	1.95	0.65
1:B:168:ALA:HB2	1:B:173:ILE:HD11	1.78	0.65
1:K:155:ARG:O	1:K:159:GLU:HG3	1.96	0.65
1:L:153:VAL:O	1:L:156:VAL:HB	1.96	0.65
1:C:116:TYR:HB3	3:C:8430:HOH:O	1.96	0.65
1:E:155:ARG:O	1:E:159:GLU:HG3	1.96	0.65
1:D:44:MET:SD	1:D:73:PRO:HG2	2.37	0.65
1:F:146:LYS:NZ	1:F:249:ASP:HB2	2.12	0.65
1:L:280:GLU:O	1:L:281:ASP:HB3	1.94	0.65
1:C:45:ASP:O	1:C:49:VAL:HG23	1.96	0.65
1:D:187:THR:O	1:D:190:GLU:HG2	1.97	0.65
1:I:20:MET:SD	1:I:97:ILE:HD12	2.36	0.65
1:F:97:ILE:HD11	1:F:161:PHE:HZ	1.62	0.65
1:D:243:LYS:HG3	1:E:247:LEU:HG	1.77	0.64
1:L:116:TYR:CE2	1:L:180:LYS:HA	2.31	0.64
1:I:45:ASP:O	1:I:49:VAL:HG23	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:PRO:HA	3:B:8038:HOH:O	1.98	0.64
1:F:24:LEU:HD21	1:F:161:PHE:HB2	1.78	0.64
1:F:197:PRO:O	1:F:201:VAL:HG23	1.97	0.64
1:I:97:ILE:HG12	1:I:117:ILE:HB	1.80	0.64
1:A:136:GLU:OE1	1:A:238:HIS:HD2	1.80	0.64
1:K:224:GLU:OE1	1:K:226:ASP:HB3	1.98	0.64
1:H:277:LYS:HB2	1:H:280:GLU:HB2	1.80	0.64
1:A:170:GLU:O	1:A:172:GLU:HG3	1.98	0.64
1:C:97:ILE:HG12	1:C:117:ILE:HB	1.80	0.64
1:D:74:ASN:HD22	1:D:77:ALA:HB2	1.63	0.64
1:I:75:PRO:HG2	1:I:102:GLY:HA3	1.80	0.63
1:L:81:SER:HA	1:L:84:ARG:HE	1.62	0.63
1:C:75:PRO:HG2	1:C:102:GLY:HA3	1.80	0.63
1:F:196:ASN:HD22	1:F:199:ALA:H	1.46	0.63
1:G:139:ILE:HG23	1:H:146:LYS:HE2	1.79	0.63
1:K:129:ARG:CZ	1:L:268:PRO:HD3	2.28	0.63
1:C:252:ARG:HG2	3:C:8289:HOH:O	1.99	0.63
1:F:44:MET:SD	1:F:73:PRO:HG2	2.38	0.63
1:G:170:GLU:O	1:G:172:GLU:HG3	1.98	0.63
1:K:146:LYS:HE2	1:K:249:ASP:HB2	1.80	0.63
1:K:196:ASN:ND2	1:K:254:LEU:HD13	2.14	0.63
1:K:196:ASN:ND2	1:K:199:ALA:H	1.97	0.63
1:B:277:LYS:HB2	1:B:280:GLU:HB2	1.81	0.62
1:L:196:ASN:HD22	1:L:199:ALA:H	1.46	0.62
1:D:196:ASN:ND2	1:D:198:TYR:H	1.96	0.62
1:F:125:LEU:HD13	1:F:132:LEU:HD22	1.81	0.62
1:F:30:ARG:HG2	1:F:32:ASP:OD2	2.00	0.62
1:L:26:GLU:HG2	1:L:27:ARG:N	2.13	0.62
1:F:196:ASN:ND2	1:F:198:TYR:H	1.97	0.62
1:J:168:ALA:HB2	1:J:173:ILE:HD11	1.81	0.62
1:B:231:VAL:HB	1:B:232:PRO:HD3	1.81	0.62
1:E:146:LYS:HE2	1:E:249:ASP:HB2	1.82	0.62
1:F:5:LYS:HG2	1:F:34:GLU:HB3	1.80	0.62
1:B:227:LYS:HA	1:B:230:TYR:CZ	2.35	0.62
1:B:246:GLU:O	1:B:250:GLU:HG3	2.00	0.62
1:D:168:ALA:HB2	1:D:173:ILE:HD11	1.81	0.62
1:D:46:PRO:HA	1:D:79:GLY:HA2	1.81	0.62
1:I:99:ASP:CG	1:I:101:PRO:HD2	2.20	0.62
1:D:43:LYS:HD2	3:D:8152:HOH:O	1.99	0.62
1:H:231:VAL:HB	1:H:232:PRO:HD3	1.79	0.62
1:H:188:LEU:HD22	3:H:8135:HOH:O	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:232:PRO:HG3	1:D:279:MET:HE1	1.81	0.61
1:J:74:ASN:HD22	1:J:77:ALA:HB2	1.64	0.61
1:L:49:VAL:HG11	1:L:79:GLY:O	1.99	0.61
1:A:239:GLU:HG3	1:F:201:VAL:HG12	1.82	0.61
1:D:262:LEU:HB2	1:D:276:ARG:NH2	2.16	0.61
1:J:31:GLU:HG2	1:J:268:PRO:O	2.01	0.61
1:K:49:VAL:HG11	1:K:79:GLY:O	2.00	0.61
1:L:24:LEU:HD11	1:L:161:PHE:CD1	2.36	0.61
1:C:20:MET:SD	1:C:97:ILE:HD12	2.40	0.61
1:I:38:VAL:HG12	1:J:38:VAL:HG12	1.81	0.61
1:C:49:VAL:CG1	1:C:83:ALA:HB2	2.31	0.61
1:D:97:ILE:HD11	1:D:161:PHE:HZ	1.66	0.61
1:E:196:ASN:ND2	1:E:199:ALA:H	1.98	0.61
1:G:126:GLY:HA3	1:G:234:VAL:HB	1.83	0.61
1:I:49:VAL:CG1	1:I:83:ALA:HB2	2.31	0.61
1:B:136:GLU:OE1	1:B:238:HIS:HD2	1.84	0.61
1:C:55:MET:HE3	1:D:36:ARG:HD2	1.82	0.61
1:D:54:GLU:O	1:D:58:ASP:HB2	2.01	0.61
1:E:49:VAL:HG11	1:E:79:GLY:O	2.01	0.61
1:J:262:LEU:HB2	1:J:276:ARG:NH2	2.16	0.61
1:G:136:GLU:OE1	1:G:238:HIS:HD2	1.84	0.60
1:J:54:GLU:O	1:J:58:ASP:HB2	2.01	0.60
1:K:42:VAL:HG21	1:L:25:ASP:O	2.01	0.60
1:F:231:VAL:HB	1:F:232:PRO:HD3	1.83	0.60
1:D:31:GLU:HG2	1:D:268:PRO:O	2.01	0.60
1:I:196:ASN:HD21	1:I:198:TYR:HB2	1.66	0.60
1:A:126:GLY:HA3	1:A:234:VAL:HB	1.83	0.60
1:D:63:PHE:O	1:D:64:GLU:HB2	2.02	0.60
1:H:32:ASP:HB2	1:H:169:LYS:HE2	1.83	0.60
1:J:189:LEU:HD21	1:K:232:PRO:HB2	1.83	0.60
1:D:75:PRO:HD2	1:D:102:GLY:CA	2.31	0.60
1:J:63:PHE:O	1:J:64:GLU:HB2	2.01	0.60
1:K:74:ASN:ND2	1:K:77:ALA:HB2	2.16	0.60
1:L:143:ASP:O	1:L:147:VAL:HG13	2.02	0.60
1:E:196:ASN:ND2	1:E:254:LEU:HD13	2.16	0.60
1:I:69:VAL:HG21	1:I:161:PHE:HE2	1.67	0.60
1:L:121:PRO:HG3	1:L:207:LEU:HD22	1.83	0.60
1:L:97:ILE:HD11	1:L:161:PHE:HZ	1.66	0.60
1:A:168:ALA:HB2	1:A:173:ILE:HD11	1.84	0.59
1:J:75:PRO:HD2	1:J:102:GLY:CA	2.32	0.59
1:L:50:GLU:O	1:L:54:GLU:HG3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:155:ARG:HG2	1:L:191:ARG:NH1	2.17	0.59
1:L:9:ILE:HG21	1:L:52:ALA:HB1	1.83	0.59
1:L:185:ARG:HG3	1:L:204:MET:O	2.02	0.59
1:B:188:LEU:HD22	3:B:8047:HOH:O	2.02	0.59
1:C:101:PRO:O	1:C:104:LYS:HE2	2.02	0.59
1:E:224:GLU:OE1	1:E:226:ASP:HB3	2.01	0.59
1:F:44:MET:HE3	1:F:80:PRO:CG	2.32	0.59
1:L:9:ILE:HA	1:L:38:VAL:O	2.03	0.59
1:C:38:VAL:HG12	1:D:38:VAL:HG12	1.85	0.59
1:J:10:LYS:HE2	1:J:20:MET:HE3	1.84	0.59
1:E:36:ARG:HD2	1:F:55:MET:SD	2.42	0.59
1:L:128:ARG:NE	1:L:221:CYS:HA	2.17	0.59
1:E:196:ASN:HD22	1:E:199:ALA:N	2.01	0.59
1:H:119:VAL:HG12	1:H:121:PRO:HD2	1.85	0.59
1:L:103:LEU:HD22	1:L:106:LYS:HD3	1.85	0.59
1:C:196:ASN:HD21	1:C:198:TYR:HB2	1.67	0.59
1:D:189:LEU:HD21	1:E:232:PRO:HB2	1.82	0.59
1:F:25:ASP:OD1	1:F:30:ARG:HB2	2.03	0.59
1:I:196:ASN:HD22	1:I:199:ALA:H	1.48	0.59
1:C:99:ASP:CG	1:C:101:PRO:HD2	2.22	0.59
1:E:129:ARG:HH12	1:F:268:PRO:HD3	1.67	0.59
1:L:19:MET:O	1:L:23:LEU:HG	2.02	0.59
1:L:55:MET:O	1:L:59:ILE:HG12	2.03	0.58
1:A:196:ASN:ND2	1:A:198:TYR:HB2	2.18	0.58
1:C:97:ILE:HD11	1:C:161:PHE:CZ	2.38	0.58
1:D:155:ARG:HH21	1:D:155:ARG:HG3	1.68	0.58
1:K:30:ARG:HG2	1:K:32:ASP:OD2	2.03	0.58
1:K:99:ASP:CG	1:K:101:PRO:HD2	2.24	0.58
1:C:49:VAL:HG11	1:C:79:GLY:O	2.03	0.58
1:G:168:ALA:HB2	1:G:173:ILE:HD11	1.84	0.58
1:I:115:GLY:H	1:I:178:LEU:HD13	1.68	0.58
1:L:131:PHE:CZ	1:L:235:ALA:HA	2.38	0.58
1:C:69:VAL:HG21	1:C:161:PHE:HE2	1.68	0.58
1:E:74:ASN:ND2	1:E:77:ALA:HB2	2.17	0.58
1:K:196:ASN:HD22	1:K:199:ALA:N	2.02	0.58
1:G:189:LEU:HD21	1:G:204:MET:HE1	1.86	0.58
1:K:266:HIS:CD2	1:K:272:VAL:HG22	2.39	0.58
1:L:124:MET:HE1	1:L:218:VAL:HA	1.85	0.58
1:B:5:LYS:HE3	1:B:64:GLU:O	2.03	0.58
1:C:196:ASN:HD22	1:C:199:ALA:H	1.50	0.58
1:D:108:GLU:O	1:D:112:GLN:HG3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:120:LYS:HG3	1:F:184:ASP:HB3	1.85	0.58
1:F:32:ASP:OD1	1:F:270:GLY:HA3	2.04	0.58
1:F:49:VAL:HG21	1:F:79:GLY:CA	2.34	0.58
1:K:126:GLY:N	1:K:238:HIS:HE1	2.01	0.58
1:C:49:VAL:HG21	1:C:79:GLY:CA	2.33	0.58
1:E:99:ASP:CG	1:E:101:PRO:HD2	2.24	0.58
1:F:215:ASP:N	1:F:215:ASP:OD2	2.37	0.58
1:L:193:GLU:HG3	1:L:262:LEU:HD23	1.86	0.58
1:A:126:GLY:H	1:A:238:HIS:CE1	2.21	0.57
1:A:139:ILE:HG23	1:B:146:LYS:HE2	1.85	0.57
1:B:239:GLU:HG3	1:C:201:VAL:HG12	1.86	0.57
1:F:31:GLU:HG2	1:F:268:PRO:O	2.04	0.57
1:I:101:PRO:O	1:I:104:LYS:HE2	2.03	0.57
1:J:97:ILE:HD11	1:J:161:PHE:HZ	1.69	0.57
1:I:232:PRO:HG3	1:J:279:MET:HE1	1.86	0.57
1:B:32:ASP:HB2	1:B:169:LYS:HE2	1.85	0.57
1:C:115:GLY:H	1:C:178:LEU:HD13	1.69	0.57
1:F:30:ARG:HE	1:F:270:GLY:HA2	1.69	0.57
1:J:40:THR:HG23	1:J:52:ALA:HB2	1.86	0.57
1:E:37:VAL:O	1:F:38:VAL:HA	2.04	0.57
1:G:229:ARG:O	1:G:233:ILE:HG13	2.04	0.57
1:J:155:ARG:HG3	1:J:155:ARG:HH21	1.69	0.57
1:L:95:VAL:CG1	1:L:179:PRO:HG3	2.34	0.57
1:F:30:ARG:HE	1:F:270:GLY:CA	2.16	0.57
1:K:42:VAL:HG13	1:L:22:MET:HG2	1.84	0.57
1:E:50:GLU:HG3	1:E:86:MET:SD	2.45	0.57
1:E:231:VAL:HB	1:E:232:PRO:HD3	1.86	0.57
1:E:66:ASP:CB	1:E:168:ALA:HB1	2.35	0.57
1:F:49:VAL:HG11	1:F:79:GLY:O	2.05	0.57
1:G:109:MET:HA	1:G:112:GLN:OE1	2.05	0.57
1:K:66:ASP:CB	1:K:168:ALA:HB1	2.34	0.57
1:L:229:ARG:O	1:L:232:PRO:HD2	2.04	0.57
1:F:12:GLY:HA2	1:F:42:VAL:O	2.04	0.57
1:L:24:LEU:HA	1:L:266:HIS:CE1	2.35	0.57
1:E:30:ARG:HG2	1:E:32:ASP:OD2	2.04	0.57
1:F:8:PHE:HB2	1:F:37:VAL:HG22	1.85	0.57
1:G:212:ASN:CG	1:L:212:ASN:HD22	2.08	0.57
1:I:151:THR:O	1:I:188:LEU:HD21	2.05	0.57
1:L:184:ASP:HB2	1:L:211:GLU:OE2	2.05	0.57
1:L:8:PHE:CD2	1:L:69:VAL:HB	2.40	0.57
1:D:209:ILE:O	1:D:213:VAL:HG23	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:126:GLY:H	1:E:238:HIS:CE1	2.19	0.57
1:K:67:PHE:HD2	1:K:173:ILE:HD13	1.70	0.56
1:L:202:LYS:HB3	1:L:247:LEU:HD22	1.86	0.56
1:E:49:VAL:HG21	1:E:79:GLY:CA	2.35	0.56
1:H:119:VAL:CG1	1:H:121:PRO:HD2	2.35	0.56
1:H:136:GLU:OE1	1:H:238:HIS:HD2	1.88	0.56
1:K:120:LYS:HG3	1:K:184:ASP:HB3	1.87	0.56
1:L:147:VAL:HG12	1:L:245:ALA:HA	1.86	0.56
1:C:144:LEU:HA	1:C:147:VAL:HG12	1.86	0.56
1:J:209:ILE:O	1:J:213:VAL:HG23	2.05	0.56
1:L:96:ILE:O	1:L:116:TYR:HA	2.05	0.56
1:G:158:GLN:HE21	1:G:266:HIS:CE1	2.23	0.56
1:K:30:ARG:HD3	1:K:33:VAL:HG21	1.88	0.56
1:L:130:GLU:OE2	1:L:130:GLU:N	2.30	0.56
1:L:99:ASP:CG	1:L:101:PRO:HD2	2.25	0.56
1:D:10:LYS:HE2	1:D:20:MET:HE3	1.87	0.56
1:J:108:GLU:O	1:J:112:GLN:HG3	2.05	0.56
1:A:14:LEU:HD13	1:A:73:PRO:HG3	1.87	0.56
1:H:239:GLU:HG3	1:I:201:VAL:HG12	1.86	0.56
1:K:106:LYS:O	1:K:110:GLU:HG3	2.06	0.56
1:K:231:VAL:HB	1:K:232:PRO:HD3	1.87	0.56
1:E:67:PHE:HD2	1:E:173:ILE:HD13	1.70	0.56
1:E:266:HIS:CD2	1:E:272:VAL:HG22	2.39	0.56
1:E:49:VAL:HG21	1:E:79:GLY:HA3	1.86	0.56
1:H:99:ASP:HB2	3:H:8057:HOH:O	2.04	0.56
1:I:144:LEU:HA	1:I:147:VAL:HG12	1.87	0.56
1:I:49:VAL:HG11	1:I:79:GLY:O	2.06	0.56
1:J:10:LYS:HE2	1:J:20:MET:CE	2.36	0.56
1:L:227:LYS:HA	1:L:230:TYR:CE1	2.40	0.56
1:L:46:PRO:HA	1:L:79:GLY:HA2	1.87	0.56
1:G:239:GLU:HG3	1:L:201:VAL:HG12	1.86	0.56
1:K:49:VAL:HG21	1:K:79:GLY:HA3	1.87	0.56
1:I:49:VAL:HG21	1:I:79:GLY:CA	2.35	0.56
1:K:165:ILE:O	1:K:169:LYS:HG3	2.06	0.56
1:H:55:MET:O	1:H:59:ILE:HG13	2.06	0.55
1:B:153:VAL:HG13	1:B:183:ILE:HG21	1.88	0.55
1:D:100:ALA:HB2	1:D:120:LYS:HD2	1.87	0.55
1:G:196:ASN:ND2	1:G:198:TYR:HB2	2.19	0.55
1:H:126:GLY:H	1:H:238:HIS:CE1	2.23	0.55
1:I:97:ILE:HD11	1:I:161:PHE:CZ	2.40	0.55
1:J:156:VAL:CG2	1:J:191:ARG:NH1	2.66	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:66:ASP:O	1:K:173:ILE:HD12	2.07	0.55
1:K:49:VAL:HG21	1:K:79:GLY:CA	2.35	0.55
1:G:129:ARG:NH1	1:H:27:ARG:HH11	2.04	0.55
1:I:134:PRO:O	1:I:137:MET:HB3	2.07	0.55
1:K:30:ARG:HD3	1:K:33:VAL:CG2	2.37	0.55
1:L:120:LYS:HG3	1:L:184:ASP:HB3	1.89	0.55
1:L:197:PRO:O	1:L:201:VAL:HG23	2.06	0.55
1:K:38:VAL:HG12	1:L:38:VAL:HG12	1.87	0.55
1:L:32:ASP:HB2	1:L:169:LYS:NZ	2.22	0.55
1:D:18:MET:HG3	3:D:8154:HOH:O	2.06	0.55
1:F:103:LEU:CD2	1:F:106:LYS:HD3	2.37	0.55
1:L:51:ALA:HA	1:L:54:GLU:OE2	2.06	0.55
1:A:201:VAL:HG12	1:F:239:GLU:HG3	1.88	0.55
1:C:243:LYS:HE2	3:C:8310:HOH:O	2.06	0.55
1:K:45:ASP:O	1:K:49:VAL:HG23	2.07	0.55
1:L:8:PHE:HA	1:L:69:VAL:O	2.06	0.55
1:C:151:THR:O	1:C:188:LEU:HD21	2.05	0.55
1:E:45:ASP:O	1:E:49:VAL:HG23	2.07	0.55
1:F:132:LEU:HD11	1:F:137:MET:HA	1.88	0.55
1:I:147:VAL:HG13	1:I:148:LEU:N	2.21	0.55
1:C:125:LEU:CD1	1:C:132:LEU:HD22	2.37	0.55
1:D:156:VAL:CG2	1:D:191:ARG:NH1	2.63	0.55
1:K:13:ASN:HD21	1:K:141:ASN:HD21	1.55	0.55
1:L:25:ASP:OD2	1:L:28:ALA:HA	2.07	0.55
1:E:120:LYS:HG3	1:E:184:ASP:HB3	1.88	0.55
1:E:13:ASN:HD21	1:E:141:ASN:HD21	1.55	0.55
1:J:100:ALA:HB2	1:J:120:LYS:HD2	1.89	0.55
1:D:49:VAL:HG11	1:D:79:GLY:O	2.07	0.54
1:E:30:ARG:HD3	1:E:33:VAL:HG21	1.88	0.54
1:F:151:THR:O	1:F:188:LEU:HD21	2.07	0.54
1:H:5:LYS:HE3	1:H:64:GLU:O	2.07	0.54
1:L:49:VAL:HG21	1:L:79:GLY:HA3	1.88	0.54
1:E:30:ARG:HD3	1:E:33:VAL:CG2	2.38	0.54
1:I:44:MET:SD	1:I:73:PRO:HG2	2.47	0.54
1:I:44:MET:O	1:I:79:GLY:HA3	2.07	0.54
1:J:103:LEU:HD11	1:J:120:LYS:HD3	1.90	0.54
1:L:45:ASP:HB2	1:L:47:GLU:OE1	2.07	0.54
1:C:252:ARG:NH1	1:D:136:GLU:OE2	2.41	0.54
1:A:243:LYS:HG3	1:F:247:LEU:HG	1.89	0.54
1:F:44:MET:HE3	1:F:80:PRO:HG2	1.89	0.54
1:B:126:GLY:H	1:B:238:HIS:CE1	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:156:VAL:HG11	1:D:183:ILE:HD12	1.89	0.54
1:D:27:ARG:HB2	1:D:29:ASP:OD2	2.07	0.54
1:E:165:ILE:O	1:E:169:LYS:HG3	2.08	0.54
1:H:91:GLU:HG2	3:H:8225:HOH:O	2.08	0.54
1:L:5:LYS:HD3	1:L:34:GLU:OE2	2.07	0.54
1:C:44:MET:SD	1:C:73:PRO:HG2	2.47	0.54
1:E:84:ARG:HH21	1:E:112:GLN:HE22	1.55	0.54
1:E:10:LYS:NZ	1:E:17:SER:O	2.39	0.54
1:J:156:VAL:HG11	1:J:183:ILE:HD12	1.90	0.54
1:J:209:ILE:HA	1:J:212:ASN:ND2	2.22	0.54
1:E:106:LYS:O	1:E:110:GLU:HG3	2.07	0.54
1:L:40:THR:O	1:L:41:SER:HB3	2.08	0.54
1:G:14:LEU:HD13	1:G:73:PRO:HG3	1.90	0.54
1:K:126:GLY:H	1:K:238:HIS:CE1	2.17	0.54
1:L:146:LYS:CE	1:L:249:ASP:HB2	2.36	0.54
1:A:158:GLN:HE21	1:A:266:HIS:CE1	2.26	0.54
1:B:198:TYR:O	1:B:202:LYS:HG3	2.08	0.54
1:C:36:ARG:NH1	1:D:51:ALA:HB1	2.22	0.54
1:H:153:VAL:HG13	1:H:183:ILE:HG21	1.88	0.54
1:J:117:ILE:HA	1:J:181:LEU:O	2.08	0.54
1:C:147:VAL:HG13	1:C:148:LEU:N	2.23	0.54
1:C:25:ASP:OD2	1:C:28:ALA:HA	2.08	0.54
1:E:66:ASP:O	1:E:173:ILE:HD12	2.08	0.54
1:C:68:ILE:O	1:C:94:ALA:HA	2.08	0.53
1:C:44:MET:O	1:C:79:GLY:HA3	2.08	0.53
1:H:198:TYR:O	1:H:202:LYS:HG3	2.07	0.53
1:C:166:GLU:O	1:C:170:GLU:HG2	2.08	0.53
1:F:32:ASP:OD1	1:F:169:LYS:NZ	2.37	0.53
1:G:227:LYS:O	1:G:231:VAL:HG23	2.08	0.53
1:L:129:ARG:CZ	1:L:129:ARG:HB2	2.38	0.53
1:L:49:VAL:HG11	1:L:83:ALA:HB2	1.89	0.53
1:C:3:VAL:HG22	1:C:32:ASP:HA	1.90	0.53
1:D:10:LYS:HE2	1:D:20:MET:CE	2.38	0.53
1:D:103:LEU:HD11	1:D:120:LYS:HD3	1.91	0.53
1:D:77:ALA:HB3	1:D:80:PRO:HD2	1.91	0.53
1:J:77:ALA:HB3	1:J:80:PRO:HD2	1.90	0.53
1:A:109:MET:HA	1:A:112:GLN:OE1	2.08	0.53
1:B:55:MET:O	1:B:59:ILE:HG13	2.08	0.53
1:L:120:LYS:N	1:L:121:PRO:HD2	2.24	0.53
1:B:119:VAL:HG12	1:B:121:PRO:HD2	1.91	0.53
1:I:252:ARG:NH1	1:J:136:GLU:OE2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:THR:HG23	1:D:52:ALA:HB2	1.89	0.53
1:E:25:ASP:O	1:F:42:VAL:HG21	2.08	0.53
1:L:84:ARG:HH21	1:L:109:MET:CG	2.22	0.53
1:D:209:ILE:HA	1:D:212:ASN:ND2	2.24	0.53
1:E:108:GLU:O	1:E:112:GLN:HG3	2.09	0.53
1:J:5:LYS:HB3	1:J:63:PHE:CZ	2.44	0.53
1:K:108:GLU:O	1:K:112:GLN:HG3	2.08	0.53
1:L:229:ARG:C	1:L:232:PRO:HD2	2.29	0.53
1:H:74:ASN:OD1	1:H:77:ALA:N	2.42	0.53
1:J:32:ASP:OD1	1:J:270:GLY:HA3	2.09	0.53
1:D:49:VAL:HG21	1:D:79:GLY:HA3	1.91	0.53
1:E:91:GLU:HG2	3:E:8132:HOH:O	2.09	0.53
1:H:229:ARG:O	1:H:232:PRO:HD2	2.09	0.53
1:E:126:GLY:N	1:E:238:HIS:HE1	2.03	0.52
1:I:125:LEU:HD11	1:I:132:LEU:HD22	1.92	0.52
1:G:236:SER:O	1:G:240:MET:HG3	2.08	0.52
1:L:16:THR:O	1:L:18:MET:N	2.43	0.52
1:A:129:ARG:NH1	1:B:27:ARG:HH11	2.07	0.52
1:J:126:GLY:HA3	1:J:234:VAL:HB	1.91	0.52
1:J:49:VAL:HG11	1:J:79:GLY:O	2.10	0.52
1:L:242:ARG:O	1:L:246:GLU:HG3	2.10	0.52
1:I:166:GLU:O	1:I:170:GLU:HG2	2.09	0.52
1:L:117:ILE:CD1	1:L:181:LEU:HB2	2.39	0.52
1:F:111:GLU:C	1:F:113:GLY:H	2.11	0.52
1:K:44:MET:SD	1:K:73:PRO:HG2	2.50	0.52
1:L:275:LYS:HD2	1:L:282:PRO:HD3	1.91	0.52
1:A:162:ASP:OD1	1:A:266:HIS:NE2	2.41	0.52
1:B:196:ASN:ND2	1:B:198:TYR:HB2	2.23	0.52
1:C:125:LEU:HD11	1:C:132:LEU:HD22	1.91	0.52
1:D:50:GLU:O	1:D:54:GLU:HG3	2.09	0.52
1:H:196:ASN:HD22	1:H:199:ALA:N	2.06	0.52
1:I:3:VAL:HG22	1:I:32:ASP:HA	1.91	0.52
1:D:117:ILE:HA	1:D:181:LEU:O	2.10	0.52
1:E:44:MET:SD	1:E:73:PRO:HG2	2.49	0.52
1:F:81:SER:CB	1:F:84:ARG:HH11	2.23	0.52
1:I:68:ILE:O	1:I:94:ALA:HA	2.08	0.52
1:J:156:VAL:HG11	1:J:183:ILE:CD1	2.40	0.52
1:K:128:ARG:HH12	1:K:225:GLN:NE2	2.07	0.52
1:K:131:PHE:O	1:L:263:ARG:HD3	2.09	0.52
1:F:72:GLY:HA3	3:F:8096:HOH:O	2.08	0.52
1:J:49:VAL:HG21	1:J:79:GLY:HA3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:16:THR:C	1:L:18:MET:H	2.13	0.52
1:C:134:PRO:O	1:C:137:MET:HB3	2.10	0.52
1:C:12:GLY:HA2	1:C:42:VAL:O	2.10	0.52
1:D:156:VAL:HG11	1:D:183:ILE:CD1	2.39	0.52
1:E:36:ARG:HD2	1:F:55:MET:CE	2.40	0.51
1:G:106:LYS:O	1:G:110:GLU:HG3	2.10	0.51
1:L:123:ALA:HB2	1:L:210:ALA:O	2.10	0.51
1:A:104:LYS:NZ	3:A:8403:HOH:O	2.43	0.51
1:B:282:PRO:O	1:B:283:GLU:HG3	2.09	0.51
1:C:55:MET:CE	1:D:36:ARG:HD2	2.40	0.51
1:L:107:ASP:O	1:L:110:GLU:N	2.44	0.51
1:E:168:ALA:HB2	1:E:173:ILE:HD11	1.93	0.51
1:I:126:GLY:H	1:I:238:HIS:HE1	1.57	0.51
1:J:27:ARG:HB2	1:J:29:ASP:OD2	2.10	0.51
1:A:189:LEU:HD21	1:A:204:MET:HE1	1.91	0.51
1:D:14:LEU:HD13	1:D:73:PRO:HB3	1.93	0.51
1:G:32:ASP:OD1	1:G:270:GLY:HA3	2.09	0.51
1:K:38:VAL:HA	1:L:37:VAL:O	2.10	0.51
1:L:215:ASP:OD2	1:L:215:ASP:N	2.41	0.51
1:B:229:ARG:O	1:B:232:PRO:HD2	2.09	0.51
1:E:197:PRO:O	1:E:200:MET:HB3	2.11	0.51
1:G:126:GLY:H	1:G:238:HIS:CE1	2.23	0.51
1:H:196:ASN:ND2	1:H:198:TYR:HB2	2.20	0.51
1:I:108:GLU:O	1:I:112:GLN:HG3	2.11	0.51
1:I:147:VAL:HG13	1:I:148:LEU:H	1.75	0.51
1:H:236:SER:CA	1:I:201:VAL:HG13	2.41	0.51
1:K:11:CYS:HB2	1:K:70:TYR:OH	2.11	0.51
1:K:206:ALA:HB2	1:K:247:LEU:HB3	1.92	0.51
1:L:220:GLY:O	1:L:230:TYR:HB2	2.10	0.51
1:B:119:VAL:CG1	1:B:121:PRO:HD2	2.40	0.51
1:E:11:CYS:HB2	1:E:70:TYR:OH	2.10	0.51
1:E:206:ALA:HB2	1:E:247:LEU:HB3	1.91	0.51
1:F:117:ILE:HD13	1:F:181:LEU:HB2	1.93	0.51
1:F:146:LYS:HZ3	1:F:249:ASP:HB2	1.75	0.51
1:H:236:SER:HA	1:I:201:VAL:HG13	1.93	0.51
1:H:282:PRO:O	1:H:283:GLU:HG3	2.10	0.51
1:I:125:LEU:CD1	1:I:132:LEU:HD22	2.41	0.51
1:I:36:ARG:NH1	1:J:51:ALA:HB1	2.24	0.51
1:K:125:LEU:HB3	1:K:140:TYR:CD2	2.46	0.51
1:K:50:GLU:O	1:K:54:GLU:HG3	2.10	0.51
1:A:49:VAL:HG11	1:A:79:GLY:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:120:LYS:NZ	1:C:184:ASP:HB3	2.25	0.51
1:C:124:MET:HE2	1:C:217:SER:CB	2.32	0.51
1:D:99:ASP:OD2	1:D:101:PRO:HD2	2.10	0.51
1:I:12:GLY:HA2	1:I:42:VAL:O	2.11	0.51
1:J:167:LYS:NZ	3:J:8222:HOH:O	2.35	0.51
1:I:55:MET:CE	1:J:36:ARG:HD2	2.40	0.51
1:L:44:MET:SD	1:L:73:PRO:HG2	2.51	0.51
1:A:106:LYS:O	1:A:110:GLU:HG3	2.10	0.51
1:E:38:VAL:HA	1:F:37:VAL:O	2.11	0.51
1:F:129:ARG:HB2	1:F:129:ARG:CZ	2.41	0.51
1:H:47:GLU:N	1:H:47:GLU:OE1	2.44	0.50
1:J:19:MET:O	1:J:23:LEU:HG	2.11	0.50
1:K:66:ASP:OD1	1:K:168:ALA:HB1	2.11	0.50
1:A:224:GLU:OE1	1:A:226:ASP:HB3	2.11	0.50
1:D:196:ASN:HD22	1:D:199:ALA:N	2.07	0.50
1:J:198:TYR:HA	1:J:201:VAL:HG22	1.93	0.50
1:L:163:GLU:C	1:L:165:ILE:H	2.13	0.50
1:L:196:ASN:ND2	1:L:198:TYR:N	2.58	0.50
1:A:188:LEU:HD11	1:A:207:LEU:CD1	2.41	0.50
1:C:109:MET:O	1:C:114:LEU:HD12	2.10	0.50
1:C:280:GLU:O	1:C:281:ASP:CB	2.58	0.50
1:I:120:LYS:NZ	1:I:184:ASP:HB3	2.26	0.50
1:K:32:ASP:OD1	1:K:270:GLY:HA3	2.11	0.50
1:K:27:ARG:HG2	1:L:127:ALA:HB1	1.92	0.50
1:L:183:ILE:HD12	1:L:187:THR:HG21	1.92	0.50
1:D:128:ARG:CG	1:D:234:VAL:HG11	2.42	0.50
1:D:126:GLY:HA3	1:D:234:VAL:HB	1.93	0.50
1:E:32:ASP:OD1	1:E:270:GLY:HA3	2.12	0.50
1:F:281:ASP:O	1:F:283:GLU:HG2	2.11	0.50
1:I:109:MET:O	1:I:114:LEU:HD12	2.11	0.50
1:K:40:THR:HG22	1:L:36:ARG:HD3	1.92	0.50
1:G:214:ALA:O	1:G:218:VAL:HG23	2.11	0.50
1:H:49:VAL:HG11	1:H:79:GLY:O	2.11	0.50
1:I:280:GLU:O	1:I:281:ASP:CB	2.58	0.50
1:J:99:ASP:OD2	1:J:101:PRO:HD2	2.11	0.50
1:C:95:VAL:HA	1:C:115:GLY:O	2.11	0.50
1:F:9:ILE:HA	1:F:38:VAL:O	2.11	0.50
1:G:42:VAL:HG21	1:H:25:ASP:O	2.12	0.50
1:K:40:THR:O	1:K:41:SER:HB3	2.11	0.50
1:L:227:LYS:HA	1:L:230:TYR:CZ	2.47	0.50
1:B:126:GLY:HA3	1:B:234:VAL:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:VAL:HG11	1:C:183:ILE:CD1	2.40	0.50
1:J:128:ARG:CG	1:J:234:VAL:HG11	2.41	0.50
1:J:46:PRO:HD3	1:J:78:PRO:HB2	1.92	0.50
1:A:38:VAL:HA	1:B:37:VAL:O	2.12	0.50
1:C:126:GLY:H	1:C:238:HIS:HE1	1.59	0.50
1:D:198:TYR:HA	1:D:201:VAL:HG22	1.94	0.50
1:D:32:ASP:OD1	1:D:270:GLY:HA3	2.11	0.50
1:A:214:ALA:O	1:A:218:VAL:HG23	2.11	0.50
1:H:97:ILE:HD13	1:H:117:ILE:HB	1.93	0.50
1:J:14:LEU:HD13	1:J:73:PRO:HB3	1.94	0.50
1:K:252:ARG:HD3	3:K:8058:HOH:O	2.11	0.50
1:L:44:MET:HE3	1:L:80:PRO:HG2	1.94	0.50
1:E:50:GLU:O	1:E:54:GLU:HG3	2.12	0.49
1:J:50:GLU:O	1:J:54:GLU:HG3	2.12	0.49
1:K:84:ARG:HH21	1:K:112:GLN:HE22	1.57	0.49
1:L:53:VAL:O	1:L:57:LEU:HG	2.12	0.49
1:E:42:VAL:HG13	1:F:22:MET:HG2	1.94	0.49
1:F:14:LEU:HB3	1:F:17:SER:HB3	1.94	0.49
1:I:156:VAL:HG11	1:I:183:ILE:CD1	2.41	0.49
1:A:227:LYS:O	1:A:231:VAL:HG23	2.11	0.49
1:E:128:ARG:HH12	1:E:225:GLN:NE2	2.10	0.49
1:I:25:ASP:OD2	1:I:28:ALA:HA	2.12	0.49
1:K:242:ARG:O	1:K:246:GLU:HG3	2.11	0.49
1:A:32:ASP:OD1	1:A:270:GLY:HA3	2.12	0.49
1:B:122:ASP:OD1	1:B:144:LEU:HD21	2.13	0.49
1:E:125:LEU:HB3	1:E:140:TYR:CD2	2.46	0.49
1:G:162:ASP:OD1	1:G:266:HIS:NE2	2.40	0.49
1:K:197:PRO:O	1:K:200:MET:HB3	2.12	0.49
1:K:33:VAL:HG11	1:K:165:ILE:HD13	1.94	0.49
1:L:46:PRO:HG2	1:L:47:GLU:OE2	2.12	0.49
1:B:196:ASN:HD22	1:B:199:ALA:N	2.08	0.49
1:C:108:GLU:O	1:C:112:GLN:HG3	2.12	0.49
1:E:252:ARG:HD3	3:E:8344:HOH:O	2.12	0.49
1:I:263:ARG:NH1	1:J:136:GLU:OE2	2.46	0.49
1:A:236:SER:O	1:A:240:MET:HG3	2.12	0.49
1:G:108:GLU:O	1:G:112:GLN:HG3	2.13	0.49
1:I:6:ALA:HB3	1:I:35:PHE:CD2	2.47	0.49
1:L:100:ALA:HB3	1:L:101:PRO:HD3	1.94	0.49
1:L:6:ALA:HA	1:L:65:PRO:HB2	1.94	0.49
1:A:229:ARG:O	1:A:233:ILE:HG13	2.13	0.49
1:C:120:LYS:HZ3	1:C:184:ASP:HB3	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:19:MET:O	1:D:23:LEU:HG	2.13	0.49
1:D:46:PRO:HD3	1:D:78:PRO:HB2	1.94	0.49
1:F:125:LEU:HD13	1:F:132:LEU:CD2	2.42	0.49
1:G:188:LEU:HD11	1:G:207:LEU:CD1	2.42	0.49
1:G:49:VAL:CG1	1:G:83:ALA:HB2	2.42	0.49
1:H:243:LYS:HG3	1:I:247:LEU:HG	1.95	0.49
1:J:196:ASN:ND2	1:J:198:TYR:N	2.61	0.49
1:C:55:MET:O	1:C:59:ILE:HG23	2.13	0.49
1:D:161:PHE:O	1:D:165:ILE:HG13	2.13	0.49
1:E:40:THR:O	1:E:41:SER:HB3	2.12	0.49
1:G:38:VAL:HA	1:H:37:VAL:O	2.12	0.49
1:I:227:LYS:HA	1:I:230:TYR:CE1	2.47	0.49
1:C:277:LYS:HB2	1:C:280:GLU:HB2	1.94	0.49
1:D:236:SER:O	1:D:240:MET:HG3	2.13	0.49
1:F:173:ILE:HG22	1:F:173:ILE:O	2.13	0.49
1:I:82:LYS:O	1:I:85:GLU:HB3	2.13	0.49
1:I:95:VAL:HA	1:I:115:GLY:O	2.12	0.49
1:K:50:GLU:HG3	1:K:86:MET:SD	2.52	0.49
1:A:100:ALA:HB3	1:A:101:PRO:HD3	1.95	0.49
1:I:263:ARG:HD2	3:I:8308:HOH:O	2.13	0.49
1:L:157:VAL:O	1:L:160:ALA:HB3	2.12	0.49
1:B:236:SER:CA	1:C:201:VAL:HG13	2.43	0.48
1:C:75:PRO:CG	1:C:102:GLY:HA3	2.43	0.48
1:C:82:LYS:HE3	1:C:86:MET:SD	2.53	0.48
1:D:196:ASN:ND2	1:D:198:TYR:HB2	2.27	0.48
1:I:171:ASP:C	1:I:172:GLU:HG3	2.34	0.48
1:I:278:PHE:HE1	1:J:232:PRO:HG3	1.78	0.48
1:K:10:LYS:NZ	1:K:17:SER:O	2.41	0.48
1:K:57:LEU:O	1:K:61:GLU:HG2	2.13	0.48
1:A:226:ASP:HB3	1:A:229:ARG:HG3	1.93	0.48
1:C:227:LYS:HA	1:C:230:TYR:CE1	2.48	0.48
1:C:278:PHE:HE1	1:D:232:PRO:HG3	1.78	0.48
1:C:96:ILE:HB	3:C:8430:HOH:O	2.11	0.48
1:D:189:LEU:HD13	1:E:229:ARG:HB3	1.95	0.48
1:H:122:ASP:OD1	1:H:144:LEU:HD21	2.13	0.48
1:K:42:VAL:CG1	1:L:22:MET:HG2	2.43	0.48
1:K:149:ALA:O	1:L:135:VAL:HG13	2.13	0.48
1:D:5:LYS:HB3	1:D:63:PHE:CZ	2.47	0.48
1:F:126:GLY:H	1:F:238:HIS:CE1	2.26	0.48
1:G:226:ASP:HB3	1:G:229:ARG:HG3	1.94	0.48
1:J:191:ARG:HB3	3:J:8224:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:53:VAL:HG11	1:L:86:MET:HB3	1.95	0.48
1:B:236:SER:HA	1:C:201:VAL:HG13	1.95	0.48
1:C:268:PRO:HD3	1:D:129:ARG:CZ	2.43	0.48
1:E:33:VAL:HG11	1:E:165:ILE:HD13	1.95	0.48
1:G:49:VAL:HG11	1:G:79:GLY:O	2.13	0.48
1:I:4:ALA:O	1:I:33:VAL:HA	2.14	0.48
1:J:161:PHE:O	1:J:165:ILE:HG13	2.13	0.48
1:K:168:ALA:HB2	1:K:173:ILE:HD11	1.95	0.48
1:K:195:GLU:HB2	1:K:276:ARG:NH2	2.28	0.48
1:K:42:VAL:HG21	1:L:25:ASP:HB3	1.94	0.48
1:L:32:ASP:HB2	1:L:169:LYS:HZ3	1.78	0.48
1:A:49:VAL:CG1	1:A:83:ALA:HB2	2.44	0.48
1:G:224:GLU:OE1	1:G:226:ASP:HB3	2.13	0.48
1:I:75:PRO:CG	1:I:102:GLY:HA3	2.44	0.48
1:I:148:LEU:HD22	1:I:153:VAL:HG11	1.96	0.48
1:K:273:LEU:HD13	1:K:282:PRO:O	2.14	0.48
1:A:97:ILE:HD13	1:A:117:ILE:HB	1.96	0.48
1:A:135:VAL:O	1:A:139:ILE:HG13	2.12	0.48
1:D:118:LEU:O	1:D:183:ILE:N	2.44	0.48
1:I:277:LYS:HB2	1:I:280:GLU:HB2	1.95	0.48
1:J:236:SER:O	1:J:240:MET:HG3	2.14	0.48
1:B:74:ASN:OD1	1:B:77:ALA:N	2.47	0.48
1:C:111:GLU:C	1:C:113:GLY:H	2.17	0.48
1:C:147:VAL:HG13	1:C:148:LEU:H	1.78	0.48
1:E:14:LEU:HD13	1:E:73:PRO:HB3	1.96	0.48
1:E:57:LEU:O	1:E:61:GLU:HG2	2.14	0.48
1:F:196:ASN:HD21	1:F:198:TYR:HB2	1.78	0.48
1:E:278:PHE:CZ	1:F:231:VAL:HG12	2.49	0.48
1:H:126:GLY:HA3	1:H:234:VAL:HB	1.95	0.48
1:K:31:GLU:HG2	1:K:268:PRO:O	2.13	0.48
1:K:77:ALA:HB3	1:K:80:PRO:HD2	1.96	0.48
1:A:108:GLU:O	1:A:112:GLN:HG3	2.14	0.48
1:B:7:ILE:HG12	1:B:36:ARG:HB2	1.95	0.48
1:C:82:LYS:O	1:C:85:GLU:HB3	2.13	0.48
1:C:263:ARG:NH1	1:D:136:GLU:OE2	2.47	0.48
1:F:280:GLU:O	1:F:281:ASP:HB3	2.13	0.48
1:G:196:ASN:HD22	1:G:199:ALA:H	1.62	0.48
1:B:47:GLU:OE1	1:B:47:GLU:N	2.45	0.48
1:D:105:VAL:O	1:D:109:MET:HG3	2.14	0.48
1:G:135:VAL:O	1:G:139:ILE:HG13	2.14	0.48
1:I:275:LYS:HA	1:I:280:GLU:OE1	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:VAL:O	1:B:38:VAL:HA	2.14	0.47
1:C:66:ASP:O	1:C:93:PRO:HD2	2.14	0.47
1:E:66:ASP:OD1	1:E:168:ALA:HB1	2.13	0.47
1:E:264:THR:HA	1:E:273:LEU:O	2.13	0.47
1:E:31:GLU:HG2	1:E:268:PRO:O	2.14	0.47
1:E:7:ILE:HG12	1:E:36:ARG:HB2	1.96	0.47
1:I:126:GLY:H	1:I:238:HIS:CE1	2.32	0.47
1:L:16:THR:C	1:L:18:MET:N	2.67	0.47
1:L:53:VAL:HG11	1:L:86:MET:CB	2.44	0.47
1:F:51:ALA:O	1:F:55:MET:HG3	2.14	0.47
1:I:202:LYS:HE3	1:I:254:LEU:HD11	1.96	0.47
1:I:236:SER:O	1:I:240:MET:HG3	2.13	0.47
1:L:132:LEU:HD11	1:L:137:MET:CA	2.42	0.47
1:L:122:ASP:HA	1:L:144:LEU:HD11	1.96	0.47
1:F:120:LYS:N	1:F:121:PRO:HD2	2.30	0.47
1:F:19:MET:O	1:F:23:LEU:HG	2.14	0.47
1:I:252:ARG:HG2	3:I:8436:HOH:O	2.13	0.47
1:J:105:VAL:O	1:J:109:MET:HG3	2.14	0.47
1:J:110:GLU:CD	1:J:180:LYS:HE3	2.35	0.47
1:J:192:GLU:O	1:J:276:ARG:NH1	2.48	0.47
1:K:19:MET:HG3	1:K:154:PHE:CE1	2.50	0.47
1:A:42:VAL:HG21	1:B:25:ASP:O	2.14	0.47
1:E:273:LEU:HD13	1:E:282:PRO:O	2.15	0.47
1:G:197:PRO:O	1:G:201:VAL:HG23	2.15	0.47
1:J:128:ARG:HG2	1:J:234:VAL:HG11	1.97	0.47
1:K:264:THR:HA	1:K:273:LEU:O	2.13	0.47
1:C:148:LEU:HD22	1:C:153:VAL:HG11	1.95	0.47
1:I:82:LYS:HE3	1:I:86:MET:SD	2.55	0.47
1:A:192:GLU:O	1:A:276:ARG:NH1	2.47	0.47
1:C:4:ALA:O	1:C:33:VAL:HA	2.14	0.47
1:H:230:TYR:CD2	1:H:231:VAL:N	2.83	0.47
1:J:125:LEU:HB3	1:J:140:TYR:CE2	2.50	0.47
1:C:202:LYS:HE3	1:C:254:LEU:HD11	1.96	0.47
1:C:257:SER:HA	1:E:254:LEU:HD22	1.97	0.47
1:C:278:PHE:CZ	1:D:231:VAL:HG12	2.50	0.47
1:G:192:GLU:O	1:G:276:ARG:NH1	2.48	0.47
1:I:115:GLY:N	1:I:178:LEU:HD13	2.29	0.47
1:D:158:GLN:NE2	3:D:8511:HOH:O	2.44	0.47
1:I:124:MET:HE2	1:I:217:SER:CB	2.34	0.47
1:I:128:ARG:HD2	1:I:230:TYR:CE2	2.50	0.47
1:I:66:ASP:O	1:I:93:PRO:HD2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:63:PHE:O	1:K:64:GLU:HB2	2.15	0.47
1:A:10:LYS:HE2	1:A:17:SER:O	2.14	0.47
1:A:147:VAL:O	1:A:151:THR:HG23	2.15	0.47
1:L:51:ALA:O	1:L:54:GLU:HB2	2.14	0.47
1:C:115:GLY:N	1:C:178:LEU:HD13	2.30	0.47
1:D:196:ASN:ND2	1:D:198:TYR:N	2.63	0.47
1:D:49:VAL:CG1	1:D:83:ALA:HB2	2.45	0.47
1:I:268:PRO:HD3	1:J:129:ARG:CZ	2.45	0.47
1:L:273:LEU:HB3	1:L:282:PRO:HB2	1.97	0.47
1:B:97:ILE:HD13	1:B:117:ILE:HB	1.97	0.47
1:C:6:ALA:HB3	1:C:35:PHE:CD2	2.49	0.47
1:D:125:LEU:HD13	1:D:132:LEU:HD22	1.96	0.47
1:E:77:ALA:HB3	1:E:80:PRO:HD2	1.96	0.47
1:J:125:LEU:HD13	1:J:132:LEU:HD22	1.96	0.47
1:J:189:LEU:HD13	1:K:229:ARG:HB3	1.96	0.47
1:K:10:LYS:HD2	1:K:37:VAL:CG1	2.45	0.47
1:C:128:ARG:HD2	1:C:230:TYR:CE2	2.50	0.46
1:C:65:PRO:HD2	1:C:92:TYR:CE1	2.50	0.46
1:D:125:LEU:HB3	1:D:140:TYR:CE2	2.51	0.46
1:D:110:GLU:CD	1:D:180:LYS:HE3	2.35	0.46
1:G:84:ARG:HD2	1:G:109:MET:HG2	1.98	0.46
1:I:25:ASP:O	1:J:42:VAL:HG21	2.15	0.46
1:L:103:LEU:CD2	1:L:106:LYS:HD3	2.44	0.46
1:B:243:LYS:HG3	1:C:247:LEU:HG	1.96	0.46
1:C:120:LYS:N	1:C:121:PRO:HD2	2.31	0.46
1:G:242:ARG:HD2	3:G:8457:HOH:O	2.15	0.46
1:I:120:LYS:HZ3	1:I:184:ASP:HB3	1.80	0.46
1:L:24:LEU:HD11	1:L:161:PHE:HD1	1.78	0.46
1:D:49:VAL:O	1:D:53:VAL:HG23	2.15	0.46
1:E:19:MET:HG3	1:E:154:PHE:CE1	2.50	0.46
1:J:5:LYS:HB3	1:J:63:PHE:CE2	2.50	0.46
1:I:273:LEU:HB3	1:I:283:GLU:OXT	2.16	0.46
1:I:55:MET:O	1:I:59:ILE:HG23	2.14	0.46
1:K:128:ARG:NH1	1:K:225:GLN:NE2	2.64	0.46
1:L:116:TYR:N	1:L:179:PRO:HG2	2.31	0.46
1:C:40:THR:O	1:C:41:SER:HB3	2.16	0.46
1:D:167:LYS:HA	1:D:170:GLU:HG2	1.98	0.46
1:E:40:THR:HG22	1:F:36:ARG:NH2	2.30	0.46
1:G:66:ASP:HB3	1:G:168:ALA:HB1	1.98	0.46
1:H:7:ILE:HG12	1:H:36:ARG:HB2	1.98	0.46
1:J:79:GLY:O	1:J:82:LYS:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:135:VAL:O	1:L:139:ILE:HG12	2.16	0.46
1:L:47:GLU:O	1:L:50:GLU:HB3	2.16	0.46
1:B:161:PHE:O	1:B:165:ILE:HG13	2.15	0.46
1:B:49:VAL:CG1	1:B:83:ALA:HB2	2.45	0.46
1:C:165:ILE:O	1:C:169:LYS:HG3	2.16	0.46
1:E:100:ALA:N	1:E:101:PRO:CD	2.79	0.46
3:G:8076:HOH:O	1:H:25:ASP:HB3	2.16	0.46
1:H:49:VAL:CG1	1:H:83:ALA:HB2	2.46	0.46
1:I:40:THR:O	1:I:41:SER:HB3	2.15	0.46
1:K:129:ARG:HH12	1:L:268:PRO:CB	2.19	0.46
1:C:275:LYS:HA	1:C:280:GLU:OE1	2.15	0.46
1:I:243:LYS:HD3	1:I:243:LYS:HA	1.76	0.46
1:I:65:PRO:HD2	1:I:92:TYR:CE1	2.50	0.46
1:J:52:ALA:HA	1:J:55:MET:HE2	1.97	0.46
1:L:98:GLY:O	1:L:118:LEU:HA	2.16	0.46
1:L:68:ILE:O	1:L:94:ALA:HA	2.15	0.46
1:A:84:ARG:HD2	1:A:109:MET:HG2	1.98	0.46
1:G:10:LYS:HE2	1:G:17:SER:O	2.15	0.46
1:H:120:LYS:N	1:H:121:PRO:CD	2.79	0.46
1:I:120:LYS:N	1:I:121:PRO:HD2	2.30	0.46
1:B:32:ASP:OD1	1:B:270:GLY:HA3	2.16	0.46
1:D:147:VAL:O	1:D:151:THR:HG23	2.16	0.46
1:F:49:VAL:HG21	1:F:79:GLY:HA3	1.97	0.46
1:I:111:GLU:C	1:I:113:GLY:H	2.17	0.46
1:L:273:LEU:CB	1:L:282:PRO:HB2	2.45	0.46
1:A:125:LEU:HD13	1:A:132:LEU:HD22	1.97	0.46
1:B:272:VAL:HG23	3:B:8467:HOH:O	2.16	0.46
1:D:267:ALA:HB3	1:D:269:ASP:OD1	2.16	0.46
1:E:128:ARG:O	1:E:129:ARG:C	2.55	0.46
1:F:155:ARG:CZ	1:F:262:LEU:HG	2.46	0.46
1:F:277:LYS:HB2	1:F:280:GLU:HB2	1.98	0.46
1:H:161:PHE:O	1:H:165:ILE:HG13	2.16	0.46
1:K:7:ILE:HG12	1:K:36:ARG:HB2	1.98	0.46
1:L:161:PHE:O	1:L:165:ILE:HG13	2.16	0.46
1:D:128:ARG:HG2	1:D:234:VAL:HG11	1.98	0.45
1:E:63:PHE:O	1:E:64:GLU:HB2	2.16	0.45
1:F:111:GLU:C	1:F:113:GLY:N	2.70	0.45
1:G:128:ARG:HH12	1:G:225:GLN:NE2	2.15	0.45
1:G:234:VAL:O	1:G:237:ALA:HB3	2.16	0.45
1:G:37:VAL:O	1:H:38:VAL:HA	2.16	0.45
1:E:3:VAL:HG13	1:E:3:VAL:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:119:VAL:HG12	1:G:121:PRO:HD2	1.98	0.45
1:G:68:ILE:O	1:G:94:ALA:HA	2.16	0.45
1:I:125:LEU:HD12	1:I:125:LEU:C	2.37	0.45
1:L:170:GLU:C	1:L:172:GLU:H	2.19	0.45
1:C:171:ASP:C	1:C:172:GLU:HG3	2.36	0.45
1:C:253:GLU:OE1	1:C:256:LYS:HD2	2.16	0.45
1:D:66:ASP:HB3	3:D:8059:HOH:O	2.17	0.45
1:F:10:LYS:HG2	1:F:20:MET:HE2	1.97	0.45
1:G:191:ARG:HD3	3:G:8136:HOH:O	2.16	0.45
1:J:167:LYS:HA	1:J:170:GLU:HG2	1.98	0.45
1:K:196:ASN:HD21	1:K:254:LEU:HD13	1.81	0.45
1:B:201:VAL:HG12	1:C:239:GLU:HG3	1.98	0.45
1:C:236:SER:O	1:C:240:MET:HG3	2.16	0.45
1:C:49:VAL:HG21	1:C:79:GLY:C	2.36	0.45
1:C:25:ASP:O	1:D:42:VAL:HG21	2.16	0.45
1:I:165:ILE:O	1:I:169:LYS:HG3	2.17	0.45
1:I:49:VAL:HG21	1:I:79:GLY:C	2.37	0.45
1:J:196:ASN:HD22	1:J:199:ALA:N	2.11	0.45
1:B:230:TYR:CD2	1:B:231:VAL:N	2.85	0.45
1:D:192:GLU:O	1:D:276:ARG:NH1	2.49	0.45
1:E:162:ASP:OD1	1:E:266:HIS:NE2	2.49	0.45
1:G:196:ASN:ND2	1:G:198:TYR:H	2.15	0.45
1:K:3:VAL:O	1:K:3:VAL:HG13	2.16	0.45
1:L:57:LEU:HD22	1:L:90:SER:HB2	1.98	0.45
1:E:156:VAL:HG22	1:E:191:ARG:NH1	2.31	0.45
1:G:100:ALA:HB3	1:G:101:PRO:HD3	1.99	0.45
1:I:278:PHE:CZ	1:J:231:VAL:HG12	2.51	0.45
1:K:100:ALA:N	1:K:101:PRO:CD	2.79	0.45
1:K:49:VAL:O	1:K:53:VAL:HG23	2.17	0.45
1:B:49:VAL:HG11	1:B:79:GLY:O	2.16	0.45
1:E:118:LEU:HD12	1:E:182:VAL:HG22	1.98	0.45
1:I:191:ARG:HB3	1:I:191:ARG:HH11	1.81	0.45
1:H:201:VAL:HG12	1:I:239:GLU:HG3	1.97	0.45
1:I:259:ASP:O	1:I:277:LYS:HD3	2.17	0.45
1:J:118:LEU:HD12	1:J:182:VAL:HG22	1.99	0.45
1:J:215:ASP:HB2	3:K:8206:HOH:O	2.17	0.45
1:J:267:ALA:HB3	1:J:269:ASP:OD1	2.16	0.45
1:K:97:ILE:O	1:K:97:ILE:HG22	2.17	0.45
1:G:201:VAL:HG13	1:L:236:SER:N	2.31	0.45
1:K:156:VAL:HG22	1:K:191:ARG:NH1	2.31	0.45
1:L:185:ARG:HA	1:L:207:LEU:HD13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:13:ASN:HD21	1:E:141:ASN:ND2	2.15	0.45
1:E:5:LYS:HG2	1:E:34:GLU:HB3	1.98	0.45
1:I:257:SER:HA	1:K:254:LEU:HD22	1.97	0.45
1:J:7:ILE:HD12	1:J:65:PRO:HG3	1.98	0.45
1:A:61:GLU:HA	1:A:61:GLU:OE2	2.17	0.45
1:A:5:LYS:NZ	1:A:63:PHE:O	2.43	0.45
1:J:49:VAL:CG1	1:J:83:ALA:HB2	2.46	0.45
1:C:32:ASP:OD1	1:C:270:GLY:HA3	2.17	0.44
1:E:101:PRO:O	1:E:104:LYS:HE2	2.17	0.44
1:E:242:ARG:O	1:E:246:GLU:HG3	2.16	0.44
1:E:195:GLU:HB2	1:E:276:ARG:NH2	2.32	0.44
1:F:45:ASP:O	1:F:49:VAL:HG23	2.16	0.44
1:G:97:ILE:HD13	1:G:117:ILE:HB	1.99	0.44
1:K:243:LYS:HA	1:K:243:LYS:HD3	1.74	0.44
1:C:161:PHE:O	1:C:165:ILE:HG13	2.17	0.44
1:E:132:LEU:HD11	1:E:137:MET:HA	1.99	0.44
1:E:170:GLU:OE2	1:E:170:GLU:HA	2.17	0.44
1:E:224:GLU:OE1	1:E:229:ARG:HB2	2.16	0.44
1:A:201:VAL:HG13	1:F:236:SER:N	2.33	0.44
1:H:32:ASP:OD1	1:H:270:GLY:HA3	2.17	0.44
1:K:107:ASP:HB2	3:K:8364:HOH:O	2.16	0.44
1:L:36:ARG:HG2	1:L:36:ARG:HH21	1.82	0.44
1:A:68:ILE:O	1:A:94:ALA:HA	2.17	0.44
1:D:36:ARG:HG2	1:D:36:ARG:HH21	1.83	0.44
1:D:5:LYS:HB3	1:D:63:PHE:CE2	2.52	0.44
1:E:168:ALA:CB	1:E:173:ILE:HD11	2.47	0.44
1:F:172:GLU:HG2	1:F:172:GLU:O	2.17	0.44
1:I:144:LEU:HD12	1:I:147:VAL:CG1	2.48	0.44
1:I:54:GLU:HG3	1:I:86:MET:HE1	1.99	0.44
1:J:49:VAL:O	1:J:53:VAL:HG23	2.18	0.44
1:K:128:ARG:O	1:K:129:ARG:C	2.55	0.44
1:K:155:ARG:HH21	1:K:155:ARG:HG3	1.81	0.44
1:K:214:ALA:O	1:K:218:VAL:HG23	2.17	0.44
1:A:128:ARG:HH12	1:A:225:GLN:NE2	2.16	0.44
1:C:125:LEU:HD12	1:C:125:LEU:C	2.38	0.44
1:C:126:GLY:H	1:C:238:HIS:CE1	2.34	0.44
1:E:49:VAL:O	1:E:53:VAL:HG23	2.18	0.44
1:I:280:GLU:O	1:I:281:ASP:HB3	2.17	0.44
1:I:53:VAL:O	1:I:57:LEU:HG	2.17	0.44
1:K:14:LEU:HD13	1:K:73:PRO:HB3	2.00	0.44
1:L:93:PRO:HG2	1:L:173:ILE:CB	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:LEU:HD13	1:B:73:PRO:HG3	1.99	0.44
1:C:84:ARG:NH2	1:C:105:VAL:HB	2.33	0.44
1:E:25:ASP:O	1:F:42:VAL:HG11	2.17	0.44
1:E:10:LYS:HD2	1:E:37:VAL:CG1	2.48	0.44
1:I:105:VAL:O	1:I:109:MET:HG3	2.17	0.44
1:I:54:GLU:HG3	1:I:86:MET:CE	2.48	0.44
1:J:118:LEU:O	1:J:183:ILE:N	2.45	0.44
1:J:127:ALA:HA	1:J:132:LEU:HD22	1.99	0.44
1:L:24:LEU:O	1:L:25:ASP:HB2	2.17	0.44
1:A:196:ASN:HD22	1:A:199:ALA:H	1.64	0.44
1:B:120:LYS:N	1:B:121:PRO:CD	2.81	0.44
1:B:49:VAL:O	1:B:53:VAL:HG23	2.18	0.44
1:C:100:ALA:HB2	1:C:120:LYS:HA	1.99	0.44
1:F:99:ASP:CG	1:F:101:PRO:HD2	2.37	0.44
1:G:32:ASP:HB3	3:G:8090:HOH:O	2.17	0.44
1:H:230:TYR:HD2	1:H:231:VAL:N	2.16	0.44
1:I:253:GLU:OE1	1:I:256:LYS:HD2	2.17	0.44
1:A:66:ASP:HB3	1:A:168:ALA:HB1	1.99	0.44
1:C:280:GLU:O	1:C:281:ASP:HB3	2.18	0.44
1:E:218:VAL:HG13	1:E:222:PHE:HD2	1.83	0.44
1:I:9:ILE:HD12	1:I:87:LEU:HD11	2.00	0.44
1:I:43:LYS:NZ	1:J:30:ARG:O	2.41	0.44
1:K:111:GLU:C	1:K:113:GLY:N	2.70	0.44
1:K:191:ARG:NH2	3:K:8032:HOH:O	2.51	0.44
1:K:198:TYR:O	1:K:202:LYS:HG3	2.18	0.44
1:L:254:LEU:HD23	1:L:254:LEU:HA	1.82	0.44
1:B:196:ASN:ND2	1:B:198:TYR:H	2.16	0.44
1:C:186:ASN:HB2	3:C:8318:HOH:O	2.17	0.44
1:D:52:ALA:HA	1:D:55:MET:HE2	2.00	0.44
1:E:196:ASN:HD21	1:E:198:TYR:HB2	1.82	0.44
1:E:75:PRO:HD2	1:E:102:GLY:CA	2.48	0.44
1:G:61:GLU:OE2	1:G:61:GLU:HA	2.16	0.44
1:I:218:VAL:HG13	1:I:222:PHE:HD2	1.83	0.44
1:J:212:ASN:ND2	1:K:212:ASN:ND2	2.66	0.44
1:J:97:ILE:HD11	1:J:161:PHE:CZ	2.52	0.44
1:L:198:TYR:O	1:L:202:LYS:HG3	2.17	0.44
1:L:146:LYS:HE2	1:L:249:ASP:HB2	2.00	0.44
1:L:44:MET:CE	1:L:80:PRO:HG2	2.48	0.44
1:C:17:SER:HA	1:C:20:MET:SD	2.58	0.44
1:E:75:PRO:HD2	1:E:102:GLY:HA3	2.00	0.44
1:L:106:LYS:O	1:L:109:MET:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:129:ARG:NH2	1:L:129:ARG:HB2	2.33	0.44
1:L:12:GLY:HA2	1:L:42:VAL:O	2.17	0.44
1:L:180:LYS:HB3	1:L:180:LYS:HE2	1.84	0.44
1:L:79:GLY:O	1:L:82:LYS:HB3	2.17	0.44
1:C:105:VAL:O	1:C:109:MET:HG3	2.17	0.43
1:E:198:TYR:O	1:E:202:LYS:HG3	2.18	0.43
1:F:165:ILE:O	1:F:169:LYS:HG3	2.17	0.43
1:H:135:VAL:O	1:H:139:ILE:HG13	2.18	0.43
1:J:196:ASN:ND2	1:J:198:TYR:HB2	2.28	0.43
1:C:243:LYS:HA	1:C:243:LYS:HD3	1.78	0.43
1:C:9:ILE:HD12	1:C:87:LEU:HD11	1.99	0.43
1:D:7:ILE:HD12	1:D:65:PRO:HG3	2.00	0.43
1:E:116:TYR:N	1:E:179:PRO:O	2.46	0.43
1:E:92:TYR:HA	1:E:93:PRO:HD3	1.92	0.43
1:F:198:TYR:O	1:F:202:LYS:HG3	2.18	0.43
1:G:125:LEU:HD13	1:G:132:LEU:HD22	1.98	0.43
1:G:201:VAL:HG13	1:L:236:SER:CA	2.49	0.43
1:G:5:LYS:NZ	1:G:63:PHE:O	2.44	0.43
1:I:107:ASP:O	1:I:110:GLU:HG3	2.18	0.43
1:K:12:GLY:HA2	1:K:42:VAL:O	2.18	0.43
1:L:107:ASP:C	1:L:109:MET:N	2.70	0.43
1:L:97:ILE:HD11	1:L:161:PHE:CZ	2.51	0.43
1:E:111:GLU:C	1:E:113:GLY:N	2.71	0.43
1:E:118:LEU:O	1:E:183:ILE:N	2.49	0.43
1:J:205:ALA:O	1:J:209:ILE:HG13	2.18	0.43
1:L:76:ALA:CB	1:L:105:VAL:HG13	2.47	0.43
1:I:161:PHE:O	1:I:165:ILE:HG13	2.17	0.43
1:K:101:PRO:O	1:K:104:LYS:HE2	2.17	0.43
1:C:46:PRO:HA	1:C:79:GLY:HA2	2.01	0.43
1:G:45:ASP:O	1:G:49:VAL:HG23	2.18	0.43
1:I:100:ALA:HB2	1:I:120:LYS:HA	2.00	0.43
1:I:156:VAL:HG11	1:I:183:ILE:HD12	2.01	0.43
1:J:250:GLU:OE2	1:K:243:LYS:NZ	2.36	0.43
1:K:196:ASN:HD21	1:K:198:TYR:HB2	1.84	0.43
1:K:5:LYS:HB3	1:K:63:PHE:CE2	2.54	0.43
1:A:196:ASN:ND2	1:A:198:TYR:H	2.15	0.43
1:C:156:VAL:HG11	1:C:183:ILE:HD12	2.00	0.43
1:D:208:GLU:HG2	1:E:240:MET:SD	2.58	0.43
1:K:75:PRO:HD2	1:K:102:GLY:CA	2.48	0.43
1:K:5:LYS:HG2	1:K:34:GLU:HB3	2.00	0.43
1:L:103:LEU:HD23	1:L:103:LEU:HA	1.92	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:97:ILE:HD11	1:D:161:PHE:CZ	2.49	0.43
1:E:214:ALA:O	1:E:218:VAL:HG23	2.18	0.43
1:K:156:VAL:CG2	1:K:191:ARG:NH1	2.81	0.43
1:K:162:ASP:OD1	1:K:266:HIS:NE2	2.49	0.43
1:K:40:THR:HG22	1:L:36:ARG:NE	2.34	0.43
1:B:32:ASP:OD2	1:B:32:ASP:N	2.52	0.43
1:G:212:ASN:ND2	1:L:212:ASN:HD22	2.17	0.43
1:K:13:ASN:HD21	1:K:141:ASN:ND2	2.16	0.43
1:K:168:ALA:CB	1:K:173:ILE:HD11	2.49	0.43
1:K:170:GLU:HA	1:K:170:GLU:OE2	2.19	0.43
1:C:77:ALA:HB1	1:C:78:PRO:CD	2.49	0.43
1:D:49:VAL:HG12	1:D:83:ALA:HB2	2.01	0.43
1:G:128:ARG:HH12	1:G:225:GLN:HE22	1.67	0.43
1:H:214:ALA:O	1:H:218:VAL:HG23	2.19	0.43
1:H:229:ARG:C	1:H:232:PRO:HD2	2.39	0.43
1:I:100:ALA:N	1:I:101:PRO:CD	2.81	0.43
1:J:193:GLU:OE2	1:J:262:LEU:HD23	2.18	0.43
1:C:218:VAL:HG13	1:C:222:PHE:HD2	1.83	0.43
1:K:75:PRO:HD2	1:K:102:GLY:HA3	2.00	0.43
1:L:30:ARG:HH12	1:L:165:ILE:HD12	1.84	0.43
1:L:57:LEU:HD22	1:L:92:TYR:CD2	2.53	0.43
1:B:147:VAL:O	1:B:151:THR:HG23	2.19	0.42
1:B:214:ALA:O	1:B:218:VAL:HG23	2.18	0.42
1:C:107:ASP:O	1:C:110:GLU:HG3	2.18	0.42
1:C:97:ILE:HD11	1:C:161:PHE:CE1	2.54	0.42
1:C:17:SER:O	1:C:20:MET:HG2	2.19	0.42
1:D:127:ALA:HA	1:D:132:LEU:HD22	2.00	0.42
1:H:14:LEU:HD13	1:H:73:PRO:HG3	2.01	0.42
1:H:150:ALA:HB3	1:H:248:ALA:HB1	2.01	0.42
1:I:84:ARG:NH2	1:I:105:VAL:HB	2.34	0.42
1:I:6:ALA:HB3	1:I:35:PHE:HD2	1.83	0.42
1:J:208:GLU:HG2	1:K:240:MET:SD	2.58	0.42
1:L:146:LYS:HE3	1:L:249:ASP:HB2	2.01	0.42
1:C:53:VAL:O	1:C:57:LEU:HG	2.19	0.42
1:D:79:GLY:O	1:D:82:LYS:HB3	2.18	0.42
1:E:156:VAL:CG2	1:E:191:ARG:NH1	2.82	0.42
1:F:262:LEU:HB2	1:F:276:ARG:CZ	2.49	0.42
1:I:263:ARG:NH1	1:J:131:PHE:CE1	2.87	0.42
1:K:118:LEU:HD12	1:K:182:VAL:HG22	2.01	0.42
1:C:144:LEU:HA	1:C:147:VAL:CG1	2.48	0.42
1:D:262:LEU:HB2	1:D:276:ARG:CZ	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:155:ARG:HG3	1:E:155:ARG:HH21	1.83	0.42
1:E:128:ARG:NH1	1:E:225:GLN:NE2	2.67	0.42
1:E:243:LYS:HD3	1:E:243:LYS:HA	1.76	0.42
1:E:49:VAL:CG1	1:E:83:ALA:HB2	2.49	0.42
1:F:196:ASN:HB2	1:F:258:ASN:ND2	2.34	0.42
1:J:147:VAL:O	1:J:151:THR:HG23	2.19	0.42
1:C:111:GLU:C	1:C:113:GLY:N	2.73	0.42
1:D:97:ILE:CD1	1:D:161:PHE:HZ	2.29	0.42
1:F:101:PRO:O	1:F:104:LYS:HE2	2.19	0.42
1:J:156:VAL:HA	1:J:191:ARG:HH12	1.83	0.42
1:J:185:ARG:NE	1:J:208:GLU:OE2	2.53	0.42
1:K:229:ARG:O	1:K:233:ILE:HG13	2.19	0.42
1:E:198:TYR:HA	1:E:201:VAL:HG22	2.00	0.42
1:F:155:ARG:NH1	1:F:262:LEU:HG	2.34	0.42
1:G:147:VAL:O	1:G:151:THR:HG23	2.20	0.42
1:G:40:THR:HG23	1:G:52:ALA:HB2	2.01	0.42
1:I:111:GLU:C	1:I:113:GLY:N	2.73	0.42
1:I:46:PRO:HA	1:I:79:GLY:HA2	2.02	0.42
1:K:111:GLU:C	1:K:113:GLY:H	2.21	0.42
1:L:107:ASP:C	1:L:109:MET:H	2.22	0.42
1:C:273:LEU:HB3	1:C:283:GLU:OXT	2.20	0.42
1:D:3:VAL:O	1:D:3:VAL:HG13	2.20	0.42
1:I:144:LEU:HA	1:I:147:VAL:CG1	2.49	0.42
1:I:229:ARG:O	1:I:233:ILE:HG13	2.20	0.42
1:J:36:ARG:HH21	1:J:36:ARG:HG2	1.84	0.42
1:J:39:GLY:HA3	3:J:8187:HOH:O	2.19	0.42
1:C:196:ASN:ND2	1:C:198:TYR:HB2	2.34	0.42
1:C:70:TYR:HB3	1:C:96:ILE:HD13	2.02	0.42
1:E:36:ARG:HH21	1:E:36:ARG:HG2	1.84	0.42
1:F:95:VAL:HA	1:F:115:GLY:O	2.20	0.42
1:I:49:VAL:O	1:I:53:VAL:HG23	2.20	0.42
1:I:77:ALA:HB1	1:I:78:PRO:CD	2.49	0.42
1:K:198:TYR:HA	1:K:201:VAL:HG22	2.01	0.42
1:K:224:GLU:OE1	1:K:229:ARG:HB2	2.19	0.42
1:L:130:GLU:CD	1:L:130:GLU:N	2.65	0.42
1:L:133:ASP:HB2	1:L:134:PRO:CD	2.50	0.42
1:A:191:ARG:HB3	1:A:191:ARG:NH1	2.34	0.42
1:A:40:THR:HG23	1:A:52:ALA:HB2	2.01	0.42
1:B:196:ASN:ND2	1:B:198:TYR:N	2.67	0.42
1:C:229:ARG:O	1:C:233:ILE:HG13	2.19	0.42
1:C:54:GLU:O	1:C:58:ASP:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:8:PHE:CD1	1:C:21:ASP:HB3	2.55	0.42
1:F:166:GLU:O	1:F:170:GLU:HG2	2.20	0.42
1:F:44:MET:O	1:F:79:GLY:HA3	2.20	0.42
1:G:243:LYS:HG3	1:L:247:LEU:HG	2.01	0.42
1:I:32:ASP:OD1	1:I:270:GLY:HA3	2.20	0.42
1:K:195:GLU:HB2	1:K:276:ARG:CZ	2.50	0.42
1:K:218:VAL:HG13	1:K:222:PHE:HD2	1.84	0.42
1:L:116:TYR:O	1:L:116:TYR:CD2	2.66	0.42
1:A:197:PRO:O	1:A:201:VAL:HG23	2.20	0.42
1:C:100:ALA:N	1:C:101:PRO:CD	2.83	0.42
1:F:271:LYS:HB3	1:F:271:LYS:NZ	2.34	0.42
1:I:54:GLU:O	1:I:58:ASP:HB3	2.20	0.42
1:K:100:ALA:C	1:K:102:GLY:H	2.23	0.42
1:K:132:LEU:HD11	1:K:137:MET:HA	2.01	0.42
1:K:42:VAL:CG2	1:L:25:ASP:HB3	2.50	0.42
1:K:40:THR:HG22	1:L:36:ARG:CZ	2.50	0.42
1:B:229:ARG:C	1:B:232:PRO:HD2	2.40	0.42
1:B:237:ALA:O	1:B:240:MET:HB2	2.20	0.42
1:C:259:ASP:O	1:C:277:LYS:HD3	2.20	0.42
1:K:55:MET:SD	1:L:59:ILE:HD12	2.59	0.42
1:L:124:MET:CE	1:L:218:VAL:HA	2.50	0.42
1:L:128:ARG:NH1	1:L:221:CYS:O	2.53	0.42
1:L:28:ALA:N	3:L:8335:HOH:O	2.53	0.42
1:B:230:TYR:HD2	1:B:231:VAL:N	2.18	0.41
1:C:252:ARG:HG3	1:C:256:LYS:HE3	2.02	0.41
1:C:273:LEU:HD22	1:C:283:GLU:OXT	2.20	0.41
1:E:95:VAL:HA	1:E:115:GLY:O	2.20	0.41
1:I:77:ALA:HB1	1:I:78:PRO:HD2	2.03	0.41
1:L:66:ASP:OD2	1:L:66:ASP:N	2.53	0.41
1:D:100:ALA:CB	1:D:120:LYS:HD2	2.50	0.41
1:D:156:VAL:HA	1:D:191:ARG:HH12	1.85	0.41
1:E:100:ALA:C	1:E:102:GLY:H	2.23	0.41
1:D:212:ASN:ND2	1:E:212:ASN:ND2	2.68	0.41
1:F:216:VAL:CG1	1:F:237:ALA:HB2	2.50	0.41
1:G:205:ALA:O	1:G:209:ILE:HG13	2.20	0.41
1:I:17:SER:O	1:I:20:MET:HG2	2.20	0.41
1:I:97:ILE:HD11	1:I:161:PHE:CE1	2.55	0.41
1:J:14:LEU:HD12	1:J:14:LEU:HA	1.91	0.41
1:J:156:VAL:HA	1:J:191:ARG:NH1	2.35	0.41
1:J:3:VAL:HG13	1:J:3:VAL:O	2.19	0.41
1:K:120:LYS:HE2	1:K:211:GLU:OE1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:66:ASP:HB3	1:K:168:ALA:HB1	2.02	0.41
1:L:262:LEU:HB2	1:L:276:ARG:CZ	2.50	0.41
1:L:269:ASP:CG	1:L:270:GLY:H	2.24	0.41
1:A:119:VAL:HG12	1:A:121:PRO:HD2	2.02	0.41
1:D:5:LYS:HB2	1:D:5:LYS:HE3	1.91	0.41
1:E:12:GLY:HA2	1:E:42:VAL:O	2.20	0.41
1:E:167:LYS:HA	1:E:167:LYS:HD3	1.88	0.41
1:E:17:SER:O	1:E:20:MET:HG2	2.20	0.41
1:E:196:ASN:ND2	1:E:199:ALA:N	2.64	0.41
1:I:119:VAL:CG1	1:I:122:ASP:HB2	2.50	0.41
1:J:262:LEU:HB2	1:J:276:ARG:CZ	2.50	0.41
1:K:95:VAL:HA	1:K:115:GLY:O	2.20	0.41
1:E:229:ARG:O	1:E:233:ILE:HG13	2.19	0.41
1:J:24:LEU:O	1:J:30:ARG:HD3	2.20	0.41
1:J:49:VAL:HG12	1:J:83:ALA:HB2	2.03	0.41
1:K:28:ALA:HB2	1:L:42:VAL:HB	2.02	0.41
1:K:40:THR:HG22	1:L:36:ARG:CD	2.50	0.41
1:L:125:LEU:H	1:L:125:LEU:HG	1.66	0.41
1:L:31:GLU:C	1:L:33:VAL:H	2.23	0.41
1:A:128:ARG:HH12	1:A:225:GLN:HE22	1.69	0.41
1:E:120:LYS:HB2	1:E:121:PRO:CD	2.50	0.41
1:F:116:TYR:N	1:F:179:PRO:O	2.48	0.41
1:J:54:GLU:O	1:J:58:ASP:CB	2.67	0.41
1:I:55:MET:HG3	1:J:59:ILE:HD13	2.02	0.41
1:J:46:PRO:CA	1:J:79:GLY:HA2	2.50	0.41
1:K:49:VAL:CG1	1:K:83:ALA:HB2	2.50	0.41
1:L:75:PRO:HD3	1:L:98:GLY:HA3	2.01	0.41
1:C:54:GLU:HG3	1:C:86:MET:CE	2.51	0.41
1:E:152:GLY:O	1:E:156:VAL:HG23	2.20	0.41
1:H:147:VAL:O	1:H:151:THR:HG23	2.21	0.41
1:H:240:MET:SD	1:I:208:GLU:HG2	2.61	0.41
1:I:132:LEU:HD11	1:I:137:MET:HA	2.02	0.41
1:I:196:ASN:ND2	1:I:198:TYR:H	2.18	0.41
1:H:250:GLU:CD	1:I:243:LYS:HZ1	2.23	0.41
1:I:252:ARG:HG3	1:I:256:LYS:HE3	2.03	0.41
1:I:75:PRO:HG2	1:I:102:GLY:CA	2.48	0.41
1:J:100:ALA:N	1:J:101:PRO:CD	2.83	0.41
1:K:278:PHE:CZ	1:L:231:VAL:HG12	2.56	0.41
1:A:162:ASP:CG	1:A:266:HIS:HE2	2.22	0.41
1:C:144:LEU:CA	1:C:147:VAL:HG12	2.50	0.41
1:D:118:LEU:HD12	1:D:182:VAL:HG22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:9:ILE:HA	1:E:38:VAL:O	2.21	0.41
1:E:49:VAL:HG12	1:E:83:ALA:HB2	2.02	0.41
1:E:97:ILE:O	1:E:97:ILE:HG22	2.19	0.41
1:F:122:ASP:HA	1:F:144:LEU:HD11	2.03	0.41
1:F:30:ARG:NE	1:F:270:GLY:HA2	2.35	0.41
1:J:97:ILE:CD1	1:J:161:PHE:HZ	2.31	0.41
1:J:45:ASP:OD2	1:J:47:GLU:HB2	2.20	0.41
1:K:36:ARG:HH21	1:K:36:ARG:HG2	1.84	0.41
1:A:50:GLU:O	1:A:54:GLU:HB2	2.21	0.41
1:A:99:ASP:CG	1:A:101:PRO:HD2	2.41	0.41
1:C:75:PRO:HG2	1:C:102:GLY:CA	2.47	0.41
1:D:30:ARG:HB3	1:D:33:VAL:HG22	2.03	0.41
1:D:54:GLU:O	1:D:58:ASP:CB	2.67	0.41
1:F:75:PRO:HG2	1:F:102:GLY:HA3	2.02	0.41
1:H:237:ALA:O	1:H:240:MET:HB2	2.21	0.41
1:I:196:ASN:ND2	1:I:198:TYR:HB2	2.34	0.41
1:J:170:GLU:O	1:J:172:GLU:HG3	2.20	0.41
1:K:118:LEU:O	1:K:183:ILE:N	2.49	0.41
1:L:182:VAL:O	1:L:183:ILE:HD13	2.20	0.41
1:K:278:PHE:CE1	1:L:231:VAL:HG12	2.56	0.41
1:L:49:VAL:O	1:L:52:ALA:HB3	2.20	0.41
1:E:111:GLU:C	1:E:113:GLY:H	2.23	0.41
1:H:174:SER:O	1:H:177:ASP:HB2	2.21	0.41
1:J:7:ILE:CD1	1:J:65:PRO:HG3	2.51	0.41
1:K:9:ILE:HA	1:K:38:VAL:O	2.20	0.41
1:L:165:ILE:O	1:L:169:LYS:N	2.49	0.41
1:L:120:LYS:HB2	1:L:184:ASP:HB3	2.03	0.41
1:L:185:ARG:HA	1:L:207:LEU:CD1	2.51	0.41
1:L:82:LYS:O	1:L:85:GLU:HB3	2.20	0.41
1:K:17:SER:O	1:K:20:MET:HG2	2.20	0.41
1:K:99:ASP:OD2	1:K:99:ASP:N	2.53	0.41
1:K:55:MET:CE	1:L:36:ARG:HD2	2.51	0.41
1:B:100:ALA:HB3	1:B:101:PRO:HD3	2.02	0.41
1:D:100:ALA:N	1:D:101:PRO:CD	2.84	0.41
1:F:280:GLU:O	1:F:281:ASP:CB	2.68	0.41
1:G:191:ARG:NH1	1:G:191:ARG:HB3	2.36	0.41
1:G:201:VAL:HG12	1:L:239:GLU:HG3	2.01	0.41
1:G:32:ASP:OD1	1:G:169:LYS:NZ	2.44	0.41
1:H:159:GLU:OE2	1:H:191:ARG:NH2	2.51	0.41
1:I:70:TYR:HB3	1:I:96:ILE:HD13	2.02	0.41
1:J:5:LYS:HE3	1:J:5:LYS:HB2	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:152:GLY:O	1:K:156:VAL:HG23	2.20	0.41
1:L:155:ARG:NH2	1:L:264:THR:HG23	2.36	0.41
1:C:191:ARG:HH11	1:C:191:ARG:HB3	1.86	0.40
1:F:32:ASP:OD1	1:F:269:ASP:O	2.39	0.40
1:F:84:ARG:O	1:F:88:ALA:HB2	2.21	0.40
1:G:75:PRO:HD2	1:G:102:GLY:CA	2.51	0.40
1:G:188:LEU:HD21	1:G:207:LEU:HD11	2.03	0.40
1:H:196:ASN:ND2	1:H:198:TYR:N	2.69	0.40
1:J:100:ALA:CB	1:J:120:LYS:HD2	2.51	0.40
1:A:234:VAL:O	1:A:237:ALA:HB3	2.22	0.40
1:C:119:VAL:CG1	1:C:122:ASP:HB2	2.52	0.40
1:H:196:ASN:ND2	1:H:198:TYR:H	2.18	0.40
1:K:84:ARG:HD2	1:K:112:GLN:OE1	2.21	0.40
1:L:231:VAL:N	1:L:232:PRO:CD	2.84	0.40
1:D:185:ARG:NE	1:D:208:GLU:OE2	2.53	0.40
1:F:120:LYS:HB2	1:F:121:PRO:HD3	2.02	0.40
1:I:17:SER:HA	1:I:20:MET:SD	2.61	0.40
1:K:120:LYS:HB2	1:K:121:PRO:CD	2.51	0.40
1:L:158:GLN:C	1:L:160:ALA:N	2.74	0.40
1:K:129:ARG:NH1	1:L:268:PRO:HD3	2.36	0.40
1:C:144:LEU:HD12	1:C:147:VAL:CG1	2.51	0.40
1:C:214:ALA:O	1:C:218:VAL:HG23	2.22	0.40
1:D:247:LEU:HG	1:E:243:LYS:HG3	2.02	0.40
1:D:24:LEU:O	1:D:30:ARG:HD3	2.22	0.40
1:F:252:ARG:HD2	3:F:8214:HOH:O	2.22	0.40
1:G:189:LEU:HD13	1:L:229:ARG:HB3	2.04	0.40
1:G:191:ARG:HH11	1:G:191:ARG:HB3	1.86	0.40
1:K:49:VAL:HG12	1:K:83:ALA:HB2	2.03	0.40
1:L:230:TYR:O	1:L:234:VAL:HG22	2.21	0.40
1:B:135:VAL:O	1:B:139:ILE:HG13	2.20	0.40
1:C:162:ASP:OD1	1:C:266:HIS:NE2	2.55	0.40
1:C:67:PHE:HA	1:C:93:PRO:O	2.22	0.40
1:E:5:LYS:HB3	1:E:63:PHE:CE2	2.56	0.40
1:F:144:LEU:HA	1:F:147:VAL:HG12	2.03	0.40
1:F:267:ALA:HB1	1:F:268:PRO:HD2	2.03	0.40
1:F:66:ASP:O	1:F:93:PRO:HD2	2.22	0.40
1:I:67:PHE:HA	1:I:93:PRO:O	2.21	0.40
1:K:5:LYS:HD2	1:K:63:PHE:CE1	2.56	0.40
1:L:152:GLY:HA3	1:L:193:GLU:OE2	2.20	0.40
1:L:256:LYS:O	1:L:259:ASP:N	2.41	0.40
1:L:2:THR:OG1	1:L:3:VAL:N	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	280/283 (99%)	262 (94%)	17 (6%)	1 (0%)	38	54
1	B	280/283 (99%)	266 (95%)	14 (5%)	0	100	100
1	C	280/283 (99%)	251 (90%)	26 (9%)	3 (1%)	17	23
1	D	280/283 (99%)	266 (95%)	12 (4%)	2 (1%)	25	37
1	E	280/283 (99%)	254 (91%)	21 (8%)	5 (2%)	10	12
1	F	280/283 (99%)	250 (89%)	27 (10%)	3 (1%)	17	23
1	G	280/283 (99%)	261 (93%)	18 (6%)	1 (0%)	38	54
1	H	280/283 (99%)	266 (95%)	14 (5%)	0	100	100
1	I	280/283 (99%)	251 (90%)	25 (9%)	4 (1%)	13	18
1	J	280/283 (99%)	265 (95%)	13 (5%)	2 (1%)	25	37
1	K	280/283 (99%)	254 (91%)	21 (8%)	5 (2%)	10	12
1	L	280/283 (99%)	226 (81%)	43 (15%)	11 (4%)	3	3
All	All	3360/3396 (99%)	3072 (91%)	251 (8%)	37 (1%)	17	23

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	129	ARG
1	K	129	ARG
1	L	25	ASP
1	E	41	SER
1	K	41	SER
1	L	32	ASP
1	L	41	SER
1	K	20	MET
1	L	17	SER

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Mol	Chain	Res	Type
1	L	78	PRO
1	L	270	GLY
1	C	41	SER
1	C	86	MET
1	C	281	ASP
1	E	20	MET
1	F	281	ASP
1	I	41	SER
1	I	86	MET
1	I	281	ASP
1	L	185	ARG
1	L	281	ASP
1	D	41	SER
1	E	74	ASN
1	E	223	VAL
1	F	112	GLN
1	J	41	SER
1	K	74	ASN
1	K	223	VAL
1	L	47	GLU
1	L	129	ARG
1	D	74	ASN
1	J	74	ASN
1	F	74	ASN
1	G	74	ASN
1	A	74	ASN
1	L	133	ASP
1	I	126	GLY

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	233/234 (100%)	227 (97%)	6 (3%)	51	72
1	B	233/234 (100%)	231 (99%)	2 (1%)	82	92
1	C	233/234 (100%)	225 (97%)	8 (3%)	42	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	233/234 (100%)	228 (98%)	5 (2%)	59	78
1	E	233/234 (100%)	226 (97%)	7 (3%)	46	67
1	F	233/234 (100%)	228 (98%)	5 (2%)	59	78
1	G	233/234 (100%)	227 (97%)	6 (3%)	51	72
1	H	233/234 (100%)	231 (99%)	2 (1%)	82	92
1	I	233/234 (100%)	225 (97%)	8 (3%)	42	63
1	J	233/234 (100%)	227 (97%)	6 (3%)	51	72
1	K	233/234 (100%)	225 (97%)	8 (3%)	42	63
1	L	233/234 (100%)	219 (94%)	14 (6%)	22	35
All	All	2796/2808 (100%)	2719 (97%)	77 (3%)	49	70

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	47	GLU
1	A	58	ASP
1	A	125	LEU
1	A	225	GLN
1	A	227	LYS
1	B	125	LEU
1	B	230	TYR
1	C	45	ASP
1	C	58	ASP
1	C	114	LEU
1	C	146	LYS
1	C	163	GLU
1	C	176	ASN
1	C	191	ARG
1	C	196	ASN
1	D	34	GLU
1	D	45	ASP
1	D	89	ASP
1	D	125	LEU
1	D	281	ASP
1	E	58	ASP
1	E	84	ARG
1	E	89	ASP
1	E	125	LEU

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Mol	Chain	Res	Type
1	E	158	GLN
1	E	230	TYR
1	E	281	ASP
1	F	114	LEU
1	F	125	LEU
1	F	192	GLU
1	F	215	ASP
1	F	230	TYR
1	G	2	THR
1	G	47	GLU
1	G	58	ASP
1	G	125	LEU
1	G	225	GLN
1	G	227	LYS
1	H	125	LEU
1	H	230	TYR
1	I	45	ASP
1	I	58	ASP
1	I	114	LEU
1	I	146	LYS
1	I	163	GLU
1	I	176	ASN
1	I	191	ARG
1	I	196	ASN
1	J	2	THR
1	J	34	GLU
1	J	45	ASP
1	J	89	ASP
1	J	125	LEU
1	J	281	ASP
1	K	58	ASP
1	K	84	ARG
1	K	89	ASP
1	K	125	LEU
1	K	158	GLN
1	K	230	TYR
1	K	247	LEU
1	K	281	ASP
1	L	19	MET
1	L	45	ASP
1	L	91	GLU
1	L	114	LEU

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Mol	Chain	Res	Type
1	L	116	TYR
1	L	125	LEU
1	L	130	GLU
1	L	147	VAL
1	L	192	GLU
1	L	215	ASP
1	L	230	TYR
1	L	247	LEU
1	L	257	SER
1	L	279	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (57) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	GLN
1	A	196	ASN
1	A	225	GLN
1	A	238	HIS
1	A	258	ASN
1	B	141	ASN
1	B	196	ASN
1	B	225	GLN
1	B	238	HIS
1	B	258	ASN
1	C	141	ASN
1	C	196	ASN
1	C	212	ASN
1	C	238	HIS
1	C	258	ASN
1	D	196	ASN
1	D	212	ASN
1	D	238	HIS
1	D	258	ASN
1	E	141	ASN
1	E	158	GLN
1	E	196	ASN
1	E	212	ASN
1	E	225	GLN
1	E	238	HIS
1	F	196	ASN
1	F	238	HIS
1	F	258	ASN

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Mol	Chain	Res	Type
1	G	158	GLN
1	G	196	ASN
1	G	225	GLN
1	G	238	HIS
1	G	258	ASN
1	H	141	ASN
1	H	196	ASN
1	H	225	GLN
1	H	238	HIS
1	H	258	ASN
1	I	141	ASN
1	I	196	ASN
1	I	212	ASN
1	I	238	HIS
1	I	258	ASN
1	J	196	ASN
1	J	212	ASN
1	J	238	HIS
1	J	258	ASN
1	K	141	ASN
1	K	158	GLN
1	K	196	ASN
1	K	212	ASN
1	K	225	GLN
1	K	238	HIS
1	L	196	ASN
1	L	212	ASN
1	L	238	HIS
1	L	266	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 carbohydrates in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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	282/283 (99%)	-0.13	1 (0%) 92 91	14, 31, 49, 61	0
1	B	282/283 (99%)	-0.13	3 (1%) 80 79	11, 27, 45, 60	0
1	C	282/283 (99%)	0.69	32 (11%) 6 5	19, 49, 80, 92	0
1	D	282/283 (99%)	0.66	23 (8%) 12 11	20, 45, 66, 77	0
1	E	282/283 (99%)	0.49	18 (6%) 20 18	21, 50, 74, 87	0
1	F	282/283 (99%)	0.91	56 (19%) 1 1	16, 50, 88, 92	0
1	G	282/283 (99%)	0.14	1 (0%) 92 91	17, 30, 47, 59	0
1	H	282/283 (99%)	0.39	8 (2%) 53 51	13, 28, 45, 63	0
1	I	282/283 (99%)	0.95	50 (17%) 2 1	22, 51, 75, 92	0
1	J	282/283 (99%)	0.52	16 (5%) 24 23	23, 47, 69, 83	0
1	K	282/283 (99%)	1.24	64 (22%) 1 1	26, 53, 79, 84	0
1	L	282/283 (99%)	1.53	84 (29%) 1 1	24, 52, 84, 92	0
All	All	3384/3396 (99%)	0.61	356 (10%) 7 6	11, 40, 76, 92	0

All (356) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	57	LEU	11.5
1	K	173	ILE	9.4
1	L	2	THR	8.0
1	L	172	GLU	7.9
1	L	53	VAL	6.9
1	L	178	LEU	6.9
1	C	171	ASP	6.2
1	F	172	GLU	6.1
1	I	115	GLY	6.0
1	F	2	THR	5.9
1	D	60	ALA	5.9

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Mol	Chain	Res	Type	RSRZ
1	K	171	ASP	5.8
1	F	168	ALA	5.8
1	I	2	THR	5.7
1	F	171	ASP	5.3
1	K	63	PHE	5.3
1	L	88	ALA	5.3
1	L	180	LYS	5.1
1	L	176	ASN	5.1
1	L	56	ALA	5.0
1	L	171	ASP	5.0
1	C	2	THR	4.9
1	F	63	PHE	4.9
1	J	85	GLU	4.8
1	K	48	CYS	4.8
1	L	113	GLY	4.7
1	L	3	VAL	4.6
1	I	271	LYS	4.5
1	I	91	GLU	4.5
1	F	3	VAL	4.5
1	E	171	ASP	4.5
1	F	61	GLU	4.5
1	D	172	GLU	4.4
1	L	167	LYS	4.4
1	K	40	THR	4.3
1	C	61	GLU	4.3
1	K	70	TYR	4.3
1	I	3	VAL	4.3
1	L	170	GLU	4.3
1	F	58	ASP	4.3
1	E	173	ILE	4.2
1	F	114	LEU	4.2
1	F	112	GLN	4.2
1	K	89	ASP	4.2
1	L	114	LEU	4.2
1	D	171	ASP	4.1
1	I	171	ASP	4.1
1	L	63	PHE	4.1
1	I	172	GLU	4.1
1	D	85	GLU	4.1
1	K	91	GLU	4.1
1	L	268	PRO	4.1
1	L	61	GLU	4.0

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Mol	Chain	Res	Type	RSRZ
1	L	31	GLU	4.0
1	L	166	GLU	4.0
1	I	94	ALA	4.0
1	L	76	ALA	4.0
1	F	62	ASP	3.9
1	J	171	ASP	3.9
1	K	54	GLU	3.9
1	I	176	ASN	3.9
1	F	170	GLU	3.9
1	K	85	GLU	3.9
1	F	165	ILE	3.8
1	D	61	GLU	3.8
1	L	46	PRO	3.8
1	I	87	LEU	3.8
1	I	114	LEU	3.8
1	D	54	GLU	3.8
1	I	113	GLY	3.8
1	C	173	ILE	3.8
1	K	3	VAL	3.8
1	L	62	ASP	3.7
1	H	2	THR	3.7
1	K	52	ALA	3.7
1	L	111	GLU	3.7
1	D	91	GLU	3.7
1	J	61	GLU	3.6
1	L	34	GLU	3.6
1	C	62	ASP	3.6
1	K	174	SER	3.6
1	L	64	GLU	3.6
1	K	2	THR	3.6
1	I	31	GLU	3.6
1	C	172	GLU	3.6
1	L	89	ASP	3.6
1	E	57	LEU	3.6
1	I	96	ILE	3.5
1	L	177	ASP	3.5
1	F	267	ALA	3.5
1	I	272	VAL	3.5
1	L	75	PRO	3.5
1	L	68	ILE	3.5
1	E	3	VAL	3.5
1	F	69	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	I	163	GLU	3.5
1	L	32	ASP	3.5
1	I	93	PRO	3.5
1	I	170	GLU	3.4
1	L	85	GLU	3.4
1	F	40	THR	3.4
1	L	94	ALA	3.4
1	K	86	MET	3.4
1	L	11	CYS	3.4
1	I	92	TYR	3.4
1	F	107	ASP	3.4
1	I	173	ILE	3.4
1	H	172	GLU	3.4
1	L	30	ARG	3.4
1	C	31	GLU	3.3
1	F	47	GLU	3.3
1	J	172	GLU	3.3
1	K	56	ALA	3.3
1	E	85	GLU	3.2
1	K	58	ASP	3.2
1	K	62	ASP	3.2
1	K	96	ILE	3.2
1	L	60	ALA	3.2
1	C	91	GLU	3.2
1	F	89	ASP	3.2
1	E	54	GLU	3.2
1	D	2	THR	3.2
1	K	111	GLU	3.2
1	K	80	PRO	3.2
1	L	169	LYS	3.1
1	D	267	ALA	3.1
1	F	34	GLU	3.1
1	I	282	PRO	3.1
1	D	62	ASP	3.1
1	J	62	ASP	3.1
1	E	48	CYS	3.1
1	K	93	PRO	3.1
1	F	65	PRO	3.0
1	C	272	VAL	3.0
1	F	173	ILE	3.0
1	L	74	ASN	3.0
1	K	78	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	E	89	ASP	3.0
1	I	177	ASP	3.0
1	K	90	SER	3.0
1	K	53	VAL	3.0
1	F	283	GLU	3.0
1	K	92	TYR	3.0
1	K	46	PRO	3.0
1	L	44	MET	3.0
1	F	169	LYS	3.0
1	J	91	GLU	2.9
1	K	67	PHE	2.9
1	C	174	SER	2.9
1	J	95	VAL	2.9
1	L	173	ILE	2.9
1	E	91	GLU	2.9
1	K	175	GLU	2.9
1	K	42	VAL	2.9
1	K	13	ASN	2.9
1	C	175	GLU	2.9
1	F	55	MET	2.8
1	F	116	TYR	2.8
1	I	103	LEU	2.8
1	L	189	LEU	2.8
1	C	95	VAL	2.8
1	F	95	VAL	2.8
1	D	170	GLU	2.8
1	J	54	GLU	2.8
1	L	107	ASP	2.8
1	C	87	LEU	2.8
1	L	12	GLY	2.8
1	L	163	GLU	2.8
1	K	87	LEU	2.8
1	K	7	ILE	2.7
1	I	111	GLU	2.7
1	I	68	ILE	2.7
1	C	89	ASP	2.7
1	C	176	ASN	2.7
1	I	4	ALA	2.7
1	F	178	LEU	2.7
1	I	67	PHE	2.7
1	F	88	ALA	2.7
1	L	106	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	F	167	LYS	2.7
1	C	42	VAL	2.7
1	K	104	LYS	2.7
1	F	64	GLU	2.7
1	L	84	ARG	2.7
1	L	5	LYS	2.7
1	H	283	GLU	2.6
1	I	61	GLU	2.6
1	K	34	GLU	2.6
1	L	58	ASP	2.6
1	I	267	ALA	2.6
1	E	96	ILE	2.6
1	F	113	GLY	2.6
1	H	64	GLU	2.6
1	K	49	VAL	2.6
1	K	113	GLY	2.6
1	L	4	ALA	2.6
1	I	178	LEU	2.6
1	K	167	LYS	2.6
1	L	67	PHE	2.6
1	F	175	GLU	2.6
1	D	167	LYS	2.6
1	D	95	VAL	2.6
1	F	96	ILE	2.6
1	F	31	GLU	2.6
1	G	170	GLU	2.6
1	D	92	TYR	2.6
1	I	62	ASP	2.6
1	L	52	ALA	2.6
1	I	110	GLU	2.6
1	J	50	GLU	2.6
1	K	64	GLU	2.6
1	K	35	PHE	2.5
1	C	79	GLY	2.5
1	E	104	LYS	2.5
1	H	28	ALA	2.5
1	I	169	LYS	2.5
1	K	105	VAL	2.5
1	L	49	VAL	2.5
1	K	179	PRO	2.5
1	K	84	ARG	2.5
1	L	272	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	170	GLU	2.5
1	K	177	ASP	2.5
1	L	69	VAL	2.5
1	L	162	ASP	2.5
1	I	79	GLY	2.5
1	I	63	PHE	2.5
1	L	112	GLN	2.5
1	K	77	ALA	2.5
1	L	70	TYR	2.5
1	F	68	ILE	2.5
1	L	117	ILE	2.5
1	A	171	ASP	2.5
1	L	282	PRO	2.5
1	B	170	GLU	2.5
1	I	89	ASP	2.5
1	C	168	ALA	2.5
1	F	110	GLU	2.5
1	L	283	GLU	2.5
1	C	3	VAL	2.4
1	B	172	GLU	2.4
1	I	85	GLU	2.4
1	F	30	ARG	2.4
1	K	129	ARG	2.4
1	L	267	ALA	2.4
1	I	95	VAL	2.4
1	J	69	VAL	2.4
1	F	85	GLU	2.4
1	C	111	GLU	2.4
1	J	47	GLU	2.4
1	F	111	GLU	2.4
1	L	87	LEU	2.4
1	C	67	PHE	2.4
1	I	283	GLU	2.4
1	D	88	ALA	2.4
1	I	273	LEU	2.4
1	F	78	PRO	2.4
1	I	221	CYS	2.4
1	F	180	LYS	2.4
1	L	97	ILE	2.4
1	H	171	ASP	2.4
1	D	76	ALA	2.4
1	F	49	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	97	ILE	2.3
1	I	109	MET	2.3
1	K	190	GLU	2.3
1	B	192	GLU	2.3
1	K	6	ALA	2.3
1	I	58	ASP	2.3
1	L	54	GLU	2.3
1	L	55	MET	2.3
1	E	92	TYR	2.3
1	E	172	GLU	2.3
1	D	89	ASP	2.3
1	K	61	GLU	2.3
1	D	96	ILE	2.3
1	F	161	PHE	2.3
1	K	11	CYS	2.3
1	L	175	GLU	2.3
1	C	165	ILE	2.3
1	L	7	ILE	2.3
1	L	159	GLU	2.3
1	L	38	VAL	2.2
1	F	94	ALA	2.2
1	D	50	GLU	2.2
1	L	124	MET	2.2
1	L	47	GLU	2.2
1	J	53	VAL	2.2
1	F	76	ALA	2.2
1	C	47	GLU	2.2
1	E	111	GLU	2.2
1	H	61	GLU	2.2
1	J	89	ASP	2.2
1	K	166	GLU	2.2
1	C	74	ASN	2.2
1	L	65	PRO	2.2
1	K	37	VAL	2.2
1	K	4	ALA	2.2
1	E	176	ASN	2.2
1	K	268	PRO	2.2
1	D	283	GLU	2.2
1	L	123	ALA	2.2
1	E	62	ASP	2.2
1	E	167	LYS	2.1
1	F	59	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	L	50	GLU	2.1
1	I	174	SER	2.1
1	C	58	ASP	2.1
1	K	69	VAL	2.1
1	L	110	GLU	2.1
1	C	282	PRO	2.1
1	K	75	PRO	2.1
1	H	190	GLU	2.1
1	K	172	GLU	2.1
1	C	51	ALA	2.1
1	F	28	ALA	2.1
1	F	46	PRO	2.1
1	K	57	LEU	2.1
1	I	36	ARG	2.1
1	L	81	SER	2.1
1	C	271	LYS	2.1
1	F	51	ALA	2.1
1	L	42	VAL	2.1
1	F	91	GLU	2.1
1	L	35	PHE	2.1
1	I	45	ASP	2.1
1	J	58	ASP	2.1
1	L	281	ASP	2.1
1	C	113	GLY	2.1
1	K	94	ALA	2.1
1	F	70	TYR	2.1
1	K	31	GLU	2.1
1	C	107	ASP	2.1
1	F	66	ASP	2.1
1	F	97	ILE	2.1
1	I	7	ILE	2.1
1	J	177	ASP	2.1
1	F	80	PRO	2.1
1	K	5	LYS	2.1
1	L	179	PRO	2.1
1	K	43	LYS	2.1
1	K	44	MET	2.0
1	D	69	VAL	2.0
1	I	175	GLU	2.0
1	D	52	ALA	2.0
1	J	76	ALA	2.0
1	F	271	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	K	12	GLY	2.0
1	E	129	ARG	2.0
1	L	66	ASP	2.0
1	I	159	GLU	2.0
1	L	86	MET	2.0
1	L	40	THR	2.0
1	C	36	ARG	2.0
1	I	116	TYR	2.0
1	L	93	PRO	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	MG	B	6004	1/1	0.78	0.21	0.63	30,30,30,30	0
2	MG	G	6006	1/1	0.90	0.19	0.59	21,21,21,21	0
2	MG	H	6007	1/1	0.67	0.21	-0.52	34,34,34,34	0
2	MG	A	6002	1/1	0.89	0.14	-0.79	25,25,25,25	0
2	MG	A	6001	1/1	0.86	0.12	-1.03	29,29,29,29	0
2	MG	B	6003	1/1	0.93	0.09	-1.69	25,25,25,25	0
2	MG	H	6008	1/1	0.84	0.11	-1.85	27,27,27,27	0
2	MG	G	6005	1/1	0.78	0.12	-	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.