



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:27 AM GMT

PDB ID : 2QJH
Title : M. jannaschii ADH synthase covalently bound to dihydroxyacetone phosphate
Authors : Ealick, S.E.; Morar, M.
Deposited on : 2007-07-07
Resolution : 2.60 Å(reported)

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

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

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

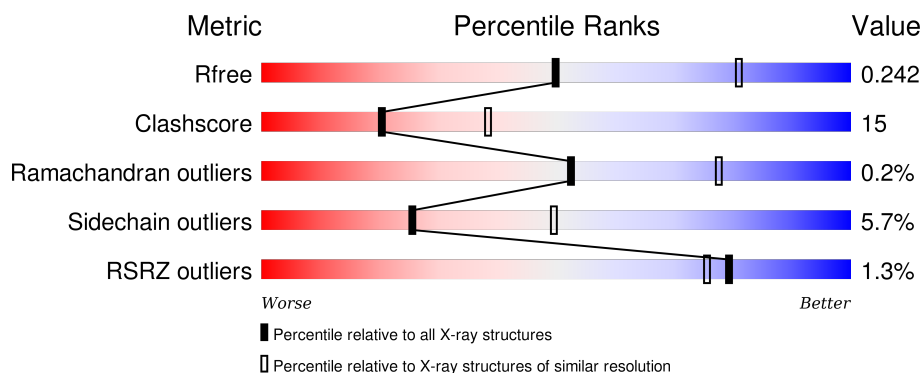
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	273	<div> <div>2%</div> <div>73%</div> <div>21%</div> <div>• •</div> </div>
1	B	273	<div> <div>2%</div> <div>68%</div> <div>26%</div> <div>• •</div> </div>
1	C	273	<div> <div>%</div> <div>73%</div> <div>22%</div> <div>• •</div> </div>
1	D	273	<div> <div>71%</div> <div>24%</div> <div>• •</div> </div>
1	E	273	<div> <div>73%</div> <div>21%</div> <div>• •</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	273	 68% 26% . .
1	G	273	 68% 26% . .
1	H	273	 68% 26% . .
1	I	273	 74% 20% . .
1	J	273	 72% 22% . .
1	K	273	 73% 21% . .
1	L	273	 71% 23% . .
1	M	273	 72% 23% . .
1	N	273	 72% 21% . .
1	O	273	 69% 25% . .
1	P	273	 71% 22% . .
1	Q	273	 70% 23% . .
1	R	273	 68% 26% . .
1	S	273	 69% 24% . .
1	T	273	 68% 27% . .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 40004 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 Putative aldolase MJ0400.

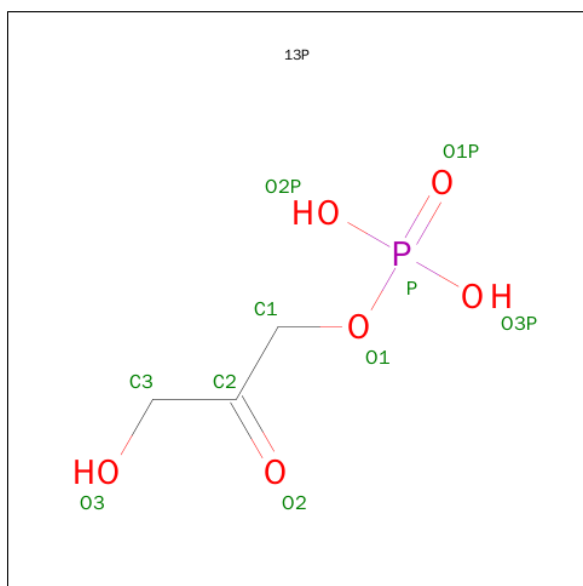
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	0	0
			1960	1231	347	371	11			
1	B	264	Total	C	N	O	S	0	0	0
			1964	1233	347	373	11			
1	C	265	Total	C	N	O	S	0	0	0
			1984	1246	350	376	12			
1	D	266	Total	C	N	O	S	0	0	0
			1995	1251	353	379	12			
1	E	264	Total	C	N	O	S	0	0	0
			1972	1238	348	375	11			
1	F	264	Total	C	N	O	S	0	0	0
			1968	1235	347	375	11			
1	G	264	Total	C	N	O	S	0	0	0
			1960	1231	347	371	11			
1	H	264	Total	C	N	O	S	0	0	0
			1964	1234	348	371	11			
1	I	264	Total	C	N	O	S	0	0	0
			1982	1244	352	375	11			
1	J	264	Total	C	N	O	S	0	0	0
			1968	1235	347	375	11			
1	K	264	Total	C	N	O	S	0	0	0
			1970	1237	351	371	11			
1	L	265	Total	C	N	O	S	0	0	0
			1979	1242	352	374	11			
1	M	264	Total	C	N	O	S	0	0	0
			1968	1237	349	371	11			
1	N	264	Total	C	N	O	S	0	0	0
			1964	1233	347	373	11			
1	O	264	Total	C	N	O	S	0	0	0
			1968	1236	348	373	11			
1	P	264	Total	C	N	O	S	0	0	0
			1966	1234	350	371	11			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	264	Total	C	N	O	S	0	0	0
			1972	1239	349	373	11			
1	R	266	Total	C	N	O	S	0	0	0
			1986	1246	350	379	11			
1	S	264	Total	C	N	O	S	0	0	0
			1961	1232	346	372	11			
1	T	264	Total	C	N	O	S	0	0	0
			1960	1231	347	371	11			

- Molecule 2 is 1,3-DIHYDROXYACETONEPHOSPHATE (three-letter code: 13P) (formula: $C_3H_7O_6P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			9	3	5	1		
2	B	1	Total	C	O	P	0	0
			9	3	5	1		
2	C	1	Total	C	O	P	0	0
			9	3	5	1		
2	D	1	Total	C	O	P	0	0
			9	3	5	1		
2	E	1	Total	C	O	P	0	0
			9	3	5	1		
2	F	1	Total	C	O	P	0	0
			9	3	5	1		
2	G	1	Total	C	O	P	0	0
			9	3	5	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	H	1	Total	C	O	P	0	0
			9	3	5	1		
2	I	1	Total	C	O	P	0	0
			9	3	5	1		
2	J	1	Total	C	O	P	0	0
			9	3	5	1		
2	K	1	Total	C	O	P	0	0
			9	3	5	1		
2	L	1	Total	C	O	P	0	0
			9	3	5	1		
2	M	1	Total	C	O	P	0	0
			9	3	5	1		
2	N	1	Total	C	O	P	0	0
			9	3	5	1		
2	O	1	Total	C	O	P	0	0
			9	3	5	1		
2	P	1	Total	C	O	P	0	0
			9	3	5	1		
2	Q	1	Total	C	O	P	0	0
			9	3	5	1		
2	R	1	Total	C	O	P	0	0
			9	3	5	1		
2	S	1	Total	C	O	P	0	0
			9	3	5	1		
2	T	1	Total	C	O	P	0	0
			9	3	5	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	13	Total	O	0	0
			13	13		
3	B	15	Total	O	0	0
			15	15		
3	C	20	Total	O	0	0
			20	20		
3	D	23	Total	O	0	0
			23	23		
3	E	23	Total	O	0	0
			23	23		
3	F	25	Total	O	0	0
			25	25		

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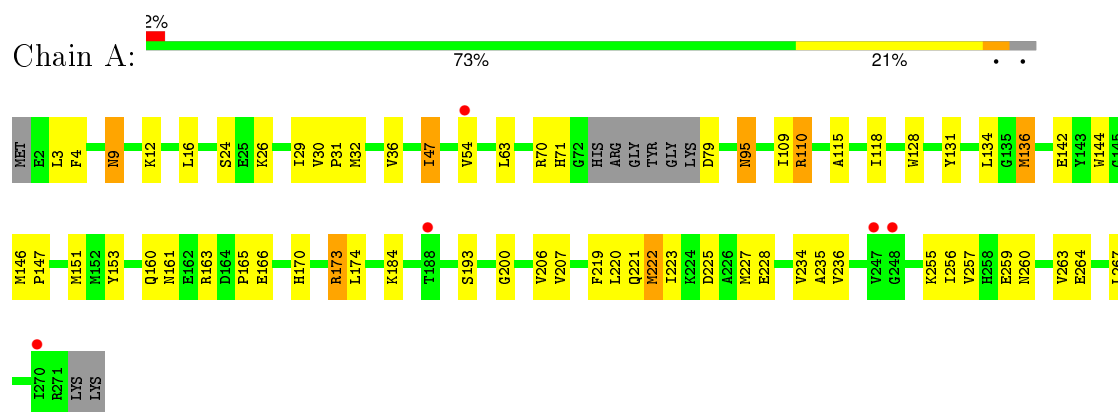
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	17	Total 17	O 17	0	0
3	H	13	Total 13	O 13	0	0
3	I	24	Total 24	O 24	0	0
3	J	19	Total 19	O 19	0	0
3	K	27	Total 27	O 27	0	0
3	L	26	Total 26	O 26	0	0
3	M	23	Total 23	O 23	0	0
3	N	20	Total 20	O 20	0	0
3	O	27	Total 27	O 27	0	0
3	P	17	Total 17	O 17	0	0
3	Q	23	Total 23	O 23	0	0
3	R	24	Total 24	O 24	0	0
3	S	20	Total 20	O 20	0	0
3	T	14	Total 14	O 14	0	0

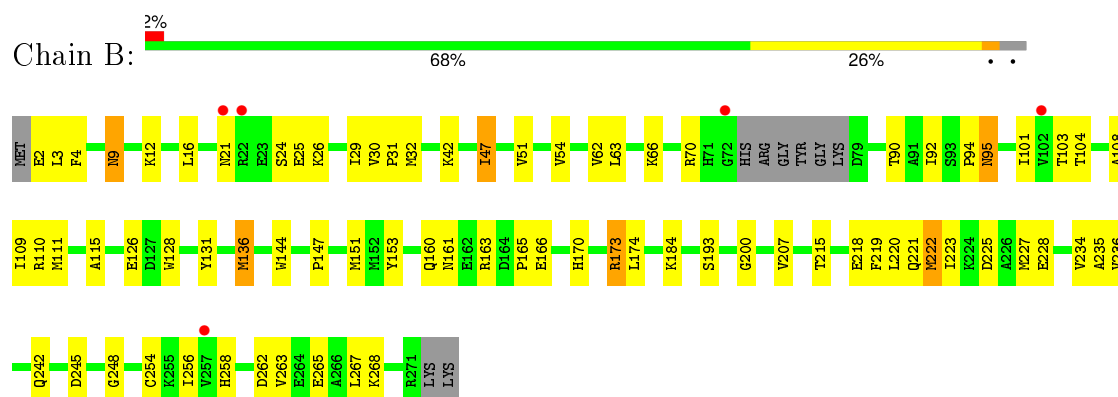
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). 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.

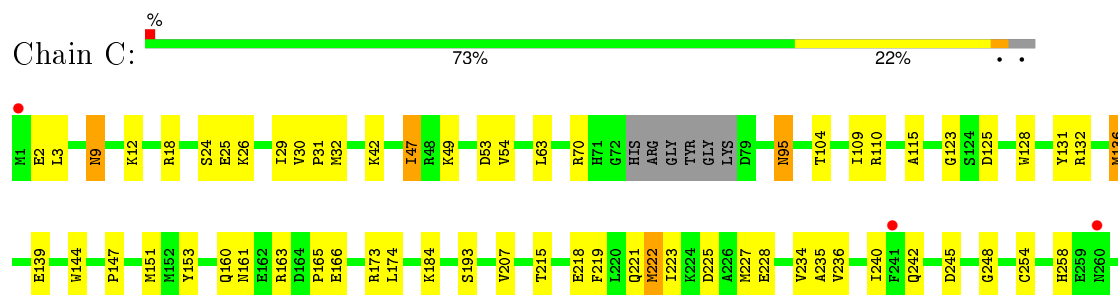
• Molecule 1: Putative aldolase MJ0400



• Molecule 1: Putative aldolase MJ0400



• Molecule 1: Putative aldolase MJ0400





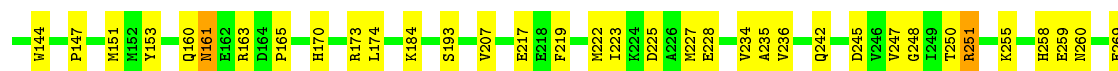
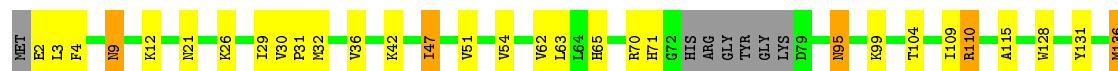
- Molecule 1: Putative aldolase MJ0400

Chain D: 71% 24%



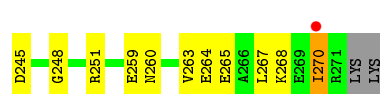
- Molecule 1: Putative aldolase MJ0400

Chain E: 73% 21%



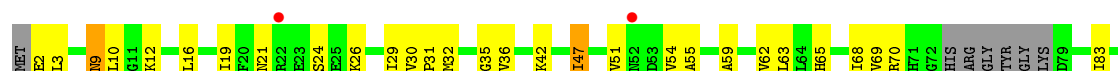
- Molecule 1: Putative aldolase MJ0400

Chain F: 68% 26%

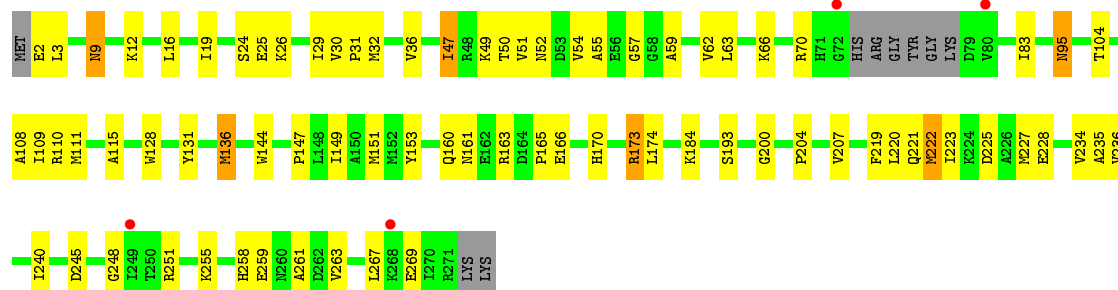


- Molecule 1: Putative aldolase MJ0400

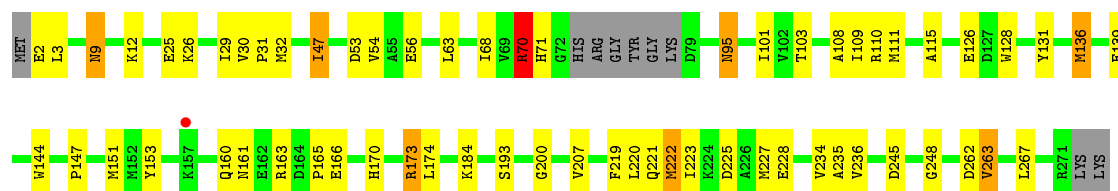
Chain G: 68% 26%



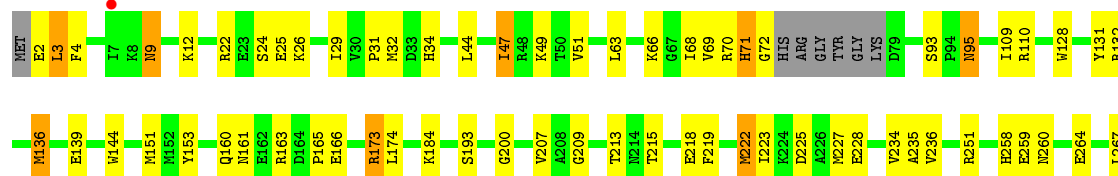
- Molecule 1: Putative aldolase MJ0400



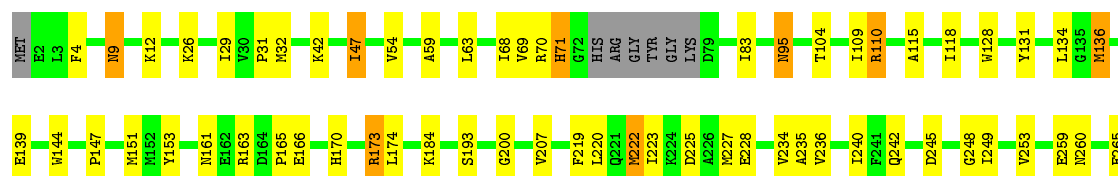
- Molecule 1: Putative aldolase MJ0400



- Molecule 1: Putative aldolase MJ0400

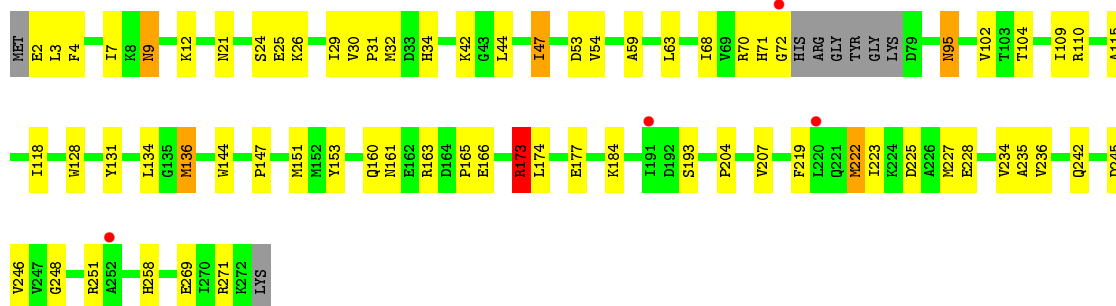


- Molecule 1: Putative aldolase MJ0400

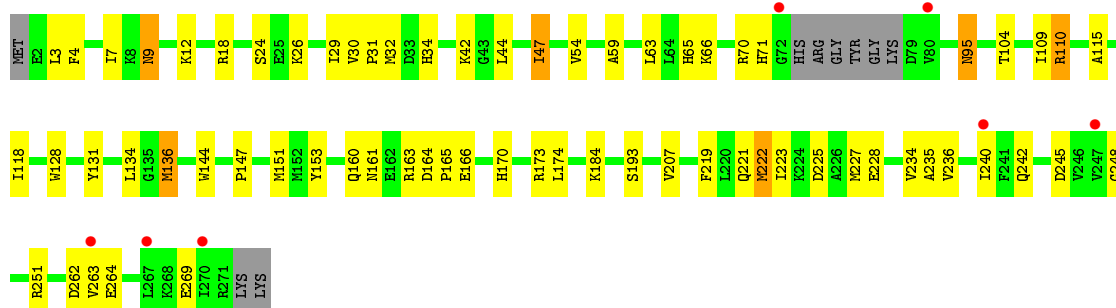


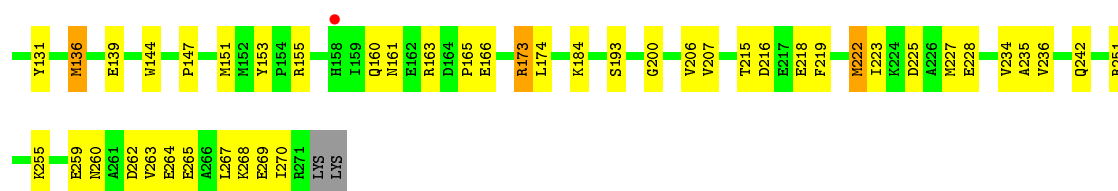


- Molecule 1: Putative aldolase MJ0400



- Molecule 1: Putative aldolase MJ0400





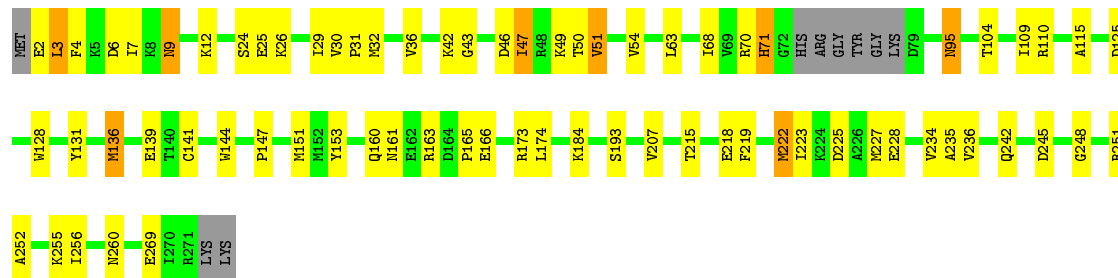
- Molecule 1: Putative aldolase MJ0400

Chain P: 71% 22%



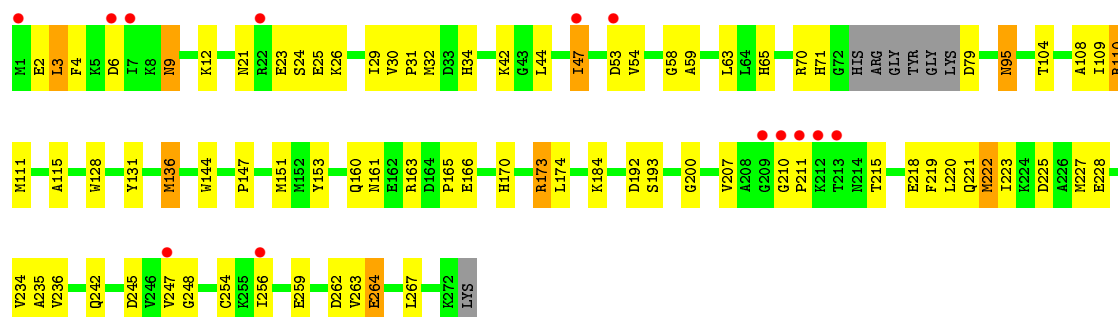
- Molecule 1: Putative aldolase MJ0400

Chain Q: 70% 23%



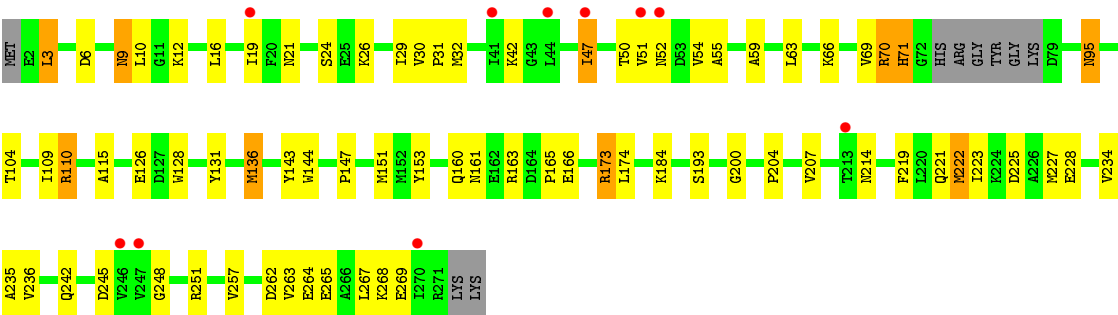
- Molecule 1: Putative aldolase MJ0400

Chain R: 5% 68% 26%

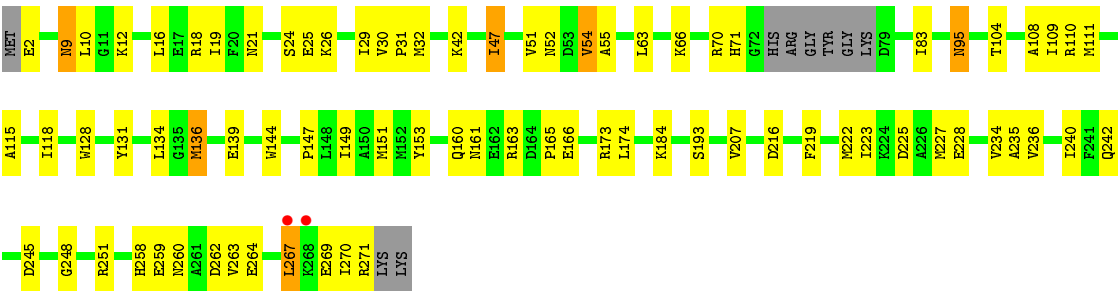


- Molecule 1: Putative aldolase MJ0400

Chain S: 4% 69% 24%



● Molecule 1: Putative aldolase MJ0400



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	94.49Å 101.86Å 154.16Å 90.31° 86.70° 82.44°	Depositor
Resolution (Å)	48.28 – 2.60 54.20 – 2.35	Depositor EDS
% Data completeness (in resolution range)	84.2 (48.28-2.60) 84.2 (54.20-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.34Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.203 , 0.244 0.202 , 0.242	Depositor DCC
R_{free} test set	13111 reflections (9.98%)	DCC
Wilson B-factor (Å ²)	51.0	Xtriage
Anisotropy	0.382	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 168893 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	40004	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 13P

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	0.37	0/1990	0.63	2/2699 (0.1%)
1	B	0.38	0/1994	0.62	0/2704
1	C	0.39	0/2014	0.64	0/2727
1	D	0.40	0/2025	0.64	0/2742
1	E	0.61	6/2002 (0.3%)	0.76	3/2713 (0.1%)
1	F	0.36	0/1998	0.61	0/2709
1	G	0.37	0/1990	0.63	0/2699
1	H	0.38	0/1994	0.61	0/2703
1	I	0.42	0/2012	0.64	0/2724
1	J	0.40	0/1998	0.64	1/2709 (0.0%)
1	K	0.40	0/2000	0.64	2/2710 (0.1%)
1	L	0.40	0/2009	1.10	6/2722 (0.2%)
1	M	0.36	0/1998	0.64	2/2707 (0.1%)
1	N	0.37	0/1994	0.63	2/2704 (0.1%)
1	O	0.39	0/1998	0.62	0/2708
1	P	0.40	0/1996	0.64	2/2706 (0.1%)
1	Q	0.40	1/2002 (0.0%)	0.66	2/2712 (0.1%)
1	R	0.38	0/2016	0.65	2/2732 (0.1%)
1	S	0.38	0/1991	0.67	2/2700 (0.1%)
1	T	0.36	0/1990	0.62	1/2699 (0.0%)
All	All	0.40	7/40011 (0.0%)	0.67	27/54229 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	251	ARG	CZ-NH1	-12.47	1.16	1.33
1	E	251	ARG	CZ-NH2	-8.12	1.22	1.33
1	E	251	ARG	N-CA	-8.02	1.30	1.46
1	E	251	ARG	NE-CZ	-6.82	1.24	1.33
1	Q	141	CYS	CB-SG	-5.84	1.72	1.81
1	E	250	THR	C-N	-5.29	1.21	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	251	ARG	C-O	-5.16	1.13	1.23

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	173	ARG	NE-CZ-NH1	-31.62	104.49	120.30
1	L	173	ARG	NE-CZ-NH2	29.11	134.85	120.30
1	L	173	ARG	CD-NE-CZ	15.64	145.49	123.60
1	E	251	ARG	NE-CZ-NH1	-13.58	113.51	120.30
1	E	251	ARG	NE-CZ-NH2	13.06	126.83	120.30
1	L	173	ARG	CG-CD-NE	-12.01	86.57	111.80
1	S	71	HIS	N-CA-C	11.60	142.32	111.00
1	Q	71	HIS	N-CA-C	8.85	134.88	111.00
1	L	71	HIS	N-CA-C	8.60	134.23	111.00
1	R	71	HIS	N-CA-C	7.88	132.28	111.00
1	M	71	HIS	N-CA-C	7.10	130.17	111.00
1	P	71	HIS	N-CA-C	7.00	129.89	111.00
1	L	71	HIS	CB-CA-C	-6.47	97.46	110.40
1	M	71	HIS	CB-CA-C	-6.46	97.48	110.40
1	K	71	HIS	CB-CA-C	-6.35	97.71	110.40
1	S	71	HIS	CB-CA-C	-6.34	97.72	110.40
1	A	71	HIS	N-CA-C	6.20	127.74	111.00
1	R	71	HIS	CB-CA-C	-6.13	98.15	110.40
1	A	71	HIS	CB-CA-C	-5.97	98.46	110.40
1	E	71	HIS	N-CA-C	5.68	126.33	111.00
1	T	71	HIS	N-CA-C	5.61	126.14	111.00
1	N	71	HIS	N-CA-C	5.61	126.14	111.00
1	J	71	HIS	CB-CA-C	-5.52	99.36	110.40
1	Q	71	HIS	CB-CA-C	-5.47	99.45	110.40
1	K	71	HIS	N-CA-C	5.17	124.96	111.00
1	P	71	HIS	CB-CA-C	-5.15	100.10	110.40
1	N	71	HIS	CB-CA-C	-5.13	100.13	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1960	0	1945	56	0
1	B	1964	0	1948	56	0
1	C	1984	0	1986	55	0
1	D	1995	0	1992	55	0
1	E	1972	0	1963	56	0
1	F	1968	0	1952	68	0
1	G	1960	0	1944	64	0
1	H	1964	0	1955	66	0
1	I	1982	0	1985	50	0
1	J	1968	0	1953	60	0
1	K	1970	0	1967	58	0
1	L	1979	0	1973	61	0
1	M	1968	0	1967	55	0
1	N	1964	0	1949	59	0
1	O	1968	0	1959	65	0
1	P	1966	0	1956	64	0
1	Q	1972	0	1971	59	0
1	R	1986	0	1975	80	0
1	S	1961	0	1944	66	0
1	T	1960	0	1944	60	0
2	A	9	0	5	2	0
2	B	9	0	5	2	0
2	C	9	0	5	2	0
2	D	9	0	5	2	0
2	E	9	0	5	2	0
2	F	9	0	5	2	0
2	G	9	0	5	2	0
2	H	9	0	5	2	0
2	I	9	0	5	2	0
2	J	9	0	5	2	0
2	K	9	0	5	2	0
2	L	9	0	5	2	0
2	M	9	0	5	2	0
2	N	9	0	5	2	0
2	O	9	0	5	2	0
2	P	9	0	5	2	0
2	Q	9	0	5	2	0
2	R	9	0	5	2	0
2	S	9	0	5	2	0
2	T	9	0	5	2	0
3	A	13	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	15	0	0	1	0
3	C	20	0	0	1	0
3	D	23	0	0	3	0
3	E	23	0	0	7	0
3	F	25	0	0	5	0
3	G	17	0	0	8	0
3	H	13	0	0	2	0
3	I	24	0	0	2	0
3	J	19	0	0	4	0
3	K	27	0	0	4	0
3	L	26	0	0	6	0
3	M	23	0	0	3	0
3	N	20	0	0	6	0
3	O	27	0	0	4	0
3	P	17	0	0	4	0
3	Q	23	0	0	2	0
3	R	24	0	0	7	0
3	S	20	0	0	4	0
3	T	14	0	0	0	0
All	All	40004	0	39328	1149	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 15.

All (1149) 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:Q:136:MET:HA	1:Q:136:MET:HE3	1.44	0.98
1:L:136:MET:HE3	1:L:136:MET:HA	1.45	0.98
1:D:136:MET:HA	1:D:136:MET:HE3	1.46	0.98
1:E:136:MET:HE3	1:E:136:MET:HA	1.47	0.97
1:H:136:MET:HE3	1:H:136:MET:HA	1.48	0.96
1:A:207:VAL:HG23	1:A:234:VAL:HG23	1.48	0.96
1:D:207:VAL:HG23	1:D:234:VAL:HG23	1.48	0.95
1:P:136:MET:HA	1:P:136:MET:HE3	1.49	0.95
1:R:207:VAL:HG23	1:R:234:VAL:HG23	1.48	0.95
1:T:207:VAL:HG23	1:T:234:VAL:HG23	1.47	0.94
1:F:136:MET:HE3	1:F:136:MET:HA	1.47	0.94
1:B:136:MET:HE3	1:B:136:MET:HA	1.45	0.94
1:N:207:VAL:HG23	1:N:234:VAL:HG23	1.48	0.94
1:J:207:VAL:HG23	1:J:234:VAL:HG23	1.49	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:207:VAL:HG23	1:K:234:VAL:HG23	1.49	0.93
1:S:30:VAL:HG21	1:S:54:VAL:HG11	1.48	0.93
1:M:207:VAL:HG23	1:M:234:VAL:HG23	1.48	0.93
1:J:136:MET:HE3	1:J:136:MET:HA	1.47	0.93
1:C:207:VAL:HG23	1:C:234:VAL:HG23	1.50	0.93
1:E:207:VAL:HG23	1:E:234:VAL:HG23	1.52	0.92
1:I:136:MET:HA	1:I:136:MET:HE3	1.48	0.92
1:L:207:VAL:HG23	1:L:234:VAL:HG23	1.52	0.92
1:H:207:VAL:HG23	1:H:234:VAL:HG23	1.50	0.92
1:A:136:MET:HE3	1:A:136:MET:HA	1.52	0.92
1:Q:207:VAL:HG23	1:Q:234:VAL:HG23	1.52	0.92
1:P:207:VAL:HG23	1:P:234:VAL:HG23	1.50	0.91
1:G:207:VAL:HG23	1:G:234:VAL:HG23	1.50	0.91
1:G:30:VAL:HG21	1:G:54:VAL:HG21	1.52	0.91
1:S:207:VAL:HG23	1:S:234:VAL:HG23	1.50	0.91
1:F:207:VAL:HG23	1:F:234:VAL:HG23	1.51	0.91
1:B:207:VAL:HG23	1:B:234:VAL:HG23	1.51	0.90
1:O:207:VAL:HG23	1:O:234:VAL:HG23	1.52	0.90
1:K:136:MET:HA	1:K:136:MET:HE3	1.54	0.89
1:I:207:VAL:HG23	1:I:234:VAL:HG23	1.52	0.89
1:J:251:ARG:HG2	1:J:269:GLU:HG2	1.53	0.88
1:H:50:THR:O	1:H:54:VAL:HG23	1.76	0.86
1:C:136:MET:HE3	1:C:136:MET:HA	1.57	0.86
1:L:3:LEU:HD21	1:L:204:PRO:HG3	1.57	0.86
1:H:255:LYS:HE2	1:H:269:GLU:HG3	1.58	0.85
1:A:146:MET:HB2	3:A:510:HOH:O	1.75	0.84
1:R:31:PRO:HB2	2:R:501:13P:H31	1.60	0.84
1:D:47:ILE:O	1:D:51:VAL:HG23	1.75	0.84
1:Q:104:THR:HG23	1:R:136:MET:HE1	1.57	0.84
1:O:251:ARG:HG2	1:O:269:GLU:OE1	1.77	0.84
1:R:263:VAL:O	1:R:267:LEU:HD23	1.78	0.83
1:N:136:MET:HA	1:N:136:MET:HE3	1.61	0.83
1:O:255:LYS:HD3	1:O:259:GLU:OE1	1.76	0.83
1:D:199:LYS:HD2	3:D:505:HOH:O	1.78	0.82
1:N:31:PRO:HB2	2:N:501:13P:H31	1.62	0.82
1:M:31:PRO:HB2	2:M:501:13P:H31	1.61	0.81
1:K:31:PRO:HB2	2:K:501:13P:H31	1.64	0.80
1:G:31:PRO:HB2	2:G:501:13P:H31	1.63	0.80
1:B:31:PRO:HB2	2:B:501:13P:H31	1.61	0.80
1:O:136:MET:HA	1:O:136:MET:HE3	1.62	0.80
1:L:104:THR:HG23	1:M:136:MET:HE1	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:136:MET:HA	1:M:136:MET:HE3	1.64	0.80
1:F:31:PRO:HB2	2:F:501:13P:H31	1.63	0.79
1:P:30:VAL:HG21	1:P:54:VAL:HG11	1.64	0.79
1:D:31:PRO:HB2	2:D:501:13P:H31	1.65	0.79
1:E:247:VAL:HB	3:E:502:HOH:O	1.82	0.79
1:I:221:GLN:OE1	1:I:263:VAL:HG21	1.81	0.79
1:S:31:PRO:HB2	2:S:501:13P:H31	1.63	0.78
1:T:31:PRO:HB2	2:T:501:13P:H31	1.65	0.78
1:C:31:PRO:HB2	2:C:501:13P:H31	1.64	0.78
1:S:136:MET:HE3	1:S:136:MET:HA	1.65	0.78
1:A:220:LEU:HD12	1:A:267:LEU:HD23	1.66	0.78
1:H:31:PRO:HB2	2:H:501:13P:H31	1.65	0.78
1:J:215:THR:OG1	1:J:218:GLU:HG3	1.83	0.78
1:D:252:ALA:O	1:D:256:ILE:HD12	1.84	0.77
1:S:262:ASP:HB3	1:S:265:GLU:HG3	1.66	0.77
1:O:31:PRO:HB2	2:O:501:13P:H31	1.66	0.77
1:O:47:ILE:O	1:O:51:VAL:HG23	1.85	0.77
1:F:8:LYS:HA	3:F:519:HOH:O	1.84	0.77
1:I:31:PRO:HB2	2:I:501:13P:H31	1.65	0.77
1:Q:31:PRO:HB2	2:Q:501:13P:H31	1.64	0.77
1:A:31:PRO:HB2	2:A:501:13P:H31	1.64	0.77
1:J:31:PRO:HB2	2:J:501:13P:H31	1.64	0.77
1:T:136:MET:HA	1:T:136:MET:HE3	1.67	0.76
1:S:50:THR:O	1:S:54:VAL:HG23	1.85	0.76
1:P:245:ASP:OD2	1:P:271:ARG:HD3	1.86	0.76
1:P:31:PRO:HB2	2:P:501:13P:H31	1.68	0.76
1:S:104:THR:HG23	1:T:136:MET:HE1	1.66	0.76
1:E:31:PRO:HB2	2:E:501:13P:H31	1.65	0.76
1:S:30:VAL:HG21	1:S:54:VAL:CG1	2.15	0.75
1:F:51:VAL:HG13	1:F:62:VAL:HG11	1.66	0.75
1:H:30:VAL:HG21	1:H:54:VAL:HG11	1.68	0.75
1:L:31:PRO:HB2	2:L:501:13P:H31	1.68	0.74
1:T:30:VAL:HG21	1:T:54:VAL:HG21	1.69	0.74
1:R:211:PRO:HD2	3:R:517:HOH:O	1.87	0.74
1:L:109:ILE:HD11	1:L:144:TRP:HB3	1.70	0.73
1:R:263:VAL:HG13	1:R:267:LEU:CD2	2.18	0.73
1:S:109:ILE:HD11	1:S:144:TRP:HB3	1.70	0.73
1:F:3:LEU:HD21	1:F:204:PRO:HB3	1.70	0.73
1:J:251:ARG:HG2	1:J:269:GLU:CG	2.19	0.73
1:E:110:ARG:HD3	3:K:508:HOH:O	1.87	0.73
1:D:109:ILE:HD11	1:D:144:TRP:HB3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:30:VAL:HG21	1:T:54:VAL:CG2	2.19	0.72
1:R:109:ILE:HD11	1:R:144:TRP:HB3	1.72	0.72
1:H:109:ILE:HD11	1:H:144:TRP:HB3	1.72	0.72
1:A:109:ILE:HD11	1:A:144:TRP:HB3	1.71	0.71
1:I:109:ILE:HD11	1:I:144:TRP:HB3	1.72	0.71
1:T:109:ILE:HD11	1:T:144:TRP:HB3	1.72	0.71
1:K:26:LYS:HE3	3:K:511:HOH:O	1.89	0.71
1:P:109:ILE:HD11	1:P:144:TRP:HB3	1.72	0.71
1:K:170:HIS:HD2	3:K:503:HOH:O	1.73	0.71
1:C:109:ILE:HD11	1:C:144:TRP:HB3	1.71	0.71
1:M:221:GLN:OE1	1:M:263:VAL:HG21	1.91	0.71
1:N:109:ILE:HD11	1:N:144:TRP:HB3	1.73	0.71
1:E:109:ILE:HD11	1:E:144:TRP:HB3	1.74	0.70
1:G:221:GLN:OE1	1:G:263:VAL:HG21	1.91	0.70
1:P:26:LYS:HE3	3:P:504:HOH:O	1.90	0.70
1:B:109:ILE:HD11	1:B:144:TRP:HB3	1.73	0.69
1:Q:109:ILE:HD11	1:Q:144:TRP:HB3	1.73	0.69
1:G:30:VAL:HG21	1:G:54:VAL:CG2	2.20	0.69
1:J:109:ILE:HD11	1:J:144:TRP:HB3	1.73	0.69
1:S:21:ASN:HB3	1:S:24:SER:OG	1.92	0.69
1:F:109:ILE:HD11	1:F:144:TRP:HB3	1.73	0.69
1:K:109:ILE:HD11	1:K:144:TRP:HB3	1.73	0.69
1:G:136:MET:HE3	1:G:136:MET:HA	1.73	0.69
1:H:30:VAL:HG21	1:H:54:VAL:CG1	2.23	0.69
1:P:30:VAL:HG21	1:P:54:VAL:CG1	2.24	0.68
1:D:160:GLN:HB2	3:D:518:HOH:O	1.94	0.68
1:S:6:ASP:HB2	3:S:508:HOH:O	1.93	0.68
1:G:109:ILE:HD11	1:G:144:TRP:HB3	1.74	0.68
1:O:109:ILE:HD11	1:O:144:TRP:HB3	1.75	0.68
1:S:47:ILE:O	1:S:51:VAL:HG23	1.93	0.68
1:E:47:ILE:O	1:E:51:VAL:HG23	1.94	0.68
1:M:109:ILE:HD11	1:M:144:TRP:HB3	1.75	0.68
1:F:47:ILE:O	1:F:51:VAL:HG23	1.94	0.68
1:R:170:HIS:HD2	3:R:504:HOH:O	1.76	0.68
1:T:263:VAL:HG12	1:T:267:LEU:HD12	1.75	0.67
1:L:251:ARG:HG2	1:L:269:GLU:OE1	1.94	0.67
1:S:251:ARG:HG2	1:S:269:GLU:OE1	1.95	0.67
1:Q:24:SER:O	1:Q:26:LYS:HG2	1.94	0.67
1:K:245:ASP:OD2	1:K:271:ARG:HG2	1.95	0.66
1:L:3:LEU:HD21	1:L:204:PRO:CG	2.26	0.66
1:G:54:VAL:HG22	1:G:59:ALA:HB2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:160:GLN:HG3	3:P:513:HOH:O	1.95	0.66
1:G:110:ARG:HD3	3:G:509:HOH:O	1.96	0.66
1:G:26:LYS:HE3	3:G:506:HOH:O	1.94	0.66
1:G:47:ILE:O	1:G:51:VAL:HG23	1.94	0.66
1:F:104:THR:HG23	1:G:136:MET:HE1	1.77	0.66
1:R:263:VAL:HG13	1:R:267:LEU:HD23	1.77	0.66
1:I:2:GLU:HA	1:I:25:GLU:OE1	1.96	0.66
1:M:136:MET:CE	1:M:136:MET:HA	2.26	0.65
1:H:255:LYS:HE2	1:H:269:GLU:CG	2.26	0.65
1:L:3:LEU:CD2	1:L:204:PRO:HG3	2.26	0.65
1:L:95:ASN:HB2	3:L:521:HOH:O	1.96	0.65
1:R:220:LEU:HD12	1:R:267:LEU:CD1	2.27	0.65
1:P:251:ARG:HG2	1:P:269:GLU:OE1	1.97	0.65
1:J:228:GLU:HG3	3:J:518:HOH:O	1.97	0.64
1:F:3:LEU:HD13	1:F:4:PHE:CE1	2.32	0.64
1:L:30:VAL:HG21	1:L:54:VAL:HG11	1.77	0.64
1:N:251:ARG:HG2	1:N:269:GLU:OE1	1.96	0.64
1:P:51:VAL:HG13	1:P:62:VAL:HG11	1.80	0.64
1:K:136:MET:CE	1:K:136:MET:HA	2.27	0.64
1:N:270:ILE:HG22	1:N:271:ARG:H	1.62	0.64
1:D:267:LEU:HD23	1:D:270:ILE:HD12	1.79	0.64
3:L:514:HOH:O	1:M:136:MET:SD	2.55	0.64
1:N:214:ASN:N	1:N:214:ASN:HD22	1.96	0.64
1:R:136:MET:HA	1:R:136:MET:CE	2.27	0.63
1:L:245:ASP:OD2	1:L:271:ARG:HD3	1.99	0.63
1:A:220:LEU:HD12	1:A:267:LEU:CD2	2.28	0.63
1:P:31:PRO:HA	1:P:63:LEU:HB3	1.79	0.63
1:F:221:GLN:OE1	1:F:263:VAL:HG21	1.99	0.63
1:J:251:ARG:CG	1:J:269:GLU:HG2	2.26	0.63
3:G:518:HOH:O	1:H:173:ARG:HB3	1.97	0.63
1:E:255:LYS:HG3	1:E:259:GLU:OE1	1.99	0.62
1:O:265:GLU:HA	1:O:268:LYS:HE3	1.79	0.62
1:M:104:THR:HG23	1:N:136:MET:HE1	1.81	0.62
1:O:51:VAL:HG13	1:O:62:VAL:HG11	1.79	0.62
1:T:136:MET:HA	1:T:136:MET:CE	2.30	0.62
1:P:221:GLN:OE1	1:P:263:VAL:HG21	2.00	0.62
1:N:31:PRO:HA	1:N:63:LEU:HB3	1.81	0.62
1:S:136:MET:CE	1:S:136:MET:HA	2.30	0.62
1:C:136:MET:CE	1:C:136:MET:HA	2.30	0.61
1:G:21:ASN:HB3	1:G:24:SER:OG	1.99	0.61
1:S:54:VAL:HG12	1:S:59:ALA:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:31:PRO:HA	1:F:63:LEU:HB3	1.82	0.61
1:L:31:PRO:HA	1:L:63:LEU:HB3	1.82	0.61
3:E:512:HOH:O	1:K:110:ARG:HD3	2.01	0.61
3:C:515:HOH:O	1:M:110:ARG:HD3	1.99	0.61
1:G:31:PRO:HA	1:G:63:LEU:HB3	1.82	0.61
1:O:2:GLU:HG3	1:O:4:PHE:H	1.65	0.61
1:S:31:PRO:HA	1:S:63:LEU:HB3	1.83	0.61
1:H:54:VAL:HG12	1:H:59:ALA:HB2	1.82	0.61
1:T:31:PRO:HA	1:T:63:LEU:HB3	1.83	0.61
1:A:151:MET:HG2	1:A:184:LYS:HD3	1.83	0.61
1:F:30:VAL:HG21	1:F:54:VAL:CG1	2.30	0.61
1:R:104:THR:HG23	1:S:136:MET:HE1	1.84	0.60
1:J:264:GLU:HA	1:J:267:LEU:HD12	1.82	0.60
1:H:31:PRO:HA	1:H:63:LEU:HB3	1.83	0.60
3:G:518:HOH:O	1:H:173:ARG:CG	2.50	0.60
1:O:215:THR:OG1	1:O:218:GLU:HB2	2.00	0.60
1:I:136:MET:CE	1:I:136:MET:HA	2.29	0.60
1:D:251:ARG:HG2	1:D:269:GLU:OE1	2.02	0.60
1:G:51:VAL:HG13	1:G:62:VAL:HG11	1.83	0.60
1:K:31:PRO:HA	1:K:63:LEU:HB3	1.84	0.60
1:P:71:HIS:O	1:Q:6:ASP:HB3	2.02	0.60
1:N:161:ASN:ND2	1:N:163:ARG:H	2.00	0.60
1:R:30:VAL:HG21	1:R:54:VAL:CG1	2.32	0.60
1:J:24:SER:OG	1:J:258:HIS:HD2	1.84	0.60
1:Q:31:PRO:HA	1:Q:63:LEU:HB3	1.83	0.59
1:R:53:ASP:HB3	1:R:247:VAL:HG22	1.84	0.59
1:E:31:PRO:HA	1:E:63:LEU:HB3	1.84	0.59
1:H:170:HIS:HD2	3:H:504:HOH:O	1.85	0.59
1:H:136:MET:CE	1:H:136:MET:HA	2.30	0.59
1:N:136:MET:HA	1:N:136:MET:CE	2.30	0.59
1:N:161:ASN:HD21	1:N:163:ARG:HB2	1.67	0.59
1:N:47:ILE:O	1:N:51:VAL:HG23	2.02	0.59
1:I:31:PRO:HA	1:I:63:LEU:HB3	1.85	0.59
1:D:215:THR:OG1	1:D:218:GLU:HG3	2.02	0.59
1:A:31:PRO:HA	1:A:63:LEU:HB3	1.83	0.59
1:G:136:MET:CE	1:G:136:MET:HA	2.33	0.59
1:T:29:ILE:O	1:T:235:ALA:HA	2.03	0.59
1:J:2:GLU:HA	1:J:25:GLU:OE2	2.03	0.59
1:A:110:ARG:HD3	3:A:507:HOH:O	2.03	0.59
1:I:29:ILE:O	1:I:235:ALA:HA	2.03	0.59
1:P:3:LEU:HD12	3:P:504:HOH:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2:GLU:HG3	1:E:4:PHE:H	1.67	0.58
1:O:216:ASP:OD2	1:O:270:ILE:HD13	2.03	0.58
1:M:29:ILE:O	1:M:235:ALA:HA	2.03	0.58
1:R:65:HIS:HE1	3:R:525:HOH:O	1.85	0.58
1:S:52:ASN:O	1:S:55:ALA:HB3	2.04	0.58
1:O:31:PRO:HA	1:O:63:LEU:HB3	1.86	0.58
1:G:29:ILE:O	1:G:235:ALA:HA	2.02	0.58
1:R:31:PRO:HA	1:R:63:LEU:HB3	1.85	0.58
1:G:10:LEU:HD21	1:S:69:VAL:HG12	1.86	0.58
1:O:65:HIS:HE1	3:O:514:HOH:O	1.87	0.58
1:E:29:ILE:O	1:E:235:ALA:HA	2.03	0.58
1:F:30:VAL:HG21	1:F:54:VAL:HG11	1.86	0.58
1:R:29:ILE:O	1:R:235:ALA:HA	2.04	0.58
1:O:155:ARG:HA	3:O:515:HOH:O	2.04	0.58
1:B:265:GLU:HA	1:B:268:LYS:NZ	2.19	0.58
1:J:136:MET:CE	1:J:136:MET:HA	2.28	0.58
1:A:4:PHE:CD1	1:A:16:LEU:HD13	2.39	0.58
1:G:54:VAL:HG22	1:G:59:ALA:CB	2.34	0.58
1:N:104:THR:HG23	1:O:136:MET:HE1	1.86	0.58
1:O:128:TRP:HA	1:O:131:TYR:CD1	2.39	0.58
1:O:30:VAL:HG21	1:O:54:VAL:HG13	1.85	0.57
1:O:136:MET:CE	1:O:136:MET:HA	2.31	0.57
1:N:32:MET:HE2	1:N:47:ILE:HG22	1.86	0.57
1:L:72:GLY:HA2	3:L:510:HOH:O	2.03	0.57
1:G:151:MET:HG2	1:G:184:LYS:HD3	1.87	0.57
1:K:29:ILE:O	1:K:235:ALA:HA	2.05	0.57
1:D:31:PRO:HA	1:D:63:LEU:HB3	1.85	0.57
1:B:31:PRO:HA	1:B:63:LEU:HB3	1.86	0.57
1:R:3:LEU:HD13	1:R:4:PHE:CE1	2.39	0.57
1:A:221:GLN:OE1	1:A:263:VAL:HG11	2.04	0.57
1:S:234:VAL:HG22	1:S:236:VAL:HG13	1.86	0.57
1:E:65:HIS:HE1	3:E:519:HOH:O	1.87	0.57
1:F:234:VAL:HG22	1:F:236:VAL:HG13	1.86	0.57
3:Q:512:HOH:O	1:R:136:MET:CE	2.51	0.57
1:C:31:PRO:HA	1:C:63:LEU:HB3	1.86	0.57
1:R:136:MET:HA	1:R:136:MET:HE3	1.85	0.57
1:K:265:GLU:HA	1:K:268:LYS:NZ	2.19	0.56
1:A:136:MET:HE1	1:E:104:THR:HG23	1.86	0.56
1:S:66:LYS:HE3	1:T:139:GLU:HG3	1.88	0.56
1:B:221:GLN:OE1	1:B:263:VAL:HG21	2.05	0.56
1:S:29:ILE:O	1:S:235:ALA:HA	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:24:SER:OG	1:C:258:HIS:HD2	1.88	0.56
1:T:128:TRP:HA	1:T:131:TYR:CD1	2.40	0.56
1:A:256:ILE:O	1:A:260:ASN:HA	2.04	0.56
1:M:170:HIS:HD2	3:M:506:HOH:O	1.88	0.56
1:N:29:ILE:O	1:N:235:ALA:HA	2.06	0.56
1:B:51:VAL:HG13	1:B:62:VAL:HG11	1.85	0.56
1:F:29:ILE:O	1:F:235:ALA:HA	2.05	0.56
1:P:128:TRP:HA	1:P:131:TYR:CD1	2.41	0.56
1:J:29:ILE:O	1:J:235:ALA:HA	2.05	0.56
1:F:128:TRP:HA	1:F:131:TYR:CD1	2.41	0.56
1:M:251:ARG:HG2	1:M:269:GLU:OE1	2.05	0.56
1:A:128:TRP:HA	1:A:131:TYR:CD1	2.41	0.56
1:S:153:TYR:OH	1:S:184:LYS:HE2	2.05	0.56
1:H:51:VAL:HG13	1:H:62:VAL:HG11	1.87	0.56
1:J:267:LEU:C	1:J:269:GLU:H	2.08	0.56
1:M:31:PRO:HA	1:M:63:LEU:HB3	1.87	0.56
1:S:264:GLU:HA	1:S:267:LEU:HD12	1.88	0.56
1:R:161:ASN:HD21	1:R:163:ARG:HB2	1.70	0.56
1:Q:46:ASP:O	1:Q:49:LYS:HB3	2.05	0.56
1:T:259:GLU:O	1:T:260:ASN:HB2	2.05	0.56
1:B:161:ASN:HD21	1:B:163:ARG:HB2	1.71	0.56
1:Q:128:TRP:HA	1:Q:131:TYR:CD1	2.40	0.56
1:A:29:ILE:O	1:A:235:ALA:HA	2.05	0.56
1:G:195:ARG:HG3	3:G:517:HOH:O	2.05	0.56
1:I:234:VAL:HG22	1:I:236:VAL:HG13	1.87	0.56
1:H:54:VAL:HG12	1:H:59:ALA:CB	2.36	0.56
1:A:263:VAL:HG23	1:A:264:GLU:N	2.19	0.56
1:K:161:ASN:HD21	1:K:163:ARG:HB2	1.71	0.56
1:Q:30:VAL:HG11	1:Q:54:VAL:HG21	1.88	0.56
1:L:29:ILE:O	1:L:235:ALA:HA	2.06	0.56
1:T:234:VAL:HG22	1:T:236:VAL:HG13	1.88	0.56
1:G:234:VAL:HG22	1:G:236:VAL:HG13	1.88	0.56
1:B:234:VAL:HG22	1:B:236:VAL:HG13	1.88	0.56
1:S:161:ASN:HD21	1:S:163:ARG:HB2	1.69	0.56
1:P:29:ILE:O	1:P:235:ALA:HA	2.05	0.56
1:J:31:PRO:HA	1:J:63:LEU:HB3	1.87	0.55
1:P:161:ASN:HD21	1:P:163:ARG:HB2	1.71	0.55
1:L:234:VAL:HG22	1:L:236:VAL:HG13	1.88	0.55
1:E:32:MET:HE2	1:E:47:ILE:HG22	1.87	0.55
1:R:151:MET:HG2	1:R:184:LYS:HD3	1.87	0.55
1:R:31:PRO:CB	2:R:501:13P:H31	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:161:ASN:HD21	1:D:163:ARG:HB2	1.71	0.55
1:M:234:VAL:HG22	1:M:236:VAL:HG13	1.89	0.55
1:H:234:VAL:HG22	1:H:236:VAL:HG13	1.89	0.55
1:A:161:ASN:HD21	1:A:163:ARG:HB2	1.71	0.55
1:C:2:GLU:HG2	1:C:25:GLU:OE1	2.07	0.55
1:R:221:GLN:OE1	1:R:263:VAL:HG21	2.07	0.55
1:N:234:VAL:HG22	1:N:236:VAL:HG13	1.88	0.55
1:P:234:VAL:HG22	1:P:236:VAL:HG13	1.88	0.55
1:E:3:LEU:HD23	1:E:3:LEU:O	2.07	0.55
1:O:30:VAL:HG11	1:O:54:VAL:HG21	1.89	0.55
1:J:128:TRP:HA	1:J:131:TYR:CD1	2.41	0.55
1:D:151:MET:HG2	1:D:184:LYS:HD3	1.88	0.55
1:D:153:TYR:OH	1:D:184:LYS:HE2	2.07	0.55
1:A:136:MET:HA	1:A:136:MET:CE	2.32	0.55
1:Q:234:VAL:HG22	1:Q:236:VAL:HG13	1.89	0.55
1:R:263:VAL:HG13	1:R:267:LEU:HD21	1.87	0.55
1:B:29:ILE:O	1:B:235:ALA:HA	2.06	0.55
1:E:161:ASN:HD21	1:E:163:ARG:HB2	1.71	0.55
1:D:234:VAL:HG22	1:D:236:VAL:HG13	1.89	0.55
1:N:128:TRP:HA	1:N:131:TYR:CD1	2.42	0.55
1:N:9:ASN:HD22	1:N:9:ASN:C	2.10	0.55
1:M:151:MET:HG2	1:M:184:LYS:HD3	1.89	0.55
1:Q:136:MET:HA	1:Q:136:MET:CE	2.28	0.55
1:F:32:MET:HE2	1:F:47:ILE:HG22	1.88	0.55
3:G:518:HOH:O	1:H:173:ARG:HG3	2.05	0.55
1:C:161:ASN:HD21	1:C:163:ARG:HB2	1.72	0.55
1:I:193:SER:HB3	3:I:522:HOH:O	2.05	0.55
1:L:161:ASN:HD21	1:L:163:ARG:HB2	1.72	0.55
1:L:2:GLU:HA	1:L:25:GLU:OE1	2.08	0.55
1:E:234:VAL:HG22	1:E:236:VAL:HG13	1.87	0.54
1:H:29:ILE:O	1:H:235:ALA:HA	2.07	0.54
1:C:29:ILE:O	1:C:235:ALA:HA	2.06	0.54
1:D:9:ASN:C	1:D:9:ASN:HD22	2.11	0.54
1:B:265:GLU:HA	1:B:268:LYS:CE	2.37	0.54
1:K:136:MET:HE1	1:O:104:THR:HG23	1.90	0.54
1:M:161:ASN:HD21	1:M:163:ARG:HB2	1.72	0.54
1:O:29:ILE:O	1:O:235:ALA:HA	2.08	0.54
1:O:161:ASN:HD21	1:O:163:ARG:HB2	1.72	0.54
1:P:269:GLU:O	1:P:271:ARG:HD2	2.07	0.54
1:E:51:VAL:HG13	1:E:62:VAL:HG11	1.90	0.54
1:L:151:MET:HG2	1:L:184:LYS:HD3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:161:ASN:HD21	1:H:163:ARG:HB2	1.72	0.54
1:A:32:MET:HE2	1:A:47:ILE:HG22	1.90	0.54
1:H:255:LYS:O	1:H:259:GLU:HB2	2.07	0.54
1:B:94:PRO:HG3	1:C:125:ASP:HA	1.88	0.54
1:O:234:VAL:HG22	1:O:236:VAL:HG13	1.88	0.54
1:B:128:TRP:HA	1:B:131:TYR:CD1	2.43	0.54
1:K:32:MET:HE2	1:K:47:ILE:HG22	1.89	0.54
1:I:220:LEU:HD12	1:I:267:LEU:HD23	1.90	0.54
1:S:70:ARG:NH1	3:S:516:HOH:O	2.20	0.54
1:R:9:ASN:C	1:R:9:ASN:HD22	2.11	0.54
1:M:32:MET:HE2	1:M:47:ILE:HG22	1.90	0.54
1:I:161:ASN:HD21	1:I:163:ARG:HB2	1.71	0.54
1:R:79:ASP:N	3:R:510:HOH:O	2.41	0.54
1:E:165:PRO:HB3	1:E:193:SER:HB2	1.90	0.54
1:I:151:MET:HG2	1:I:184:LYS:HD3	1.89	0.54
1:F:153:TYR:OH	1:F:184:LYS:HE2	2.08	0.54
1:J:49:LYS:CB	3:J:508:HOH:O	2.55	0.54
1:C:153:TYR:OH	1:C:184:LYS:HE2	2.07	0.54
1:F:3:LEU:HD13	1:F:4:PHE:CZ	2.42	0.54
1:T:267:LEU:HD23	1:T:270:ILE:HD12	1.89	0.54
1:F:151:MET:HG2	1:F:184:LYS:HD3	1.90	0.54
1:N:221:GLN:OE1	1:N:263:VAL:HG21	2.08	0.54
1:K:228:GLU:HG3	3:K:507:HOH:O	2.08	0.54
1:C:234:VAL:HG22	1:C:236:VAL:HG13	1.89	0.53
1:N:31:PRO:CB	2:N:501:13P:H31	2.37	0.53
1:G:153:TYR:OH	1:G:184:LYS:HE2	2.07	0.53
1:C:215:THR:OG1	1:C:218:GLU:HG3	2.08	0.53
1:F:139:GLU:HG3	1:J:66:LYS:HE3	1.89	0.53
1:I:128:TRP:HA	1:I:131:TYR:CD1	2.43	0.53
1:H:32:MET:HE2	1:H:47:ILE:HG22	1.89	0.53
1:D:104:THR:HG23	1:E:136:MET:HE1	1.88	0.53
1:T:270:ILE:HG22	1:T:271:ARG:N	2.23	0.53
1:N:151:MET:HG2	1:N:184:LYS:HD3	1.90	0.53
1:R:263:VAL:CG1	1:R:267:LEU:HD23	2.38	0.53
1:D:29:ILE:O	1:D:235:ALA:HA	2.08	0.53
1:B:9:ASN:C	1:B:9:ASN:HD22	2.12	0.53
1:Q:161:ASN:HD21	1:Q:163:ARG:HB2	1.72	0.53
1:S:26:LYS:HD2	1:S:227:MET:HE1	1.91	0.53
1:B:151:MET:HG2	1:B:184:LYS:HD3	1.90	0.53
1:H:104:THR:HG23	1:I:136:MET:HE1	1.91	0.53
1:O:30:VAL:HG21	1:O:54:VAL:CG1	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:9:ASN:HD22	1:L:9:ASN:C	2.12	0.53
1:T:262:ASP:OD1	1:T:264:GLU:HB3	2.09	0.53
1:L:30:VAL:HG21	1:L:54:VAL:CG1	2.39	0.53
1:N:270:ILE:HG22	1:N:271:ARG:N	2.23	0.53
1:R:54:VAL:HG12	1:R:59:ALA:CB	2.38	0.53
1:B:4:PHE:CD1	1:B:16:LEU:HD13	2.43	0.53
1:R:53:ASP:HB3	1:R:247:VAL:CG2	2.38	0.53
1:J:161:ASN:HD21	1:J:163:ARG:HB2	1.74	0.53
1:L:128:TRP:HA	1:L:131:TYR:CD1	2.43	0.53
1:C:221:GLN:OE1	1:C:263:VAL:HG21	2.09	0.53
1:T:9:ASN:HD22	1:T:9:ASN:C	2.11	0.53
1:K:128:TRP:HA	1:K:131:TYR:CD1	2.43	0.53
1:O:9:ASN:C	1:O:9:ASN:HD22	2.12	0.53
1:H:128:TRP:HA	1:H:131:TYR:CD1	2.43	0.53
1:H:151:MET:HG2	1:H:184:LYS:HD3	1.91	0.53
1:C:30:VAL:HG21	1:C:54:VAL:HG13	1.91	0.53
1:C:31:PRO:CB	2:C:501:13P:H31	2.38	0.52
1:F:3:LEU:HB3	1:F:4:PHE:CD1	2.44	0.52
1:G:161:ASN:HD21	1:G:163:ARG:HB2	1.74	0.52
1:A:234:VAL:HG22	1:A:236:VAL:HG13	1.92	0.52
1:J:234:VAL:HG22	1:J:236:VAL:HG13	1.91	0.52
1:D:109:ILE:CD1	1:D:144:TRP:HB3	2.39	0.52
1:I:32:MET:HE2	1:I:47:ILE:HG22	1.91	0.52
1:Q:3:LEU:HD13	1:Q:4:PHE:CE1	2.44	0.52
1:O:153:TYR:OH	1:O:184:LYS:HE2	2.09	0.52
1:S:128:TRP:HA	1:S:131:TYR:CD1	2.44	0.52
1:M:30:VAL:HG11	1:M:54:VAL:HG21	1.91	0.52
1:J:251:ARG:HB3	1:J:269:GLU:HG2	1.91	0.52
1:E:153:TYR:OH	1:E:184:LYS:HE2	2.09	0.52
1:E:151:MET:HG2	1:E:184:LYS:HD3	1.90	0.52
1:D:128:TRP:HA	1:D:131:TYR:CD1	2.43	0.52
1:M:164:ASP:OD2	1:S:214:ASN:CB	2.57	0.52
1:F:161:ASN:HD21	1:F:163:ARG:HB2	1.75	0.52
1:T:24:SER:O	1:T:25:GLU:HB2	2.09	0.52
1:T:32:MET:HE2	1:T:47:ILE:HG22	1.90	0.52
1:G:31:PRO:CB	2:G:501:13P:H31	2.38	0.52
1:B:153:TYR:OH	1:B:184:LYS:HE2	2.09	0.52
1:M:262:ASP:OD2	1:M:264:GLU:HB3	2.10	0.52
1:R:128:TRP:HA	1:R:131:TYR:CD1	2.44	0.52
1:G:26:LYS:HD2	1:G:227:MET:HE1	1.92	0.52
1:T:153:TYR:OH	1:T:184:LYS:HE2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:259:GLU:O	1:K:260:ASN:HB2	2.09	0.52
1:H:26:LYS:HD2	1:H:227:MET:HE1	1.91	0.52
1:E:9:ASN:C	1:E:9:ASN:HD22	2.13	0.52
1:Q:29:ILE:O	1:Q:235:ALA:HA	2.09	0.52
1:P:165:PRO:HB3	1:P:193:SER:HB2	1.92	0.52
1:I:161:ASN:ND2	1:I:163:ARG:H	2.07	0.52
1:T:151:MET:HG2	1:T:184:LYS:HD3	1.91	0.52
1:M:9:ASN:HD22	1:M:9:ASN:C	2.13	0.52
1:E:128:TRP:HA	1:E:131:TYR:CD1	2.44	0.52
1:K:153:TYR:OH	1:K:184:LYS:HE2	2.09	0.52
1:Q:151:MET:HG2	1:Q:184:LYS:HD3	1.92	0.52
1:P:66:LYS:HD2	3:P:514:HOH:O	2.10	0.52
1:S:9:ASN:C	1:S:9:ASN:HD22	2.13	0.52
1:C:32:MET:HE2	1:C:47:ILE:HG22	1.91	0.52
1:C:9:ASN:HD22	1:C:9:ASN:C	2.12	0.52
1:K:109:ILE:CD1	1:K:144:TRP:HB3	2.40	0.52
1:D:215:THR:N	1:D:218:GLU:OE2	2.39	0.52
1:E:161:ASN:ND2	1:E:163:ARG:H	2.08	0.52
1:Q:252:ALA:O	1:Q:255:LYS:HB2	2.10	0.52
1:J:32:MET:HE2	1:J:47:ILE:HG22	1.91	0.52
1:N:65:HIS:HE1	3:N:516:HOH:O	1.93	0.52
1:Q:32:MET:HE2	1:Q:47:ILE:HG22	1.92	0.52
1:L:32:MET:HE2	1:L:47:ILE:HG22	1.91	0.52
1:H:165:PRO:HB3	1:H:193:SER:HB2	1.92	0.52
1:J:259:GLU:O	1:J:260:ASN:HB2	2.09	0.52
1:K:234:VAL:HG22	1:K:236:VAL:HG13	1.92	0.52
1:L:161:ASN:ND2	1:L:163:ARG:H	2.08	0.52
1:I:153:TYR:OH	1:I:184:LYS:HE2	2.09	0.52
1:H:220:LEU:HD12	1:H:267:LEU:CD2	2.40	0.52
1:R:21:ASN:HB3	1:R:24:SER:HG	1.74	0.52
1:G:128:TRP:HA	1:G:131:TYR:CD1	2.45	0.52
1:H:173:ARG:HG2	1:H:200:GLY:O	2.10	0.51
1:T:161:ASN:HD21	1:T:163:ARG:HB2	1.75	0.51
1:P:9:ASN:C	1:P:9:ASN:HD22	2.14	0.51
1:D:32:MET:HE2	1:D:47:ILE:HG22	1.92	0.51
1:N:71:HIS:N	1:N:71:HIS:ND1	2.58	0.51
1:K:161:ASN:ND2	1:K:163:ARG:H	2.08	0.51
1:J:209:GLY:HA3	3:J:510:HOH:O	2.11	0.51
1:R:220:LEU:HD12	1:R:267:LEU:HD11	1.91	0.51
1:T:30:VAL:HG11	1:T:54:VAL:HG21	1.93	0.51
1:A:109:ILE:CD1	1:A:144:TRP:HB3	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:54:VAL:HG12	1:R:59:ALA:HB3	1.91	0.51
1:N:263:VAL:O	1:N:267:LEU:HG	2.09	0.51
1:F:161:ASN:ND2	1:F:163:ARG:H	2.09	0.51
1:Q:71:HIS:O	1:R:6:ASP:OD2	2.28	0.51
1:B:170:HIS:HD2	3:B:509:HOH:O	1.94	0.51
1:R:30:VAL:HG21	1:R:54:VAL:HG13	1.93	0.51
1:S:161:ASN:ND2	1:S:163:ARG:H	2.08	0.51
1:J:151:MET:HG2	1:J:184:LYS:HD3	1.93	0.51
1:M:128:TRP:HA	1:M:131:TYR:CD1	2.46	0.51
1:Q:26:LYS:HD2	1:Q:227:MET:CE	2.41	0.51
1:O:2:GLU:HG3	1:O:3:LEU:N	2.26	0.51
1:A:263:VAL:HG23	1:A:264:GLU:H	1.76	0.51
1:J:153:TYR:OH	1:J:184:LYS:HE2	2.11	0.51
1:J:26:LYS:HD2	1:J:227:MET:HE1	1.93	0.51
1:G:109:ILE:CD1	1:G:144:TRP:HB3	2.41	0.51
1:G:9:ASN:HD22	1:G:9:ASN:C	2.13	0.51
1:K:9:ASN:C	1:K:9:ASN:HD22	2.13	0.51
1:D:26:LYS:HD2	1:D:227:MET:CE	2.41	0.51
1:P:3:LEU:HD23	1:P:3:LEU:O	2.11	0.51
1:B:161:ASN:ND2	1:B:163:ARG:H	2.09	0.51
1:B:136:MET:HA	1:B:136:MET:CE	2.29	0.51
1:R:32:MET:HE2	1:R:47:ILE:HG22	1.93	0.51
1:A:161:ASN:ND2	1:A:163:ARG:H	2.10	0.50
1:E:9:ASN:ND2	1:E:12:LYS:H	2.10	0.50
1:J:165:PRO:HB3	1:J:193:SER:HB2	1.93	0.50
1:I:53:ASP:O	1:I:56:GLU:HB3	2.10	0.50
1:I:109:ILE:CD1	1:I:144:TRP:HB3	2.41	0.50
1:R:161:ASN:ND2	1:R:163:ARG:H	2.08	0.50
1:P:161:ASN:ND2	1:P:163:ARG:H	2.09	0.50
1:S:115:ALA:HB2	1:S:147:PRO:HG2	1.93	0.50
1:S:109:ILE:CD1	1:S:144:TRP:HB3	2.39	0.50
1:M:165:PRO:HB3	1:M:193:SER:HB2	1.93	0.50
1:K:95:ASN:HD22	1:K:95:ASN:C	2.14	0.50
1:R:234:VAL:HG22	1:R:236:VAL:HG13	1.92	0.50
1:R:220:LEU:HD12	1:R:267:LEU:CD2	2.41	0.50
1:O:32:MET:HE2	1:O:47:ILE:HG22	1.92	0.50
1:Q:161:ASN:ND2	1:Q:163:ARG:H	2.09	0.50
1:Q:32:MET:HE1	1:Q:51:VAL:HG23	1.92	0.50
1:Q:71:HIS:HE1	3:R:513:HOH:O	1.94	0.50
1:Q:9:ASN:HD22	1:Q:9:ASN:C	2.14	0.50
1:A:30:VAL:HG21	1:A:54:VAL:HG11	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:216:ASP:OD2	1:F:270:ILE:HD13	2.11	0.50
1:G:54:VAL:HG13	1:G:55:ALA:N	2.26	0.50
1:N:153:TYR:OH	1:N:184:LYS:HE2	2.12	0.50
1:G:69:VAL:HG12	1:S:10:LEU:HD21	1.93	0.50
1:H:9:ASN:C	1:H:9:ASN:HD22	2.15	0.50
1:S:3:LEU:HD21	1:S:204:PRO:HB3	1.92	0.50
1:T:216:ASP:HB2	1:T:267:LEU:HD21	1.94	0.50
1:A:9:ASN:C	1:A:9:ASN:HD22	2.14	0.50
1:L:3:LEU:HD22	1:L:4:PHE:CZ	2.46	0.50
1:L:109:ILE:CD1	1:L:144:TRP:HB3	2.39	0.50
1:T:109:ILE:CD1	1:T:144:TRP:HB3	2.42	0.50
1:N:51:VAL:HG13	1:N:62:VAL:HG11	1.93	0.50
1:D:161:ASN:ND2	1:D:163:ARG:H	2.10	0.50
1:B:165:PRO:HB3	1:B:193:SER:HB2	1.94	0.50
1:T:251:ARG:HG2	1:T:269:GLU:OE1	2.12	0.50
1:D:219:PHE:CZ	1:D:223:ILE:HD11	2.47	0.50
1:Q:95:ASN:C	1:Q:95:ASN:HD22	2.15	0.50
1:M:153:TYR:OH	1:M:184:LYS:HE2	2.11	0.50
1:Q:3:LEU:HB3	1:Q:4:PHE:CD1	2.47	0.50
1:R:24:SER:O	1:R:26:LYS:HG2	2.11	0.50
1:N:71:HIS:CE1	3:N:505:HOH:O	2.63	0.50
1:C:128:TRP:HA	1:C:131:TYR:CD1	2.47	0.50
1:N:30:VAL:HG21	1:N:54:VAL:CG1	2.42	0.50
1:B:30:VAL:HG21	1:B:54:VAL:CG1	2.42	0.50
1:B:104:THR:HG23	1:C:136:MET:HE1	1.94	0.49
1:H:255:LYS:NZ	1:H:269:GLU:OE2	2.44	0.49
1:D:214:ASN:HB2	1:D:218:GLU:OE2	2.11	0.49
1:M:161:ASN:ND2	1:M:163:ARG:H	2.09	0.49
1:H:153:TYR:OH	1:H:184:LYS:HE2	2.11	0.49
1:K:54:VAL:HG13	1:K:59:ALA:HB2	1.93	0.49
1:P:30:VAL:CG2	1:P:54:VAL:HG11	2.40	0.49
1:Q:31:PRO:CB	2:Q:501:13P:H31	2.40	0.49
1:L:109:ILE:HD11	1:L:144:TRP:CB	2.42	0.49
1:I:26:LYS:HD2	1:I:227:MET:CE	2.43	0.49
1:I:9:ASN:C	1:I:9:ASN:HD22	2.15	0.49
1:F:9:ASN:C	1:F:9:ASN:HD22	2.15	0.49
1:O:267:LEU:HD23	1:O:270:ILE:HD12	1.95	0.49
1:Q:32:MET:CE	1:Q:51:VAL:HG23	2.43	0.49
1:Q:215:THR:OG1	1:Q:218:GLU:HG3	2.11	0.49
1:S:151:MET:HG2	1:S:184:LYS:HD3	1.92	0.49
1:R:215:THR:OG1	1:R:218:GLU:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:3:LEU:HD21	1:P:204:PRO:HG3	1.94	0.49
1:G:32:MET:HE2	1:G:47:ILE:HG22	1.94	0.49
1:A:153:TYR:OH	1:A:184:LYS:HE2	2.11	0.49
1:N:165:PRO:HB3	1:N:193:SER:HB2	1.94	0.49
1:H:3:LEU:HD21	1:H:204:PRO:HB3	1.94	0.49
1:R:153:TYR:OH	1:R:184:LYS:HE2	2.11	0.49
1:I:165:PRO:HB3	1:I:193:SER:HB2	1.93	0.49
1:R:165:PRO:HB3	1:R:193:SER:HB2	1.94	0.49
1:N:26:LYS:HD2	1:N:227:MET:HE1	1.95	0.49
1:P:153:TYR:OH	1:P:184:LYS:HE2	2.12	0.49
1:B:2:GLU:HA	1:B:25:GLU:OE2	2.12	0.49
1:T:95:ASN:C	1:T:95:ASN:HD22	2.16	0.49
1:K:220:LEU:HD12	1:K:267:LEU:CD2	2.43	0.49
1:K:31:PRO:CB	2:K:501:13P:H31	2.39	0.49
1:R:26:LYS:HD2	1:R:227:MET:CE	2.43	0.49
1:C:165:PRO:HB3	1:C:193:SER:HB2	1.94	0.49
1:B:31:PRO:CB	2:B:501:13P:H31	2.36	0.49
1:E:109:ILE:CD1	1:E:144:TRP:HB3	2.41	0.49
1:T:161:ASN:ND2	1:T:163:ARG:H	2.10	0.49
1:P:32:MET:HE2	1:P:47:ILE:HG22	1.94	0.49
1:R:23:GLU:CB	3:R:512:HOH:O	2.60	0.49
1:B:115:ALA:HB2	1:B:147:PRO:HG2	1.95	0.49
1:G:143:TYR:O	1:S:110:ARG:NH1	2.43	0.49
1:F:165:PRO:HB3	1:F:193:SER:HB2	1.94	0.49
1:O:26:LYS:HD2	1:O:227:MET:HE1	1.94	0.49
1:B:32:MET:HE2	1:B:47:ILE:HG22	1.94	0.49
1:Q:109:ILE:CD1	1:Q:144:TRP:HB3	2.42	0.49
1:T:21:ASN:HB2	1:T:258:HIS:CE1	2.47	0.49
1:B:95:ASN:C	1:B:95:ASN:HD22	2.16	0.49
1:M:31:PRO:CB	2:M:501:13P:H31	2.36	0.48
1:I:262:ASP:O	1:I:263:VAL:C	2.50	0.48
1:F:2:GLU:HG3	1:F:3:LEU:N	2.28	0.48
1:C:30:VAL:HG21	1:C:54:VAL:CG1	2.43	0.48
1:N:54:VAL:HG12	1:N:59:ALA:HB3	1.94	0.48
1:D:165:PRO:HB3	1:D:193:SER:HB2	1.95	0.48
1:A:26:LYS:HD2	1:A:227:MET:HE1	1.95	0.48
1:D:31:PRO:CB	2:D:501:13P:H31	2.41	0.48
1:J:31:PRO:CB	2:J:501:13P:H31	2.40	0.48
1:F:95:ASN:HD22	1:F:95:ASN:C	2.15	0.48
1:A:146:MET:SD	3:A:510:HOH:O	2.61	0.48
1:N:109:ILE:CD1	1:N:144:TRP:HB3	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:109:ILE:CD1	1:M:144:TRP:HB3	2.42	0.48
1:H:161:ASN:ND2	1:H:163:ARG:H	2.11	0.48
1:K:151:MET:HG2	1:K:184:LYS:HD3	1.94	0.48
1:I:9:ASN:ND2	1:I:12:LYS:H	2.11	0.48
1:Q:165:PRO:HB3	1:Q:193:SER:HB2	1.95	0.48
1:M:66:LYS:HE3	1:N:139:GLU:HG3	1.94	0.48
1:F:26:LYS:HD2	1:F:227:MET:CE	2.43	0.48
1:E:95:ASN:C	1:E:95:ASN:HD22	2.15	0.48
1:P:31:PRO:CB	2:P:501:13P:H31	2.42	0.48
1:G:161:ASN:ND2	1:G:163:ARG:H	2.11	0.48
1:E:30:VAL:HG11	1:E:54:VAL:HG21	1.95	0.48
1:J:9:ASN:C	1:J:9:ASN:HD22	2.17	0.48
1:D:104:THR:HG23	1:E:136:MET:CE	2.43	0.48
1:E:26:LYS:HD2	1:E:227:MET:CE	2.44	0.48
1:E:31:PRO:CB	2:E:501:13P:H31	2.40	0.48
1:F:54:VAL:HG12	1:F:59:ALA:HB3	1.94	0.48
1:L:26:LYS:HD2	1:L:227:MET:CE	2.43	0.48
1:N:21:ASN:HB3	1:N:24:SER:OG	2.13	0.48
1:M:30:VAL:HG21	1:M:54:VAL:CG1	2.43	0.48
1:H:24:SER:OG	1:H:258:HIS:HD2	1.96	0.48
1:C:95:ASN:HD22	1:C:95:ASN:C	2.14	0.48
1:I:31:PRO:CB	2:I:501:13P:H31	2.40	0.48
1:L:153:TYR:OH	1:L:184:LYS:HE2	2.13	0.48
1:F:219:PHE:CZ	1:F:223:ILE:HD11	2.49	0.48
1:G:95:ASN:C	1:G:95:ASN:HD22	2.17	0.48
1:A:30:VAL:HG21	1:A:54:VAL:CG1	2.44	0.48
1:I:26:LYS:HD2	1:I:227:MET:HE1	1.95	0.48
1:R:262:ASP:OD1	1:R:264:GLU:HB2	2.14	0.48
1:S:165:PRO:HB3	1:S:193:SER:HB2	1.96	0.48
1:D:95:ASN:HD22	1:D:95:ASN:C	2.16	0.48
1:J:95:ASN:C	1:J:95:ASN:HD22	2.17	0.48
1:F:136:MET:CE	1:F:136:MET:HA	2.30	0.48
1:Q:2:GLU:HA	1:Q:25:GLU:OE2	2.13	0.48
1:E:110:ARG:NH2	3:E:524:HOH:O	2.47	0.47
1:A:151:MET:HA	1:A:184:LYS:HB3	1.95	0.47
1:C:161:ASN:ND2	1:C:163:ARG:H	2.12	0.47
1:O:66:LYS:HD2	3:O:508:HOH:O	2.14	0.47
1:R:109:ILE:CD1	1:R:144:TRP:HB3	2.42	0.47
1:O:263:VAL:O	1:O:267:LEU:HD12	2.14	0.47
1:A:26:LYS:HD2	1:A:227:MET:CE	2.44	0.47
1:N:115:ALA:HB2	1:N:147:PRO:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:165:PRO:HB3	1:T:193:SER:HB2	1.95	0.47
1:K:26:LYS:HD2	1:K:227:MET:CE	2.44	0.47
1:A:151:MET:CG	1:A:184:LYS:HD3	2.44	0.47
1:P:94:PRO:HG3	1:Q:125:ASP:HA	1.96	0.47
1:O:165:PRO:HB3	1:O:193:SER:HB2	1.95	0.47
1:A:95:ASN:C	1:A:95:ASN:HD22	2.17	0.47
1:P:109:ILE:CD1	1:P:144:TRP:HB3	2.40	0.47
1:S:151:MET:HA	1:S:184:LYS:HB3	1.97	0.47
1:E:247:VAL:O	1:E:251:ARG:HB2	2.14	0.47
1:C:109:ILE:CD1	1:C:144:TRP:HB3	2.43	0.47
1:R:30:VAL:HG21	1:R:54:VAL:HG11	1.97	0.47
1:O:161:ASN:ND2	1:O:163:ARG:H	2.11	0.47
1:C:151:MET:HG2	1:C:184:LYS:HD3	1.96	0.47
1:A:9:ASN:ND2	1:A:12:LYS:H	2.13	0.47
1:F:18:ARG:NE	1:T:18:ARG:NE	2.62	0.47
1:P:139:GLU:HG3	1:T:66:LYS:HE3	1.97	0.47
1:B:254:CYS:O	1:B:258:HIS:HB2	2.14	0.47
1:M:95:ASN:C	1:M:95:ASN:HD22	2.17	0.47
1:R:95:ASN:HD22	1:R:95:ASN:C	2.18	0.47
1:H:251:ARG:HG2	1:H:269:GLU:OE1	2.14	0.47
1:F:263:VAL:HG12	1:F:267:LEU:CD1	2.45	0.47
1:Q:153:TYR:OH	1:Q:184:LYS:HE2	2.13	0.47
1:J:26:LYS:HD2	1:J:227:MET:CE	2.45	0.47
1:K:9:ASN:ND2	1:K:12:LYS:H	2.12	0.47
1:P:151:MET:HG2	1:P:184:LYS:HD3	1.96	0.47
1:O:31:PRO:CB	2:O:501:13P:H31	2.41	0.47
1:F:151:MET:HA	1:F:184:LYS:HB3	1.97	0.47
1:B:151:MET:HA	1:B:184:LYS:HB3	1.97	0.47
1:T:115:ALA:HB2	1:T:147:PRO:HG2	1.96	0.47
1:N:95:ASN:C	1:N:95:ASN:HD22	2.16	0.47
1:O:225:ASP:O	1:O:228:GLU:HB2	2.15	0.47
1:L:165:PRO:HB3	1:L:193:SER:HB2	1.96	0.47
1:B:220:LEU:HB3	1:B:256:ILE:HD11	1.97	0.47
1:P:95:ASN:C	1:P:95:ASN:HD22	2.17	0.47
1:G:109:ILE:HD11	1:G:144:TRP:CB	2.44	0.47
1:D:26:LYS:HD2	1:D:227:MET:HE1	1.97	0.47
1:H:115:ALA:HB2	1:H:147:PRO:HG2	1.96	0.47
1:R:2:GLU:HB3	1:R:25:GLU:OE2	2.15	0.47
1:S:31:PRO:CB	2:S:501:13P:H31	2.38	0.47
1:P:26:LYS:HD2	1:P:227:MET:CE	2.45	0.47
1:O:26:LYS:HD2	1:O:227:MET:CE	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:245:ASP:OD2	1:T:248:GLY:HA3	2.14	0.47
1:C:115:ALA:HB2	1:C:147:PRO:HG2	1.96	0.47
1:P:220:LEU:HD12	1:P:267:LEU:CD2	2.45	0.47
1:S:221:GLN:OE1	1:S:263:VAL:HG21	2.14	0.47
1:G:65:HIS:HE1	3:G:508:HOH:O	1.96	0.47
1:O:259:GLU:O	1:O:260:ASN:HB2	2.15	0.47
1:K:245:ASP:OD2	1:K:248:GLY:HA3	2.15	0.47
1:N:151:MET:HA	1:N:184:LYS:HB3	1.95	0.47
1:H:26:LYS:HD2	1:H:227:MET:CE	2.43	0.47
1:J:71:HIS:O	1:J:72:GLY:C	2.54	0.47
1:C:267:LEU:CD2	1:C:270:ILE:HD12	2.45	0.47
1:O:95:ASN:HD22	1:O:95:ASN:C	2.16	0.47
1:F:31:PRO:CB	2:F:501:13P:H31	2.39	0.46
1:K:271:ARG:HH11	1:K:271:ARG:CG	2.28	0.46
1:P:71:HIS:O	1:Q:6:ASP:OD2	2.33	0.46
1:M:151:MET:HA	1:M:184:LYS:HB3	1.97	0.46
1:C:151:MET:HA	1:C:184:LYS:HB3	1.97	0.46
1:O:9:ASN:ND2	1:O:12:LYS:H	2.12	0.46
1:J:9:ASN:ND2	1:J:12:LYS:H	2.13	0.46
1:J:69:VAL:C	1:J:71:HIS:H	2.19	0.46
1:G:259:GLU:O	1:G:260:ASN:HB2	2.15	0.46
1:G:165:PRO:HB3	1:G:193:SER:HB2	1.96	0.46
1:N:255:LYS:CB	3:N:517:HOH:O	2.64	0.46
1:L:225:ASP:O	1:L:228:GLU:HB2	2.15	0.46
1:S:95:ASN:C	1:S:95:ASN:HD22	2.18	0.46
1:J:109:ILE:CD1	1:J:144:TRP:HB3	2.43	0.46
1:O:109:ILE:CD1	1:O:144:TRP:HB3	2.42	0.46
1:E:2:GLU:HG3	1:E:3:LEU:N	2.29	0.46
1:N:30:VAL:HG21	1:N:54:VAL:HG11	1.96	0.46
1:A:165:PRO:HB3	1:A:193:SER:HB2	1.96	0.46
1:R:173:ARG:HG2	1:R:200:GLY:O	2.15	0.46
1:O:109:ILE:HD11	1:O:144:TRP:CB	2.45	0.46
1:D:271:ARG:HG3	1:D:271:ARG:HH11	1.80	0.46
1:C:254:CYS:O	1:C:258:HIS:HB2	2.15	0.46
1:J:161:ASN:ND2	1:J:163:ARG:H	2.13	0.46
1:T:151:MET:HA	1:T:184:LYS:HB3	1.97	0.46
1:A:220:LEU:CD1	1:A:267:LEU:HD23	2.41	0.46
1:H:31:PRO:CB	2:H:501:13P:H31	2.40	0.46
1:I:151:MET:HA	1:I:184:LYS:HB3	1.96	0.46
1:P:151:MET:HA	1:P:184:LYS:HB3	1.96	0.46
1:I:103:THR:HA	1:J:139:GLU:OE2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:GLU:HG2	3:E:524:HOH:O	2.15	0.46
1:S:9:ASN:ND2	1:S:12:LYS:H	2.12	0.46
1:J:151:MET:HA	1:J:184:LYS:HB3	1.96	0.46
1:C:26:LYS:HD2	1:C:227:MET:CE	2.45	0.46
1:S:71:HIS:CD2	3:S:515:HOH:O	2.68	0.46
1:B:109:ILE:CD1	1:B:144:TRP:HB3	2.43	0.46
1:F:109:ILE:CD1	1:F:144:TRP:HB3	2.42	0.46
1:S:26:LYS:HD2	1:S:227:MET:CE	2.46	0.46
1:H:221:GLN:OE1	1:H:263:VAL:HG21	2.15	0.46
1:K:165:PRO:HB3	1:K:193:SER:HB2	1.98	0.46
1:I:222:MET:HE1	1:I:223:ILE:HA	1.98	0.46
1:F:220:LEU:HD12	1:F:267:LEU:HD23	1.98	0.46
1:Q:151:MET:HA	1:Q:184:LYS:HB3	1.97	0.46
1:P:9:ASN:ND2	1:P:12:LYS:H	2.13	0.46
1:G:9:ASN:ND2	1:G:12:LYS:H	2.13	0.46
1:B:30:VAL:HG21	1:B:54:VAL:HG13	1.98	0.46
1:L:26:LYS:HD2	1:L:227:MET:HE1	1.98	0.46
1:K:71:HIS:HD2	3:L:516:HOH:O	1.99	0.46
1:M:4:PHE:HB3	1:M:7:ILE:HD12	1.98	0.46
1:E:99:LYS:HE2	3:E:515:HOH:O	2.15	0.46
1:T:52:ASN:O	1:T:55:ALA:HB3	2.16	0.46
1:F:225:ASP:O	1:F:228:GLU:HB2	2.15	0.46
1:O:160:GLN:HA	1:O:160:GLN:HE21	1.80	0.46
1:T:109:ILE:HD11	1:T:144:TRP:CB	2.43	0.46
1:L:54:VAL:HG13	1:L:59:ALA:HB2	1.97	0.46
1:L:151:MET:CG	1:L:184:LYS:HD3	2.46	0.46
1:T:9:ASN:ND2	1:T:12:LYS:H	2.14	0.46
1:I:151:MET:CG	1:I:184:LYS:HD3	2.46	0.46
1:N:151:MET:CG	1:N:184:LYS:HD3	2.46	0.46
1:O:151:MET:HA	1:O:184:LYS:HB3	1.97	0.46
1:F:259:GLU:O	1:F:260:ASN:HB2	2.15	0.46
1:I:173:ARG:HG2	1:I:200:GLY:O	2.15	0.46
1:K:109:ILE:HD11	1:K:144:TRP:CB	2.43	0.45
1:Q:26:LYS:HD2	1:Q:227:MET:HE1	1.98	0.45
1:G:110:ARG:NH1	1:S:143:TYR:O	2.48	0.45
1:F:30:VAL:HG21	1:F:54:VAL:HG13	1.98	0.45
1:F:131:TYR:OH	1:J:93:SER:HB2	2.16	0.45
1:B:4:PHE:CE1	1:B:16:LEU:HD13	2.51	0.45
1:R:42:LYS:O	1:R:242:GLN:HG2	2.16	0.45
1:R:219:PHE:CZ	1:R:223:ILE:HD11	2.52	0.45
1:F:160:GLN:HE21	1:F:160:GLN:HA	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:PRO:CB	2:A:501:13P:H31	2.40	0.45
1:J:109:ILE:HD11	1:J:144:TRP:CB	2.45	0.45
1:A:219:PHE:CZ	1:A:223:ILE:HD11	2.52	0.45
1:K:173:ARG:HG2	1:K:200:GLY:O	2.16	0.45
1:P:160:GLN:HE21	1:P:160:GLN:HA	1.81	0.45
1:R:9:ASN:ND2	1:R:12:LYS:H	2.14	0.45
1:M:115:ALA:HB2	1:M:147:PRO:HG2	1.99	0.45
1:L:115:ALA:HB2	1:L:147:PRO:HG2	1.98	0.45
1:P:173:ARG:HG2	1:P:200:GLY:O	2.16	0.45
1:D:221:GLN:OE1	1:D:263:VAL:HG21	2.15	0.45
1:S:160:GLN:HE21	1:S:160:GLN:HA	1.81	0.45
1:S:264:GLU:O	1:S:268:LYS:HG3	2.16	0.45
1:H:109:ILE:HD11	1:H:144:TRP:CB	2.44	0.45
1:H:109:ILE:CD1	1:H:144:TRP:HB3	2.42	0.45
1:Q:43:GLY:O	1:Q:50:THR:OG1	2.29	0.45
1:S:225:ASP:O	1:S:228:GLU:HB2	2.17	0.45
1:A:118:ILE:HG21	1:A:134:LEU:HD13	1.98	0.45
1:H:95:ASN:HD22	1:H:95:ASN:C	2.19	0.45
1:S:265:GLU:HA	1:S:268:LYS:HD2	1.99	0.45
1:E:109:ILE:HD11	1:E:144:TRP:CB	2.44	0.45
1:F:220:LEU:HD12	1:F:267:LEU:CD2	2.47	0.45
1:L:9:ASN:ND2	1:L:12:LYS:H	2.14	0.45
1:T:225:ASP:O	1:T:228:GLU:HB2	2.16	0.45
1:E:115:ALA:HB2	1:E:147:PRO:HG2	1.97	0.45
1:K:115:ALA:HB2	1:K:147:PRO:HG2	1.99	0.45
1:I:160:GLN:HE21	1:I:160:GLN:HA	1.81	0.45
1:R:220:LEU:HB3	1:R:256:ILE:HD11	1.98	0.45
1:T:30:VAL:HG21	1:T:54:VAL:HG22	1.95	0.45
1:S:109:ILE:HD11	1:S:144:TRP:CB	2.43	0.45
1:P:3:LEU:HD23	1:P:3:LEU:C	2.37	0.45
1:K:225:ASP:O	1:K:228:GLU:HB2	2.16	0.45
1:C:9:ASN:ND2	1:C:12:LYS:H	2.14	0.45
1:F:170:HIS:HD2	3:F:521:HOH:O	1.99	0.45
1:C:225:ASP:O	1:C:228:GLU:HB2	2.16	0.45
1:B:66:LYS:HE3	1:C:139:GLU:HG3	1.97	0.45
1:G:173:ARG:HG2	1:G:200:GLY:O	2.17	0.45
1:D:225:ASP:O	1:D:228:GLU:HB2	2.16	0.45
1:H:104:THR:HG23	1:I:136:MET:CE	2.46	0.45
1:J:251:ARG:CB	1:J:269:GLU:HG2	2.46	0.45
3:L:514:HOH:O	1:M:136:MET:CE	2.65	0.45
1:E:245:ASP:OD2	1:E:248:GLY:HA3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:MET:CE	1:A:257:VAL:HG13	2.47	0.45
1:R:58:GLY:HA3	1:R:254:CYS:SG	2.56	0.45
1:L:173:ARG:HD3	1:L:177:GLU:HG2	1.99	0.45
1:P:225:ASP:O	1:P:228:GLU:HB2	2.17	0.45
1:H:49:LYS:O	1:H:52:ASN:HB3	2.17	0.45
1:P:3:LEU:N	1:P:25:GLU:OE1	2.50	0.45
1:R:3:LEU:O	1:R:3:LEU:CD2	2.65	0.45
1:J:32:MET:CE	1:J:51:VAL:HG23	2.47	0.45
1:I:70:ARG:C	1:I:71:HIS:HD2	2.20	0.45
1:F:215:THR:HG23	1:F:218:GLU:OE2	2.17	0.45
1:N:109:ILE:HD11	1:N:144:TRP:CB	2.45	0.45
1:E:151:MET:HA	1:E:184:LYS:HB3	1.99	0.45
1:A:227:MET:HE1	1:A:257:VAL:HG13	1.99	0.45
1:L:21:ASN:HB3	1:L:24:SER:OG	2.17	0.45
1:F:265:GLU:HA	1:F:268:LYS:HD2	1.99	0.45
1:N:245:ASP:OD2	1:N:248:GLY:HA3	2.17	0.45
1:P:115:ALA:HB2	1:P:147:PRO:HG2	1.98	0.45
1:N:160:GLN:HE21	1:N:160:GLN:HA	1.81	0.45
1:R:220:LEU:HD13	1:R:267:LEU:HD22	1.99	0.45
1:S:32:MET:HE2	1:S:47:ILE:HG22	1.99	0.45
1:K:245:ASP:CG	1:K:271:ARG:HH11	2.20	0.45
1:G:151:MET:HA	1:G:184:LYS:HB3	1.98	0.45
1:S:227:MET:CE	1:S:257:VAL:HG13	2.47	0.45
1:H:9:ASN:ND2	1:H:12:LYS:H	2.14	0.45
1:O:115:ALA:HB2	1:O:147:PRO:HG2	1.99	0.45
1:P:136:MET:HA	1:P:136:MET:CE	2.31	0.44
1:R:109:ILE:HD11	1:R:144:TRP:CB	2.46	0.44
1:O:151:MET:HG2	1:O:184:LYS:HD3	1.99	0.44
1:M:54:VAL:HG13	1:M:59:ALA:HB2	1.99	0.44
1:N:26:LYS:HD2	1:N:227:MET:CE	2.47	0.44
1:D:36:VAL:O	1:E:170:HIS:HE1	2.00	0.44
1:H:66:LYS:HE3	1:I:139:GLU:HG3	1.99	0.44
1:S:222:MET:HE1	1:S:223:ILE:HA	1.99	0.44
1:N:173:ARG:HG2	1:N:200:GLY:O	2.16	0.44
1:R:225:ASP:O	1:R:228:GLU:HB2	2.17	0.44
1:M:26:LYS:HD2	1:M:227:MET:CE	2.47	0.44
1:R:160:GLN:HA	1:R:160:GLN:HE21	1.82	0.44
1:S:104:THR:HG23	1:T:136:MET:CE	2.42	0.44
1:R:151:MET:HA	1:R:184:LYS:HB3	1.99	0.44
1:H:225:ASP:O	1:H:228:GLU:HB2	2.17	0.44
1:A:255:LYS:O	1:A:259:GLU:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:512:HOH:O	1:T:10:LEU:HD11	2.18	0.44
1:L:245:ASP:OD2	1:L:248:GLY:HA3	2.17	0.44
1:N:263:VAL:HG23	3:N:515:HOH:O	2.18	0.44
1:H:151:MET:HA	1:H:184:LYS:HB3	1.99	0.44
1:D:24:SER:O	1:D:26:LYS:HG2	2.17	0.44
1:E:26:LYS:HD2	1:E:227:MET:HE1	1.99	0.44
1:T:219:PHE:CZ	1:T:223:ILE:HD11	2.52	0.44
1:C:104:THR:HG23	1:D:136:MET:CE	2.48	0.44
1:L:3:LEU:HD21	1:L:204:PRO:CB	2.47	0.44
1:D:160:GLN:HA	1:D:160:GLN:HE21	1.83	0.44
1:S:151:MET:CG	1:S:184:LYS:HD3	2.48	0.44
1:R:151:MET:CG	1:R:184:LYS:HD3	2.47	0.44
1:B:9:ASN:ND2	1:B:12:LYS:H	2.16	0.44
1:A:170:HIS:HE1	1:E:36:VAL:O	2.00	0.44
1:B:26:LYS:HD2	1:B:227:MET:HE1	2.00	0.44
1:E:219:PHE:CZ	1:E:223:ILE:HD11	2.53	0.44
1:G:104:THR:HG23	1:H:136:MET:HE1	2.00	0.44
1:R:220:LEU:CD1	1:R:267:LEU:HD22	2.48	0.44
1:D:9:ASN:ND2	1:D:12:LYS:H	2.16	0.44
1:M:54:VAL:HG13	1:M:59:ALA:CB	2.48	0.44
1:Q:9:ASN:ND2	1:Q:12:LYS:H	2.16	0.44
1:B:26:LYS:HD2	1:B:227:MET:CE	2.48	0.44
1:J:22:ARG:NH2	3:J:504:HOH:O	2.45	0.44
1:I:95:ASN:C	1:I:95:ASN:HD22	2.19	0.44
1:T:47:ILE:O	1:T:51:VAL:HG23	2.17	0.44
1:J:219:PHE:CZ	1:J:223:ILE:HD11	2.53	0.44
1:E:225:ASP:O	1:E:228:GLU:HB2	2.17	0.44
1:R:3:LEU:O	1:R:3:LEU:HD22	2.17	0.44
1:D:151:MET:HA	1:D:184:LYS:HB3	2.00	0.44
1:M:160:GLN:HE21	1:M:160:GLN:HA	1.83	0.44
1:M:236:VAL:CG2	1:M:240:ILE:HG13	2.47	0.44
1:L:95:ASN:HD22	1:L:95:ASN:C	2.21	0.44
1:J:225:ASP:O	1:J:228:GLU:HB2	2.17	0.44
1:F:26:LYS:HD2	1:F:227:MET:HE1	1.99	0.44
1:I:219:PHE:CZ	1:I:223:ILE:HD11	2.53	0.44
1:I:225:ASP:O	1:I:228:GLU:HB2	2.17	0.44
1:R:34:HIS:HB2	1:R:44:LEU:CD1	2.48	0.44
1:D:245:ASP:OD2	1:D:248:GLY:HA3	2.17	0.44
1:B:42:LYS:O	1:B:242:GLN:HG2	2.18	0.44
1:E:160:GLN:HE21	1:E:160:GLN:HA	1.82	0.44
1:T:31:PRO:CB	2:T:501:13P:H31	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:109:ILE:HD11	1:D:144:TRP:CB	2.45	0.44
1:F:109:ILE:HD11	1:F:144:TRP:CB	2.46	0.44
1:O:265:GLU:HA	1:O:268:LYS:CE	2.45	0.44
1:C:26:LYS:HD2	1:C:227:MET:HE1	2.00	0.44
1:N:225:ASP:O	1:N:228:GLU:HB2	2.18	0.44
1:B:219:PHE:CZ	1:B:223:ILE:HD11	2.53	0.44
1:K:118:ILE:HG21	1:K:134:LEU:HD13	2.00	0.44
1:Q:219:PHE:CZ	1:Q:223:ILE:HD11	2.53	0.44
1:Q:245:ASP:OD2	1:Q:248:GLY:HA3	2.17	0.44
1:H:160:GLN:HE21	1:H:160:GLN:HA	1.83	0.44
1:C:104:THR:HG23	1:D:136:MET:HE1	2.00	0.43
1:E:136:MET:HA	1:E:136:MET:CE	2.27	0.43
1:G:36:VAL:O	1:H:170:HIS:HE1	2.01	0.43
1:R:2:GLU:O	1:R:2:GLU:HG3	2.16	0.43
1:Q:115:ALA:HB2	1:Q:147:PRO:HG2	1.99	0.43
1:G:225:ASP:O	1:G:228:GLU:HB2	2.18	0.43
1:G:236:VAL:CG2	1:G:240:ILE:HG13	2.48	0.43
1:P:245:ASP:OD2	1:P:248:GLY:HA3	2.17	0.43
1:B:215:THR:O	1:B:218:GLU:HB2	2.17	0.43
1:F:173:ARG:HG2	1:F:200:GLY:O	2.19	0.43
1:A:160:GLN:HE21	1:A:160:GLN:HA	1.84	0.43
1:J:160:GLN:HE21	1:J:160:GLN:HA	1.82	0.43
1:K:151:MET:HA	1:K:184:LYS:HB3	2.00	0.43
1:B:225:ASP:O	1:B:228:GLU:HB2	2.17	0.43
1:C:219:PHE:CZ	1:C:223:ILE:HD11	2.54	0.43
1:B:245:ASP:OD2	1:B:248:GLY:HA3	2.17	0.43
1:F:115:ALA:HB2	1:F:147:PRO:HG2	2.01	0.43
1:N:110:ARG:NH1	3:N:509:HOH:O	2.28	0.43
1:B:151:MET:CG	1:B:184:LYS:HD3	2.48	0.43
1:M:9:ASN:ND2	1:M:12:LYS:H	2.16	0.43
1:N:26:LYS:HE3	3:N:510:HOH:O	2.18	0.43
1:I:115:ALA:HB2	1:I:147:PRO:HG2	1.99	0.43
1:K:222:MET:HE2	1:K:223:ILE:HA	2.00	0.43
1:S:264:GLU:O	1:S:267:LEU:HB2	2.19	0.43
1:G:26:LYS:HD2	1:G:227:MET:CE	2.48	0.43
1:H:3:LEU:O	1:H:3:LEU:HD23	2.19	0.43
1:A:115:ALA:HB2	1:A:147:PRO:HG2	2.00	0.43
1:N:236:VAL:CG2	1:N:240:ILE:HG13	2.48	0.43
1:E:251:ARG:NH1	1:E:269:GLU:OE1	2.51	0.43
1:G:151:MET:CG	1:G:184:LYS:HD3	2.48	0.43
1:L:151:MET:HA	1:L:184:LYS:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:69:VAL:C	1:K:71:HIS:H	2.20	0.43
1:G:115:ALA:HB2	1:G:147:PRO:HG2	2.01	0.43
1:J:3:LEU:HD13	1:J:4:PHE:CZ	2.53	0.43
1:T:2:GLU:OE2	1:T:2:GLU:HA	2.18	0.43
1:F:103:THR:HA	1:G:139:GLU:OE2	2.19	0.43
1:K:265:GLU:HA	1:K:268:LYS:HZ2	1.83	0.43
1:S:42:LYS:O	1:S:242:GLN:HG2	2.19	0.43
1:T:83:ILE:HD13	1:T:149:ILE:CD1	2.49	0.43
1:H:245:ASP:OD2	1:H:248:GLY:HA3	2.19	0.43
1:C:49:LYS:HG2	1:C:53:ASP:OD2	2.19	0.43
1:N:103:THR:HA	1:O:139:GLU:OE2	2.17	0.43
1:A:225:ASP:O	1:A:228:GLU:HB2	2.18	0.43
1:T:151:MET:CG	1:T:184:LYS:HD3	2.48	0.43
1:D:95:ASN:HB2	3:D:510:HOH:O	2.18	0.43
1:J:69:VAL:CG1	1:P:10:LEU:HD21	2.49	0.43
1:M:42:LYS:O	1:M:242:GLN:HG2	2.18	0.43
1:M:219:PHE:CZ	1:M:223:ILE:HD11	2.54	0.43
1:C:160:GLN:HA	1:C:160:GLN:HE21	1.84	0.43
1:T:236:VAL:CG2	1:T:240:ILE:HG13	2.49	0.43
1:S:54:VAL:HG12	1:S:59:ALA:CB	2.47	0.43
1:H:83:ILE:HD13	1:H:149:ILE:CD1	2.49	0.43
1:F:118:ILE:HG21	1:F:134:LEU:HD13	2.01	0.43
1:K:245:ASP:OD1	1:K:271:ARG:NH1	2.51	0.43
1:N:9:ASN:ND2	1:N:12:LYS:H	2.17	0.43
1:M:151:MET:CG	1:M:184:LYS:HD3	2.48	0.43
1:M:34:HIS:HA	3:M:509:HOH:O	2.19	0.43
1:D:151:MET:CG	1:D:184:LYS:HD3	2.48	0.42
1:C:267:LEU:HD23	1:C:270:ILE:CD1	2.49	0.42
1:T:26:LYS:HD2	1:T:227:MET:CE	2.48	0.42
1:S:173:ARG:HG2	1:S:200:GLY:O	2.19	0.42
1:P:222:MET:HE1	1:P:223:ILE:HA	2.01	0.42
1:O:42:LYS:O	1:O:242:GLN:HG2	2.19	0.42
1:G:160:GLN:HA	1:G:160:GLN:HE21	1.84	0.42
1:B:173:ARG:HG2	1:B:200:GLY:O	2.18	0.42
1:F:4:PHE:CD2	1:F:16:LEU:HD13	2.55	0.42
1:E:259:GLU:O	1:E:260:ASN:HB2	2.19	0.42
1:Q:151:MET:CG	1:Q:184:LYS:HD3	2.49	0.42
1:R:26:LYS:HD2	1:R:227:MET:HE1	2.01	0.42
1:B:90:THR:HG23	1:C:131:TYR:CE1	2.53	0.42
1:A:222:MET:HE2	1:A:223:ILE:HA	2.00	0.42
1:Q:223:ILE:HG22	1:Q:256:ILE:HG21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:245:ASP:OD2	1:I:248:GLY:HA3	2.19	0.42
1:B:160:GLN:HE21	1:B:160:GLN:HA	1.83	0.42
1:P:42:LYS:O	1:P:242:GLN:HG2	2.19	0.42
1:Q:36:VAL:O	1:R:170:HIS:HE1	2.02	0.42
1:E:151:MET:CG	1:E:184:LYS:HD3	2.48	0.42
1:A:36:VAL:O	1:B:170:HIS:HE1	2.01	0.42
1:A:173:ARG:HG2	1:A:200:GLY:O	2.20	0.42
1:Q:225:ASP:O	1:Q:228:GLU:HB2	2.19	0.42
1:L:7:ILE:HG22	1:L:7:ILE:O	2.18	0.42
1:L:102:VAL:C	3:L:514:HOH:O	2.57	0.42
1:N:214:ASN:N	1:N:214:ASN:ND2	2.66	0.42
1:G:10:LEU:HD21	1:S:69:VAL:CG1	2.47	0.42
1:E:99:LYS:CE	3:E:515:HOH:O	2.67	0.42
1:M:245:ASP:OD2	1:M:248:GLY:HA3	2.19	0.42
1:P:26:LYS:HD2	1:P:227:MET:HE1	2.01	0.42
1:Q:26:LYS:HE3	3:Q:506:HOH:O	2.19	0.42
1:L:54:VAL:HG23	1:L:246:VAL:CG1	2.50	0.42
1:N:193:SER:O	1:N:196:ASP:HB2	2.20	0.42
1:A:24:SER:O	1:A:26:LYS:HG2	2.19	0.42
1:P:108:ALA:HA	1:P:111:MET:HE2	2.00	0.42
3:H:508:HOH:O	1:R:110:ARG:HD3	2.20	0.42
1:F:42:LYS:O	1:F:242:GLN:HG2	2.20	0.42
1:D:222:MET:HE2	1:D:223:ILE:HA	2.01	0.42
1:L:24:SER:O	1:L:26:LYS:HG2	2.20	0.42
1:J:222:MET:HE2	1:J:223:ILE:HA	2.01	0.42
1:H:219:PHE:CZ	1:H:223:ILE:HD11	2.54	0.42
1:K:42:LYS:O	1:K:242:GLN:HG2	2.19	0.42
1:P:66:LYS:HE3	1:Q:139:GLU:HG3	2.02	0.42
1:L:47:ILE:HD12	1:L:68:ILE:HG23	2.02	0.42
1:D:173:ARG:HG2	1:D:200:GLY:O	2.19	0.42
1:G:42:LYS:O	1:G:242:GLN:HG2	2.20	0.42
1:P:249:ILE:O	1:P:253:VAL:HG23	2.19	0.42
1:L:160:GLN:HE21	1:L:160:GLN:HA	1.84	0.42
1:L:31:PRO:CB	2:L:501:13P:H31	2.42	0.42
1:F:151:MET:CG	1:F:184:LYS:HD3	2.49	0.42
1:O:173:ARG:HG2	1:O:200:GLY:O	2.20	0.42
1:L:34:HIS:HB2	1:L:44:LEU:CD1	2.50	0.42
1:I:170:HIS:HD2	3:I:514:HOH:O	2.01	0.42
1:T:108:ALA:HA	1:T:111:MET:HE2	2.01	0.42
1:Q:160:GLN:HE21	1:Q:160:GLN:HA	1.84	0.42
1:T:160:GLN:HA	1:T:160:GLN:HE21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:3:LEU:HD21	1:P:204:PRO:HB3	2.02	0.42
1:O:206:VAL:HG11	1:O:235:ALA:HB2	2.02	0.42
1:Q:47:ILE:HD12	1:Q:68:ILE:HG23	2.01	0.42
1:G:245:ASP:OD2	1:G:248:GLY:HA3	2.20	0.42
1:H:16:LEU:HD23	1:H:19:ILE:HD11	2.02	0.42
1:O:16:LEU:HD23	1:O:19:ILE:HD11	2.02	0.42
1:O:255:LYS:CD	1:O:259:GLU:OE1	2.60	0.42
1:J:213:THR:HB	1:J:218:GLU:OE1	2.20	0.42
1:R:210:GLY:HA3	3:R:517:HOH:O	2.19	0.42
1:G:47:ILE:HD12	1:G:68:ILE:HG23	2.02	0.42
1:T:262:ASP:OD1	1:T:264:GLU:N	2.53	0.42
1:K:151:MET:CG	1:K:184:LYS:HD3	2.50	0.42
1:J:69:VAL:HG12	1:P:10:LEU:CD2	2.50	0.42
1:S:219:PHE:CZ	1:S:223:ILE:HD11	2.55	0.42
1:T:26:LYS:HD2	1:T:227:MET:HE1	2.02	0.42
1:P:219:PHE:CZ	1:P:223:ILE:HD11	2.55	0.42
1:G:16:LEU:HD23	1:G:19:ILE:HD11	2.02	0.42
1:B:21:ASN:HB3	1:B:24:SER:OG	2.19	0.42
1:E:21:ASN:HB2	1:E:258:HIS:CE1	2.55	0.42
1:O:262:ASP:OD1	1:O:264:GLU:HB3	2.20	0.42
1:D:255:LYS:HD2	1:D:259:GLU:OE1	2.20	0.42
1:H:55:ALA:C	1:H:57:GLY:H	2.22	0.42
1:J:173:ARG:HG2	1:J:200:GLY:O	2.19	0.42
1:A:79:ASP:OD1	1:A:79:ASP:O	2.37	0.42
1:I:109:ILE:HD11	1:I:144:TRP:CB	2.46	0.41
1:K:47:ILE:HD12	1:K:68:ILE:HG23	2.01	0.41
1:Q:4:PHE:CD2	1:Q:7:ILE:HD12	2.54	0.41
1:J:32:MET:HE1	1:J:51:VAL:HG23	2.02	0.41
1:D:271:ARG:NH1	1:D:271:ARG:HG3	2.34	0.41
1:K:219:PHE:CZ	1:K:223:ILE:HD11	2.55	0.41
1:C:18:ARG:NE	1:M:18:ARG:NE	2.67	0.41
1:R:115:ALA:HB2	1:R:147:PRO:HG2	2.01	0.41
1:B:101:ILE:O	1:C:132:ARG:NH1	2.50	0.41
1:K:104:THR:HG23	1:L:136:MET:CE	2.50	0.41
1:D:236:VAL:CG2	1:D:240:ILE:HG13	2.50	0.41
1:K:236:VAL:CG2	1:K:240:ILE:HG13	2.50	0.41
1:A:136:MET:CE	1:E:104:THR:HG23	2.47	0.41
1:F:54:VAL:HG12	1:F:59:ALA:CB	2.49	0.41
1:H:220:LEU:HD12	1:H:267:LEU:HD23	2.02	0.41
1:T:118:ILE:HG21	1:T:134:LEU:HD13	2.02	0.41
1:H:2:GLU:OE2	1:H:25:GLU:OE2	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:245:ASP:OD2	1:F:248:GLY:HA3	2.20	0.41
1:C:151:MET:CG	1:C:184:LYS:HD3	2.50	0.41
1:O:151:MET:CG	1:O:184:LYS:HD3	2.50	0.41
1:P:34:HIS:HB2	1:P:44:LEU:CD1	2.50	0.41
1:L:118:ILE:HG21	1:L:134:LEU:HD13	2.02	0.41
1:Q:251:ARG:HG2	1:Q:269:GLU:OE1	2.20	0.41
1:G:35:GLY:C	3:G:518:HOH:O	2.58	0.41
1:E:95:ASN:C	1:E:95:ASN:ND2	2.74	0.41
1:J:69:VAL:C	1:J:71:HIS:N	2.73	0.41
1:F:215:THR:HG1	1:F:218:GLU:HG3	1.85	0.41
1:M:222:MET:HE2	1:M:223:ILE:HA	2.03	0.41
1:B:108:ALA:HA	1:B:111:MET:HE2	2.02	0.41
1:S:16:LEU:HD23	1:S:19:ILE:HD11	2.02	0.41
1:F:108:ALA:HA	1:F:111:MET:HE3	2.03	0.41
1:I:30:VAL:HG11	1:I:54:VAL:HG21	2.02	0.41
1:Q:222:MET:HE2	1:Q:223:ILE:HA	2.02	0.41
1:N:66:LYS:HE3	1:O:139:GLU:HG3	2.01	0.41
1:D:118:ILE:HG21	1:D:134:LEU:HD13	2.02	0.41
1:C:245:ASP:OD2	1:C:248:GLY:HA3	2.20	0.41
1:L:219:PHE:CZ	1:L:223:ILE:HD11	2.54	0.41
1:E:42:LYS:O	1:E:242:GLN:HG2	2.19	0.41
1:L:3:LEU:O	1:L:3:LEU:HD23	2.19	0.41
1:S:214:ASN:CB	3:S:505:HOH:O	2.69	0.41
1:J:47:ILE:HD12	1:J:68:ILE:HG23	2.03	0.41
1:Q:95:ASN:ND2	1:Q:95:ASN:C	2.74	0.41
1:L:222:MET:HE1	1:L:223:ILE:HA	2.02	0.41
1:Q:42:LYS:O	1:Q:242:GLN:HG2	2.21	0.41
1:C:42:LYS:O	1:C:242:GLN:HG2	2.21	0.41
1:G:118:ILE:HG21	1:G:134:LEU:HD13	2.02	0.41
1:L:136:MET:CE	1:L:136:MET:HA	2.28	0.41
1:C:109:ILE:HD11	1:C:144:TRP:CB	2.44	0.41
1:F:215:THR:OG1	1:F:218:GLU:HG3	2.20	0.41
1:D:42:LYS:O	1:D:242:GLN:HG2	2.20	0.41
1:I:108:ALA:HA	1:I:111:MET:HE3	2.01	0.41
1:K:249:ILE:O	1:K:253:VAL:HG23	2.21	0.41
1:M:118:ILE:HG21	1:M:134:LEU:HD13	2.02	0.41
1:G:219:PHE:CZ	1:G:223:ILE:HD11	2.55	0.41
1:Q:3:LEU:HD13	1:Q:4:PHE:CZ	2.56	0.41
1:B:103:THR:HA	1:C:139:GLU:OE2	2.21	0.41
1:O:219:PHE:CZ	1:O:223:ILE:HD11	2.55	0.41
1:D:115:ALA:HB2	1:D:147:PRO:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:3:LEU:HD21	1:L:204:PRO:HB3	2.03	0.41
1:E:248:GLY:O	1:E:251:ARG:HB3	2.21	0.41
1:A:109:ILE:HD11	1:A:144:TRP:CB	2.44	0.41
1:P:109:ILE:HD11	1:P:144:TRP:CB	2.44	0.41
1:G:10:LEU:CD2	1:S:69:VAL:HG12	2.50	0.41
1:F:95:ASN:ND2	1:F:95:ASN:C	2.74	0.41
1:C:95:ASN:C	1:C:95:ASN:ND2	2.73	0.41
1:K:139:GLU:HG3	1:O:66:LYS:HE3	2.02	0.41
1:N:95:ASN:ND2	1:N:95:ASN:C	2.74	0.41
1:K:83:ILE:HA	1:K:115:ALA:O	2.21	0.41
1:M:34:HIS:HB2	1:M:44:LEU:CD1	2.51	0.41
1:H:36:VAL:O	1:I:170:HIS:HE1	2.04	0.41
1:O:222:MET:HE1	1:O:223:ILE:HA	2.03	0.41
1:J:34:HIS:HB2	1:J:44:LEU:CD1	2.51	0.41
1:G:83:ILE:HD13	1:G:149:ILE:HD12	2.02	0.41
1:R:245:ASP:OD2	1:R:248:GLY:HA3	2.20	0.41
1:D:34:HIS:HB2	1:D:44:LEU:CD1	2.51	0.41
1:G:83:ILE:HD13	1:G:149:ILE:CD1	2.50	0.41
1:T:42:LYS:O	1:T:242:GLN:HG2	2.21	0.41
1:M:225:ASP:O	1:M:228:GLU:HB2	2.20	0.41
1:M:109:ILE:HD11	1:M:144:TRP:CB	2.46	0.41
1:C:267:LEU:HD23	1:C:270:ILE:HD12	2.02	0.41
1:B:222:MET:HE2	1:B:223:ILE:HA	2.02	0.41
1:C:222:MET:HE1	1:C:223:ILE:HA	2.02	0.41
1:L:34:HIS:HB2	1:L:44:LEU:HD12	2.03	0.41
1:P:34:HIS:HB2	1:P:44:LEU:HD12	2.02	0.41
1:N:219:PHE:CZ	1:N:223:ILE:HD11	2.56	0.41
1:O:108:ALA:HA	1:O:111:MET:HE2	2.03	0.41
1:K:26:LYS:HD2	1:K:227:MET:HE1	2.03	0.40
1:Q:109:ILE:HD11	1:Q:144:TRP:CB	2.46	0.40
1:I:47:ILE:HD12	1:I:68:ILE:HG23	2.02	0.40
1:P:151:MET:CG	1:P:184:LYS:HD3	2.51	0.40
1:O:70:ARG:NH1	3:O:508:HOH:O	2.52	0.40
1:K:69:VAL:C	1:K:71:HIS:N	2.75	0.40
1:R:222:MET:HE2	1:R:223:ILE:HA	2.04	0.40
1:S:245:ASP:OD2	1:S:248:GLY:HA3	2.21	0.40
1:R:108:ALA:HA	1:R:111:MET:HE2	2.02	0.40
1:M:65:HIS:CD2	3:M:502:HOH:O	2.74	0.40
1:I:101:ILE:O	1:J:132:ARG:NH1	2.53	0.40
1:M:236:VAL:HG23	1:M:240:ILE:HG13	2.03	0.40
1:B:109:ILE:HD11	1:B:144:TRP:CB	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:54:VAL:HG12	1:O:59:ALA:HB3	2.02	0.40
1:A:206:VAL:HG11	1:A:235:ALA:HB2	2.03	0.40
1:H:151:MET:CG	1:H:184:LYS:HD3	2.50	0.40
1:F:69:VAL:C	1:F:71:HIS:N	2.75	0.40
1:C:236:VAL:CG2	1:C:240:ILE:HG13	2.50	0.40
1:R:53:ASP:CB	1:R:247:VAL:HG22	2.49	0.40
1:L:21:ASN:HB2	1:L:258:HIS:CE1	2.57	0.40
1:J:69:VAL:HG12	1:P:10:LEU:HD21	2.03	0.40
1:I:71:HIS:CD2	1:I:71:HIS:N	2.87	0.40
1:M:24:SER:O	1:M:26:LYS:HG2	2.21	0.40
1:R:34:HIS:HB2	1:R:44:LEU:HD12	2.02	0.40
1:F:71:HIS:CE1	3:F:520:HOH:O	2.74	0.40
1:F:251:ARG:CZ	3:F:516:HOH:O	2.70	0.40
1:B:92:ILE:O	1:C:123:GLY:HA2	2.21	0.40
1:H:236:VAL:CG2	1:H:240:ILE:HG13	2.51	0.40
1:R:267:LEU:HA	1:R:267:LEU:HD13	1.87	0.40
1:L:54:VAL:CG1	1:L:59:ALA:HB2	2.52	0.40
1:K:95:ASN:ND2	1:K:95:ASN:C	2.74	0.40
1:K:139:GLU:OE2	1:O:103:THR:HA	2.22	0.40
1:O:95:ASN:ND2	1:O:95:ASN:C	2.75	0.40
1:L:42:LYS:O	1:L:242:GLN:HG2	2.21	0.40
1:P:136:MET:HE1	1:T:104:THR:HG23	2.04	0.40
1:Q:71:HIS:O	1:R:6:ASP:HB3	2.21	0.40
1:F:222:MET:HE2	1:F:223:ILE:HA	2.03	0.40
1:H:222:MET:HE2	1:H:223:ILE:HA	2.03	0.40
1:T:16:LEU:HD23	1:T:19:ILE:HD11	2.03	0.40
1:G:108:ALA:HA	1:G:111:MET:HE2	2.03	0.40
1:H:108:ALA:HA	1:H:111:MET:HE3	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	260/273 (95%)	247 (95%)	13 (5%)	0	100	100
1	B	260/273 (95%)	249 (96%)	10 (4%)	1 (0%)	39	65
1	C	261/273 (96%)	247 (95%)	14 (5%)	0	100	100
1	D	262/273 (96%)	252 (96%)	10 (4%)	0	100	100
1	E	260/273 (95%)	249 (96%)	11 (4%)	0	100	100
1	F	260/273 (95%)	249 (96%)	8 (3%)	3 (1%)	16	33
1	G	260/273 (95%)	244 (94%)	16 (6%)	0	100	100
1	H	260/273 (95%)	247 (95%)	12 (5%)	1 (0%)	39	65
1	I	260/273 (95%)	247 (95%)	11 (4%)	2 (1%)	24	46
1	J	260/273 (95%)	247 (95%)	12 (5%)	1 (0%)	39	65
1	K	260/273 (95%)	245 (94%)	15 (6%)	0	100	100
1	L	261/273 (96%)	249 (95%)	12 (5%)	0	100	100
1	M	260/273 (95%)	243 (94%)	16 (6%)	1 (0%)	39	65
1	N	260/273 (95%)	243 (94%)	16 (6%)	1 (0%)	39	65
1	O	260/273 (95%)	250 (96%)	10 (4%)	0	100	100
1	P	260/273 (95%)	248 (95%)	12 (5%)	0	100	100
1	Q	260/273 (95%)	245 (94%)	14 (5%)	1 (0%)	39	65
1	R	262/273 (96%)	250 (95%)	12 (5%)	0	100	100
1	S	260/273 (95%)	248 (95%)	12 (5%)	0	100	100
1	T	260/273 (95%)	247 (95%)	13 (5%)	0	100	100
All	All	5206/5460 (95%)	4946 (95%)	249 (5%)	11 (0%)	52	77

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	267	LEU
1	J	268	LYS
1	F	270	ILE
1	I	263	VAL
1	M	3	LEU
1	F	264	GLU
1	H	261	ALA
1	I	70	ARG
1	F	70	ARG
1	N	70	ARG
1	Q	51	VAL

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	203/220 (92%)	192 (95%)	11 (5%)	27	52
1	B	204/220 (93%)	191 (94%)	13 (6%)	22	43
1	C	208/220 (94%)	197 (95%)	11 (5%)	28	53
1	D	209/220 (95%)	196 (94%)	13 (6%)	23	45
1	E	206/220 (94%)	195 (95%)	11 (5%)	28	53
1	F	205/220 (93%)	194 (95%)	11 (5%)	27	52
1	G	203/220 (92%)	191 (94%)	12 (6%)	24	47
1	H	204/220 (93%)	194 (95%)	10 (5%)	31	57
1	I	208/220 (94%)	196 (94%)	12 (6%)	25	49
1	J	205/220 (93%)	194 (95%)	11 (5%)	27	52
1	K	205/220 (93%)	193 (94%)	12 (6%)	24	47
1	L	206/220 (94%)	195 (95%)	11 (5%)	28	53
1	M	205/220 (93%)	195 (95%)	10 (5%)	31	57
1	N	204/220 (93%)	190 (93%)	14 (7%)	19	38
1	O	205/220 (93%)	194 (95%)	11 (5%)	27	52
1	P	204/220 (93%)	193 (95%)	11 (5%)	27	52
1	Q	206/220 (94%)	194 (94%)	12 (6%)	25	49
1	R	207/220 (94%)	193 (93%)	14 (7%)	20	39
1	S	203/220 (92%)	191 (94%)	12 (6%)	24	47
1	T	203/220 (92%)	191 (94%)	12 (6%)	24	47
All	All	4103/4400 (93%)	3869 (94%)	234 (6%)	25	49

All (234) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	9	ASN
1	A	47	ILE

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Mol	Chain	Res	Type
1	A	70	ARG
1	A	95	ASN
1	A	110	ARG
1	A	136	MET
1	A	166	GLU
1	A	173	ARG
1	A	174	LEU
1	A	222	MET
1	B	3	LEU
1	B	9	ASN
1	B	47	ILE
1	B	70	ARG
1	B	95	ASN
1	B	110	ARG
1	B	126	GLU
1	B	136	MET
1	B	166	GLU
1	B	173	ARG
1	B	174	LEU
1	B	222	MET
1	B	262	ASP
1	C	3	LEU
1	C	9	ASN
1	C	47	ILE
1	C	70	ARG
1	C	95	ASN
1	C	110	ARG
1	C	136	MET
1	C	166	GLU
1	C	173	ARG
1	C	174	LEU
1	C	222	MET
1	D	3	LEU
1	D	9	ASN
1	D	47	ILE
1	D	70	ARG
1	D	95	ASN
1	D	110	ARG
1	D	126	GLU
1	D	136	MET
1	D	166	GLU
1	D	173	ARG

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Mol	Chain	Res	Type
1	D	174	LEU
1	D	217	GLU
1	D	222	MET
1	E	9	ASN
1	E	47	ILE
1	E	70	ARG
1	E	95	ASN
1	E	110	ARG
1	E	136	MET
1	E	161	ASN
1	E	173	ARG
1	E	174	LEU
1	E	217	GLU
1	E	222	MET
1	F	3	LEU
1	F	9	ASN
1	F	47	ILE
1	F	70	ARG
1	F	95	ASN
1	F	110	ARG
1	F	136	MET
1	F	166	GLU
1	F	173	ARG
1	F	174	LEU
1	F	222	MET
1	G	2	GLU
1	G	3	LEU
1	G	9	ASN
1	G	47	ILE
1	G	70	ARG
1	G	95	ASN
1	G	110	ARG
1	G	136	MET
1	G	166	GLU
1	G	173	ARG
1	G	174	LEU
1	G	222	MET
1	H	9	ASN
1	H	47	ILE
1	H	70	ARG
1	H	95	ASN
1	H	110	ARG

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Mol	Chain	Res	Type
1	H	136	MET
1	H	166	GLU
1	H	173	ARG
1	H	174	LEU
1	H	222	MET
1	I	3	LEU
1	I	9	ASN
1	I	47	ILE
1	I	70	ARG
1	I	95	ASN
1	I	110	ARG
1	I	126	GLU
1	I	136	MET
1	I	166	GLU
1	I	173	ARG
1	I	174	LEU
1	I	222	MET
1	J	3	LEU
1	J	9	ASN
1	J	47	ILE
1	J	70	ARG
1	J	95	ASN
1	J	110	ARG
1	J	136	MET
1	J	166	GLU
1	J	173	ARG
1	J	174	LEU
1	J	222	MET
1	K	4	PHE
1	K	9	ASN
1	K	47	ILE
1	K	70	ARG
1	K	95	ASN
1	K	110	ARG
1	K	136	MET
1	K	166	GLU
1	K	173	ARG
1	K	174	LEU
1	K	222	MET
1	K	271	ARG
1	L	9	ASN
1	L	47	ILE

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Mol	Chain	Res	Type
1	L	53	ASP
1	L	70	ARG
1	L	95	ASN
1	L	110	ARG
1	L	136	MET
1	L	166	GLU
1	L	173	ARG
1	L	174	LEU
1	L	222	MET
1	M	9	ASN
1	M	47	ILE
1	M	70	ARG
1	M	95	ASN
1	M	110	ARG
1	M	136	MET
1	M	166	GLU
1	M	173	ARG
1	M	174	LEU
1	M	222	MET
1	N	3	LEU
1	N	9	ASN
1	N	47	ILE
1	N	70	ARG
1	N	71	HIS
1	N	95	ASN
1	N	110	ARG
1	N	136	MET
1	N	161	ASN
1	N	166	GLU
1	N	173	ARG
1	N	174	LEU
1	N	214	ASN
1	N	222	MET
1	O	3	LEU
1	O	9	ASN
1	O	47	ILE
1	O	70	ARG
1	O	95	ASN
1	O	110	ARG
1	O	136	MET
1	O	166	GLU
1	O	173	ARG

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Mol	Chain	Res	Type
1	O	174	LEU
1	O	222	MET
1	P	9	ASN
1	P	47	ILE
1	P	70	ARG
1	P	95	ASN
1	P	110	ARG
1	P	136	MET
1	P	166	GLU
1	P	173	ARG
1	P	174	LEU
1	P	222	MET
1	P	271	ARG
1	Q	3	LEU
1	Q	9	ASN
1	Q	47	ILE
1	Q	70	ARG
1	Q	95	ASN
1	Q	110	ARG
1	Q	136	MET
1	Q	166	GLU
1	Q	173	ARG
1	Q	174	LEU
1	Q	222	MET
1	Q	260	ASN
1	R	3	LEU
1	R	9	ASN
1	R	47	ILE
1	R	70	ARG
1	R	95	ASN
1	R	110	ARG
1	R	136	MET
1	R	166	GLU
1	R	173	ARG
1	R	174	LEU
1	R	192	ASP
1	R	222	MET
1	R	259	GLU
1	R	264	GLU
1	S	3	LEU
1	S	9	ASN
1	S	47	ILE

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Mol	Chain	Res	Type
1	S	70	ARG
1	S	95	ASN
1	S	110	ARG
1	S	126	GLU
1	S	136	MET
1	S	166	GLU
1	S	173	ARG
1	S	174	LEU
1	S	222	MET
1	T	9	ASN
1	T	47	ILE
1	T	54	VAL
1	T	70	ARG
1	T	95	ASN
1	T	110	ARG
1	T	136	MET
1	T	166	GLU
1	T	173	ARG
1	T	174	LEU
1	T	222	MET
1	T	267	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (122) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	95	ASN
1	A	160	GLN
1	A	161	ASN
1	A	214	ASN
1	A	258	HIS
1	B	9	ASN
1	B	95	ASN
1	B	160	GLN
1	B	161	ASN
1	B	170	HIS
1	B	214	ASN
1	B	258	HIS
1	C	9	ASN
1	C	71	HIS
1	C	95	ASN
1	C	160	GLN

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Mol	Chain	Res	Type
1	C	161	ASN
1	C	214	ASN
1	C	258	HIS
1	D	9	ASN
1	D	95	ASN
1	D	160	GLN
1	D	161	ASN
1	D	214	ASN
1	E	9	ASN
1	E	65	HIS
1	E	95	ASN
1	E	160	GLN
1	E	161	ASN
1	E	214	ASN
1	F	9	ASN
1	F	95	ASN
1	F	160	GLN
1	F	161	ASN
1	G	9	ASN
1	G	65	HIS
1	G	95	ASN
1	G	160	GLN
1	G	161	ASN
1	G	214	ASN
1	G	258	HIS
1	H	9	ASN
1	H	95	ASN
1	H	160	GLN
1	H	161	ASN
1	H	170	HIS
1	H	214	ASN
1	H	258	HIS
1	I	9	ASN
1	I	95	ASN
1	I	160	GLN
1	I	161	ASN
1	I	170	HIS
1	I	214	ASN
1	J	9	ASN
1	J	95	ASN
1	J	160	GLN
1	J	161	ASN

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Mol	Chain	Res	Type
1	J	214	ASN
1	J	258	HIS
1	K	9	ASN
1	K	71	HIS
1	K	95	ASN
1	K	160	GLN
1	K	161	ASN
1	K	170	HIS
1	K	214	ASN
1	L	9	ASN
1	L	52	ASN
1	L	95	ASN
1	L	160	GLN
1	L	161	ASN
1	L	214	ASN
1	M	9	ASN
1	M	95	ASN
1	M	160	GLN
1	M	161	ASN
1	M	170	HIS
1	M	258	HIS
1	N	9	ASN
1	N	65	HIS
1	N	95	ASN
1	N	160	GLN
1	N	161	ASN
1	N	214	ASN
1	O	9	ASN
1	O	65	HIS
1	O	95	ASN
1	O	158	HIS
1	O	160	GLN
1	O	161	ASN
1	O	214	ASN
1	P	9	ASN
1	P	95	ASN
1	P	160	GLN
1	P	161	ASN
1	P	214	ASN
1	Q	9	ASN
1	Q	71	HIS
1	Q	95	ASN

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Mol	Chain	Res	Type
1	Q	160	GLN
1	Q	161	ASN
1	Q	214	ASN
1	R	9	ASN
1	R	65	HIS
1	R	95	ASN
1	R	160	GLN
1	R	161	ASN
1	R	170	HIS
1	R	214	ASN
1	R	258	HIS
1	S	9	ASN
1	S	71	HIS
1	S	95	ASN
1	S	160	GLN
1	S	161	ASN
1	T	9	ASN
1	T	95	ASN
1	T	160	GLN
1	T	161	ASN
1	T	214	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

20 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link

column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	13P	A	501	1	8,8,9	1.45	1 (12%)	9,10,12	1.24	2 (22%)
2	13P	B	501	1	8,8,9	1.45	1 (12%)	9,10,12	1.23	1 (11%)
2	13P	C	501	1	8,8,9	1.46	1 (12%)	9,10,12	1.23	2 (22%)
2	13P	D	501	1	8,8,9	1.44	1 (12%)	9,10,12	1.23	2 (22%)
2	13P	E	501	1	8,8,9	1.45	1 (12%)	9,10,12	1.23	2 (22%)
2	13P	F	501	1	8,8,9	1.46	1 (12%)	9,10,12	1.23	2 (22%)
2	13P	G	501	1	8,8,9	1.46	1 (12%)	9,10,12	1.24	2 (22%)
2	13P	H	501	1	8,8,9	1.44	1 (12%)	9,10,12	1.23	1 (11%)
2	13P	I	501	1	8,8,9	1.42	1 (12%)	9,10,12	1.24	2 (22%)
2	13P	J	501	1	8,8,9	1.44	1 (12%)	9,10,12	1.24	2 (22%)
2	13P	K	501	1	8,8,9	1.42	1 (12%)	9,10,12	1.23	2 (22%)
2	13P	L	501	1	8,8,9	1.45	1 (12%)	9,10,12	1.22	2 (22%)
2	13P	M	501	1	8,8,9	1.46	1 (12%)	9,10,12	1.23	1 (11%)
2	13P	N	501	1	8,8,9	1.45	1 (12%)	9,10,12	1.23	2 (22%)
2	13P	O	501	1	8,8,9	1.44	1 (12%)	9,10,12	1.24	2 (22%)
2	13P	P	501	1	8,8,9	1.44	1 (12%)	9,10,12	1.23	2 (22%)
2	13P	Q	501	1	8,8,9	1.43	1 (12%)	9,10,12	1.23	2 (22%)
2	13P	R	501	1	8,8,9	1.45	1 (12%)	9,10,12	1.23	2 (22%)
2	13P	S	501	1	8,8,9	1.45	1 (12%)	9,10,12	1.23	2 (22%)
2	13P	T	501	1	8,8,9	1.46	1 (12%)	9,10,12	1.22	1 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	13P	A	501	1	-	0/6/6/8	0/0/0/0
2	13P	B	501	1	-	0/6/6/8	0/0/0/0
2	13P	C	501	1	-	0/6/6/8	0/0/0/0
2	13P	D	501	1	-	0/6/6/8	0/0/0/0
2	13P	E	501	1	-	0/6/6/8	0/0/0/0
2	13P	F	501	1	-	0/6/6/8	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	13P	G	501	1	-	0/6/6/8	0/0/0/0
2	13P	H	501	1	-	0/6/6/8	0/0/0/0
2	13P	I	501	1	-	0/6/6/8	0/0/0/0
2	13P	J	501	1	-	0/6/6/8	0/0/0/0
2	13P	K	501	1	-	0/6/6/8	0/0/0/0
2	13P	L	501	1	-	0/6/6/8	0/0/0/0
2	13P	M	501	1	-	0/6/6/8	0/0/0/0
2	13P	N	501	1	-	0/6/6/8	0/0/0/0
2	13P	O	501	1	-	0/6/6/8	0/0/0/0
2	13P	P	501	1	-	0/6/6/8	0/0/0/0
2	13P	Q	501	1	-	0/6/6/8	0/0/0/0
2	13P	R	501	1	-	0/6/6/8	0/0/0/0
2	13P	S	501	1	-	0/6/6/8	0/0/0/0
2	13P	T	501	1	-	0/6/6/8	0/0/0/0

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	501	13P	P-O1P	2.96	1.60	1.51
2	K	501	13P	P-O1P	2.97	1.61	1.51
2	J	501	13P	P-O1P	2.98	1.61	1.51
2	P	501	13P	P-O1P	2.99	1.61	1.51
2	O	501	13P	P-O1P	2.99	1.61	1.51
2	D	501	13P	P-O1P	2.99	1.61	1.51
2	Q	501	13P	P-O1P	2.99	1.61	1.51
2	B	501	13P	P-O1P	3.00	1.61	1.51
2	H	501	13P	P-O1P	3.01	1.61	1.51
2	L	501	13P	P-O1P	3.01	1.61	1.51
2	E	501	13P	P-O1P	3.01	1.61	1.51
2	R	501	13P	P-O1P	3.02	1.61	1.51
2	A	501	13P	P-O1P	3.02	1.61	1.51
2	N	501	13P	P-O1P	3.03	1.61	1.51
2	T	501	13P	P-O1P	3.04	1.61	1.51
2	F	501	13P	P-O1P	3.05	1.61	1.51
2	S	501	13P	P-O1P	3.05	1.61	1.51
2	C	501	13P	P-O1P	3.05	1.61	1.51
2	G	501	13P	P-O1P	3.05	1.61	1.51
2	M	501	13P	P-O1P	3.06	1.61	1.51

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	13P	O3P-P-O1	2.00	112.33	106.56
2	Q	501	13P	O3P-P-O1	2.00	112.33	106.56
2	R	501	13P	O3P-P-O1	2.00	112.33	106.56
2	P	501	13P	O3P-P-O1	2.01	112.34	106.56
2	E	501	13P	O3P-P-O1	2.01	112.34	106.56
2	L	501	13P	O3P-P-O1	2.01	112.35	106.56
2	N	501	13P	O3P-P-O1	2.01	112.36	106.56
2	S	501	13P	O3P-P-O1	2.01	112.36	106.56
2	G	501	13P	O3P-P-O1	2.01	112.36	106.56
2	J	501	13P	O3P-P-O1	2.01	112.36	106.56
2	F	501	13P	O3P-P-O1	2.02	112.37	106.56
2	K	501	13P	O3P-P-O1	2.02	112.38	106.56
2	O	501	13P	O3P-P-O1	2.03	112.40	106.56
2	C	501	13P	O3P-P-O1	2.03	112.41	106.56
2	I	501	13P	O3P-P-O1	2.03	112.41	106.56
2	D	501	13P	O3P-P-O1	2.04	112.44	106.56
2	D	501	13P	C1-C2-C3	2.37	119.59	113.71
2	L	501	13P	C1-C2-C3	2.37	119.59	113.71
2	C	501	13P	C1-C2-C3	2.37	119.60	113.71
2	T	501	13P	C1-C2-C3	2.37	119.60	113.71
2	E	501	13P	C1-C2-C3	2.38	119.61	113.71
2	F	501	13P	C1-C2-C3	2.38	119.62	113.71
2	B	501	13P	C1-C2-C3	2.38	119.62	113.71
2	H	501	13P	C1-C2-C3	2.39	119.64	113.71
2	S	501	13P	C1-C2-C3	2.39	119.64	113.71
2	R	501	13P	C1-C2-C3	2.39	119.64	113.71
2	N	501	13P	C1-C2-C3	2.39	119.64	113.71
2	I	501	13P	C1-C2-C3	2.39	119.64	113.71
2	P	501	13P	C1-C2-C3	2.39	119.65	113.71
2	Q	501	13P	C1-C2-C3	2.40	119.66	113.71
2	K	501	13P	C1-C2-C3	2.40	119.66	113.71
2	M	501	13P	C1-C2-C3	2.40	119.67	113.71
2	J	501	13P	C1-C2-C3	2.40	119.67	113.71
2	O	501	13P	C1-C2-C3	2.41	119.69	113.71
2	A	501	13P	C1-C2-C3	2.41	119.70	113.71
2	G	501	13P	C1-C2-C3	2.43	119.73	113.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

20 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	13P	2	0
2	B	501	13P	2	0
2	C	501	13P	2	0
2	D	501	13P	2	0
2	E	501	13P	2	0
2	F	501	13P	2	0
2	G	501	13P	2	0
2	H	501	13P	2	0
2	I	501	13P	2	0
2	J	501	13P	2	0
2	K	501	13P	2	0
2	L	501	13P	2	0
2	M	501	13P	2	0
2	N	501	13P	2	0
2	O	501	13P	2	0
2	P	501	13P	2	0
2	Q	501	13P	2	0
2	R	501	13P	2	0
2	S	501	13P	2	0
2	T	501	13P	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	264/273 (96%)	-0.01	5 (1%) 70 64	33, 58, 98, 119	0
1	B	264/273 (96%)	-0.01	5 (1%) 70 64	34, 57, 85, 115	0
1	C	265/273 (97%)	0.02	3 (1%) 82 79	34, 55, 86, 122	0
1	D	266/273 (97%)	-0.37	0 100 100	32, 54, 86, 107	0
1	E	264/273 (96%)	-0.27	0 100 100	36, 52, 85, 130	0
1	F	264/273 (96%)	-0.08	2 (0%) 87 85	37, 61, 95, 115	0
1	G	264/273 (96%)	0.09	5 (1%) 70 64	34, 62, 90, 110	0
1	H	264/273 (96%)	0.08	4 (1%) 76 71	36, 60, 91, 124	0
1	I	264/273 (96%)	-0.24	1 (0%) 93 91	31, 51, 79, 119	0
1	J	264/273 (96%)	-0.21	1 (0%) 93 91	30, 52, 83, 122	0
1	K	264/273 (96%)	-0.39	0 100 100	35, 54, 82, 118	0
1	L	265/273 (97%)	-0.22	4 (1%) 76 71	36, 57, 88, 115	0
1	M	264/273 (96%)	0.01	7 (2%) 58 51	38, 59, 94, 129	0
1	N	264/273 (96%)	-0.04	6 (2%) 64 57	35, 59, 88, 130	0
1	O	264/273 (96%)	-0.27	2 (0%) 87 85	34, 54, 84, 163	0
1	P	264/273 (96%)	-0.33	1 (0%) 93 91	36, 56, 83, 115	0
1	Q	264/273 (96%)	-0.29	0 100 100	32, 53, 82, 109	0
1	R	266/273 (97%)	0.07	13 (4%) 33 26	39, 60, 98, 141	0
1	S	264/273 (96%)	0.13	10 (3%) 44 36	35, 66, 98, 122	0
1	T	264/273 (96%)	-0.16	2 (0%) 87 85	41, 61, 92, 107	0
All	All	5286/5460 (96%)	-0.13	71 (1%) 79 75	30, 57, 90, 163	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	S	246	VAL	5.5
1	S	47	ILE	5.1
1	T	268	LYS	4.2
1	C	1	MET	4.2
1	R	211	PRO	4.0
1	M	247	VAL	3.9
1	O	158	HIS	3.8
1	B	72	GLY	3.7
1	R	212	LYS	3.7
1	O	79	ASP	3.5
1	A	188	THR	3.5
1	R	7	ILE	3.5
1	N	246	VAL	3.4
1	R	53	ASP	3.3
1	B	257	VAL	3.2
1	M	270	ILE	3.2
1	N	214	ASN	3.1
1	R	1	MET	3.1
1	R	6	ASP	3.1
1	R	210	GLY	3.1
1	R	213	THR	3.1
1	L	191	ILE	3.0
1	N	44	LEU	3.0
1	G	258	HIS	3.0
1	L	72	GLY	3.0
1	R	209	GLY	3.0
1	F	226	ALA	3.0
1	H	72	GLY	2.9
1	H	249	ILE	2.9
1	R	247	VAL	2.9
1	J	7	ILE	2.9
1	F	270	ILE	2.8
1	S	52	ASN	2.8
1	N	249	ILE	2.8
1	B	21	ASN	2.8
1	S	44	LEU	2.7
1	N	251	ARG	2.7
1	A	270	ILE	2.7
1	G	257	VAL	2.5
1	S	213	THR	2.5
1	M	240	ILE	2.5
1	S	270	ILE	2.5
1	R	22	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	P	71	HIS	2.3
1	S	247	VAL	2.3
1	G	270	ILE	2.3
1	M	80	VAL	2.3
1	M	267	LEU	2.3
1	L	252	ALA	2.3
1	N	210	GLY	2.3
1	T	267	LEU	2.2
1	S	51	VAL	2.2
1	S	41	ILE	2.2
1	H	80	VAL	2.2
1	M	263	VAL	2.2
1	R	47	ILE	2.2
1	L	220	LEU	2.1
1	C	241	PHE	2.1
1	M	72	GLY	2.1
1	A	247	VAL	2.1
1	C	260	ASN	2.1
1	H	268	LYS	2.1
1	A	248	GLY	2.1
1	B	22	ARG	2.1
1	R	256	ILE	2.1
1	S	19	ILE	2.1
1	A	54	VAL	2.1
1	B	102	VAL	2.1
1	G	52	ASN	2.1
1	I	157	LYS	2.1
1	G	22	ARG	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	13P	Q	501	9/10	0.96	0.18	1.22	65,66,68,68	0
2	13P	D	501	9/10	0.93	0.19	1.18	61,63,65,65	0
2	13P	K	501	9/10	0.97	0.17	1.10	64,66,67,67	0
2	13P	I	501	9/10	0.96	0.18	0.91	58,61,64,64	0
2	13P	E	501	9/10	0.98	0.18	0.83	63,65,67,69	0
2	13P	P	501	9/10	0.96	0.17	0.78	64,65,66,66	0
2	13P	B	501	9/10	0.97	0.17	0.69	62,63,66,66	0
2	13P	O	501	9/10	0.92	0.15	0.61	62,64,65,65	0
2	13P	F	501	9/10	0.94	0.17	0.13	65,67,72,72	0
2	13P	L	501	9/10	0.96	0.14	0.06	64,65,67,67	0
2	13P	G	501	9/10	0.95	0.16	-0.10	66,66,67,68	0
2	13P	T	501	9/10	0.96	0.14	-0.16	64,66,67,67	0
2	13P	H	501	9/10	0.95	0.15	-0.25	64,65,66,67	0
2	13P	M	501	9/10	0.95	0.13	-0.41	66,68,68,70	0
2	13P	J	501	9/10	0.97	0.14	-0.52	62,64,67,67	0
2	13P	A	501	9/10	0.94	0.16	-0.58	66,66,68,69	0
2	13P	N	501	9/10	0.96	0.14	-0.68	64,65,67,67	0
2	13P	R	501	9/10	0.96	0.13	-0.75	68,69,71,72	0
2	13P	C	501	9/10	0.96	0.13	-1.07	66,67,69,69	0
2	13P	S	501	9/10	0.92	0.14	-1.26	67,69,70,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.