



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 10:46 PM GMT

PDB ID : 5D2L
Title : Crystal structure of TCR C7 in complex with HCMV NLV epitope presented by HLA-A2
Authors : Gao, M.; Mariuzza, R.A.
Deposited on : 2015-08-05
Resolution : 3.51 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 : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

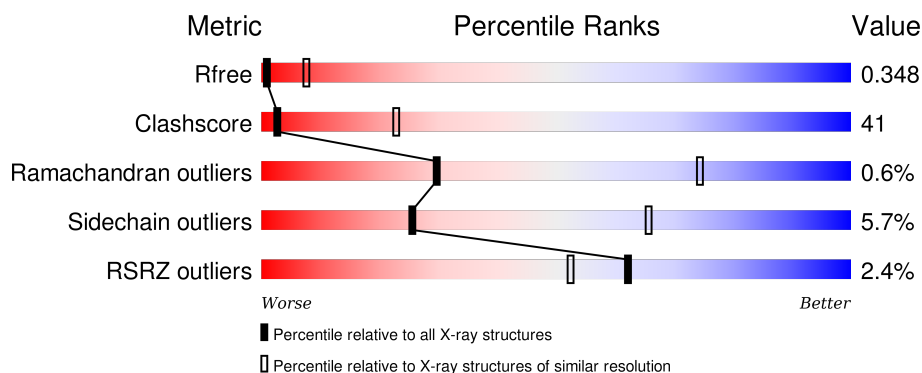
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.51 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.





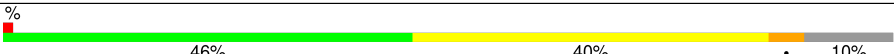
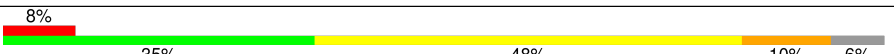
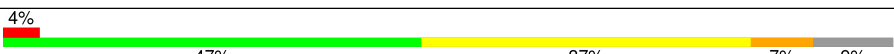
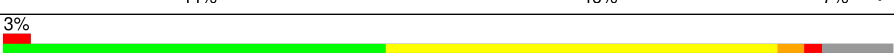




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1089 (3.64-3.40)
Clashscore	102246	1197 (3.64-3.40)
Ramachandran outliers	100387	1159 (3.64-3.40)
Sidechain outliers	100360	1160 (3.64-3.40)
RSRZ outliers	91569	1096 (3.64-3.40)

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	276	<div> <div>58%</div> <div>40%</div> <div>..</div> </div>
1	C	276	<div> <div>61%</div> <div>35%</div> <div>..</div> </div>
1	G	276	<div> <div>2%</div> <div>46%</div> <div>47%</div> <div>..</div> </div>
1	M	276	<div> <div>%</div> <div>48%</div> <div>48%</div> <div>..</div> </div>
2	B	100	<div> <div>3%</div> <div>48%</div> <div>50%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	100	
2	H	100	
2	N	100	
3	E	205	
3	I	205	
3	K	205	
3	O	205	
4	F	245	
4	J	245	
4	L	245	
4	P	245	
5	Q	9	
5	R	9	
5	T	9	
5	U	9	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 25272 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 HLA class I histocompatibility antigen, A-2 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	0	0
			2242	1401	408	424	9			
1	G	270	Total	C	N	O	S	0	0	0
			2199	1379	395	416	9			
1	M	273	Total	C	N	O	S	0	0	0
			2210	1379	401	421	9			
1	C	274	Total	C	N	O	S	0	0	0
			2242	1401	408	424	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P01892
G	0	MET	-	initiating methionine	UNP P01892
M	0	MET	-	initiating methionine	UNP P01892
C	0	MET	-	initiating methionine	UNP P01892

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	0	0
			823	522	140	158	3			
2	H	96	Total	C	N	O	S	0	0	0
			777	494	128	152	3			
2	N	100	Total	C	N	O	S	0	0	0
			825	524	138	159	4			
2	D	100	Total	C	N	O	S	0	0	0
			827	527	137	159	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
H	0	MET	-	initiating methionine	UNP P61769
N	0	MET	-	initiating methionine	UNP P61769
D	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called C7 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	185	Total	C	N	O	S	0	0	0
			1404	878	227	293	6			
3	K	192	Total	C	N	O	S	0	0	0
			1452	912	237	296	7			
3	O	187	Total	C	N	O	S	0	0	0
			1435	900	234	294	7			
3	E	187	Total	C	N	O	S	0	0	0
			1432	897	234	294	7			

- Molecule 4 is a protein called C7 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	J	226	Total	C	N	O	S	0	0	0
			1759	1108	303	343	5			
4	L	226	Total	C	N	O	S	0	0	0
			1699	1064	299	331	5			
4	P	235	Total	C	N	O	S	0	0	0
			1784	1122	306	351	5			
4	F	238	Total	C	N	O	S	0	0	0
			1852	1163	323	361	5			

- Molecule 5 is a protein called ASN-LEU-VAL-PRO-MET-VAL-ALA-THR-VAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	Q	9	Total	C	N	O	S	0	0	0
			64	42	10	11	1			
5	U	9	Total	C	N	O	S	0	0	0
			64	42	10	11	1			
5	T	9	Total	C	N	O	S	0	0	0
			64	42	10	11	1			
5	R	9	Total	C	N	O	S	0	0	0
			64	42	10	11	1			

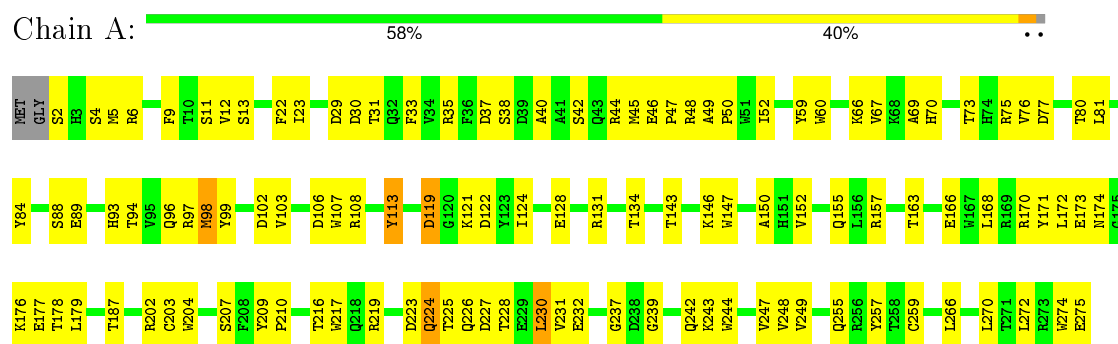
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	9	Total O 9 9	0	0
6	B	1	Total O 1 1	0	0
6	I	3	Total O 3 3	0	0
6	J	2	Total O 2 2	0	0
6	G	7	Total O 7 7	0	0
6	K	2	Total O 2 2	0	0
6	M	3	Total O 3 3	0	0
6	N	5	Total O 5 5	0	0
6	O	5	Total O 5 5	0	0
6	P	5	Total O 5 5	0	0
6	C	8	Total O 8 8	0	0
6	D	2	Total O 2 2	0	0
6	E	2	Total O 2 2	0	0

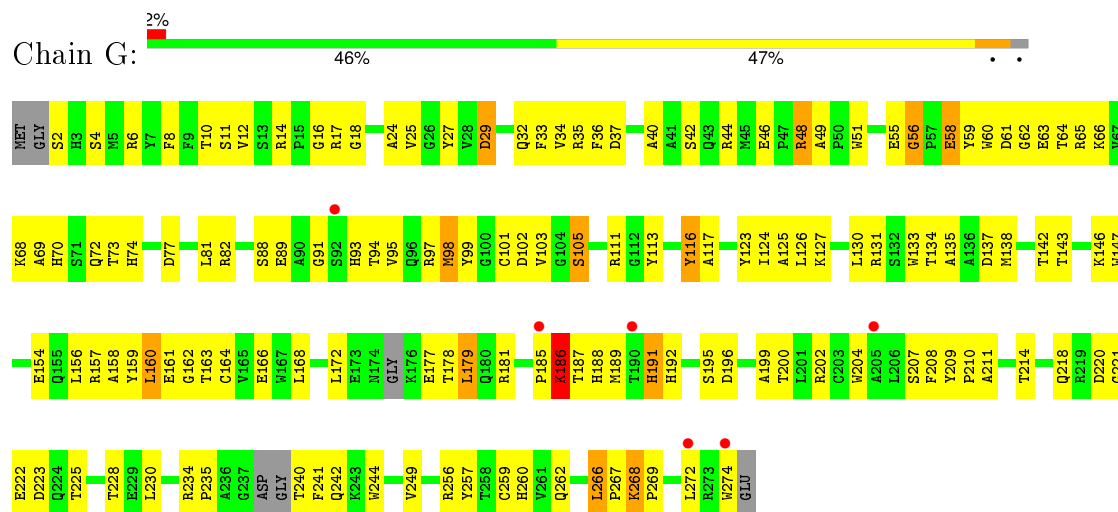
3 Residue-property plots

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

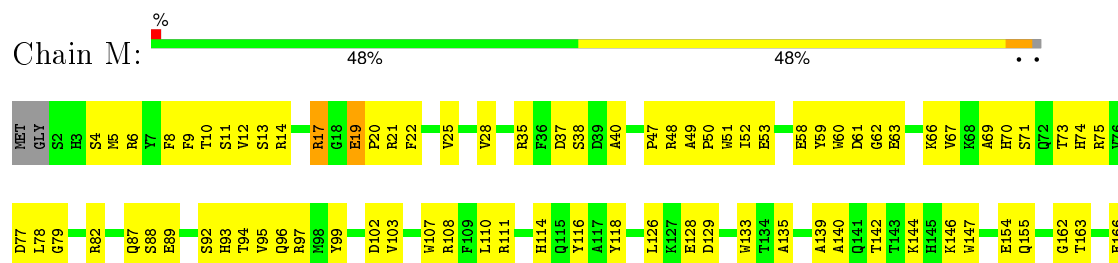
- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain

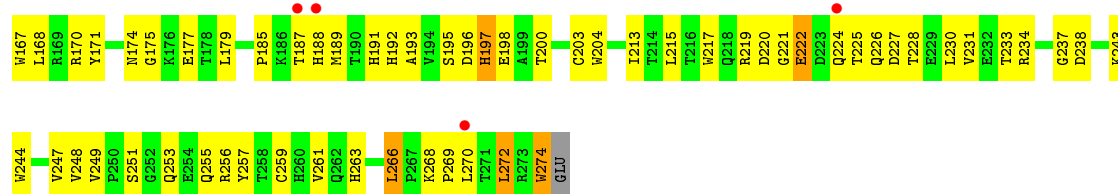


- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain



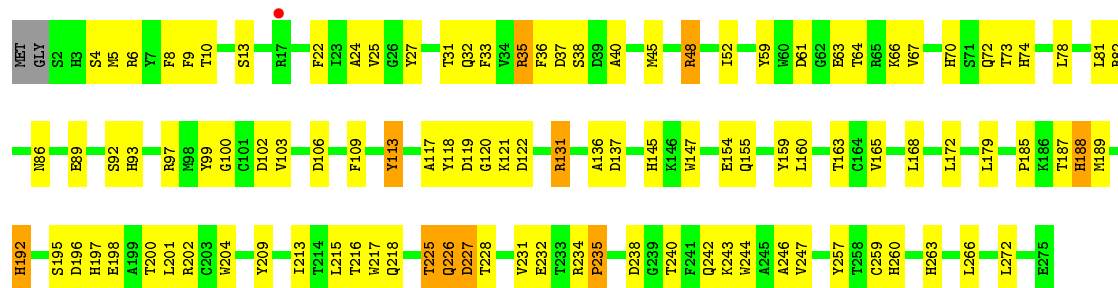
- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain





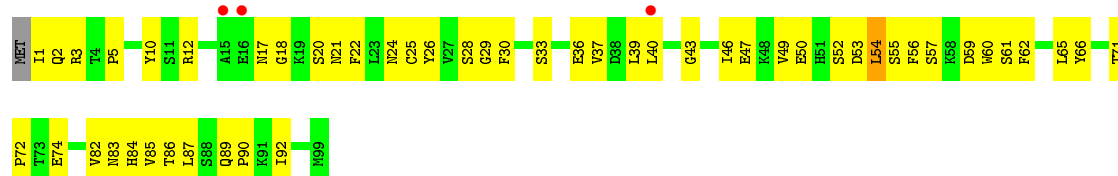
• Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain

Chain C: 61% 35%



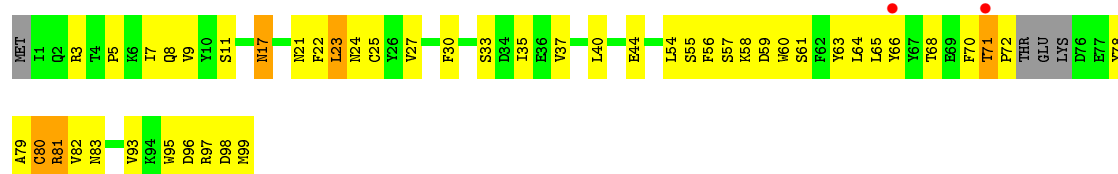
• Molecule 2: Beta-2-microglobulin

Chain B: 3% 48% 50%



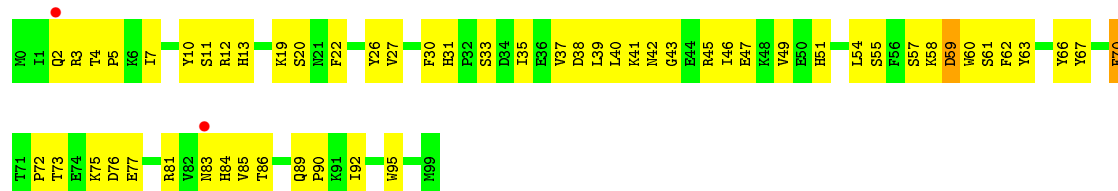
• Molecule 2: Beta-2-microglobulin

Chain H: 2% 49% 42% 5%

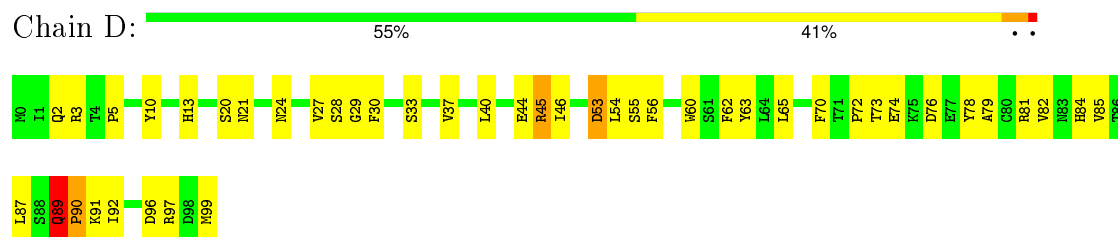


• Molecule 2: Beta-2-microglobulin

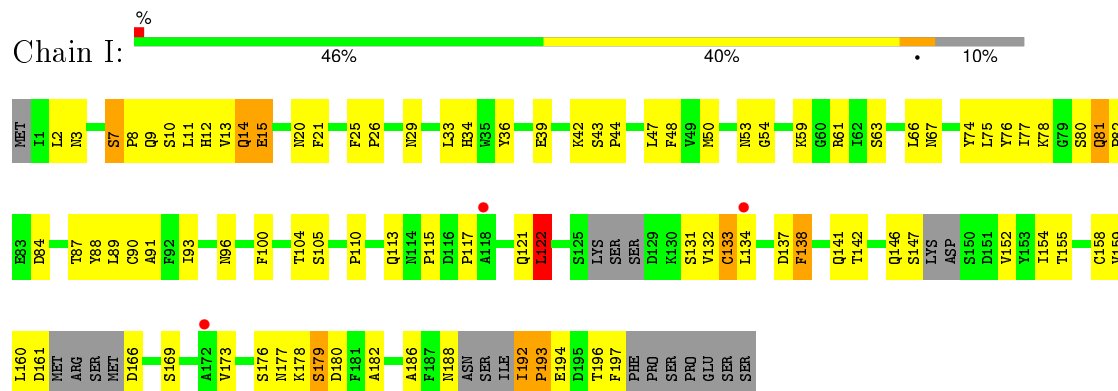
Chain N: 2% 44% 54%



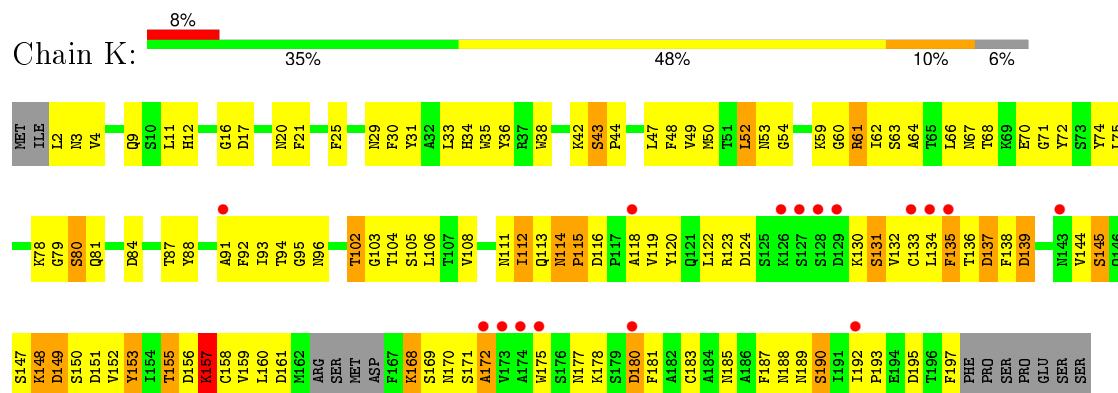
- Molecule 2: Beta-2-microglobulin



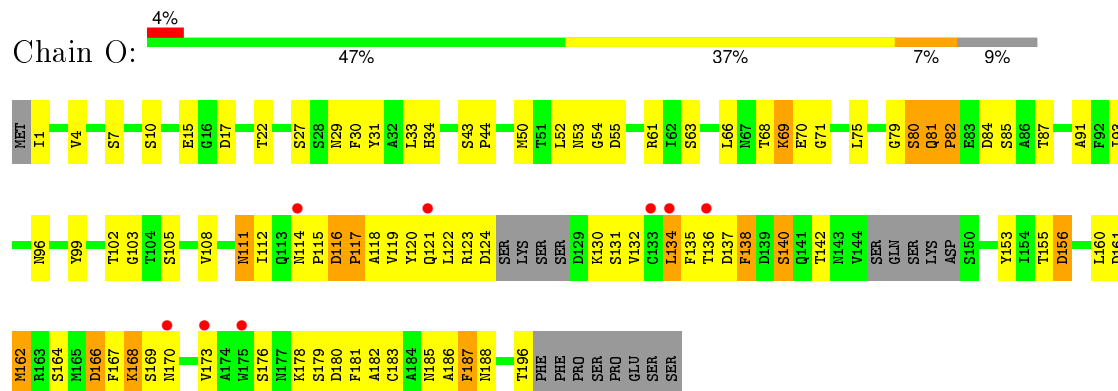
- Molecule 3: C7 TCR alpha chain



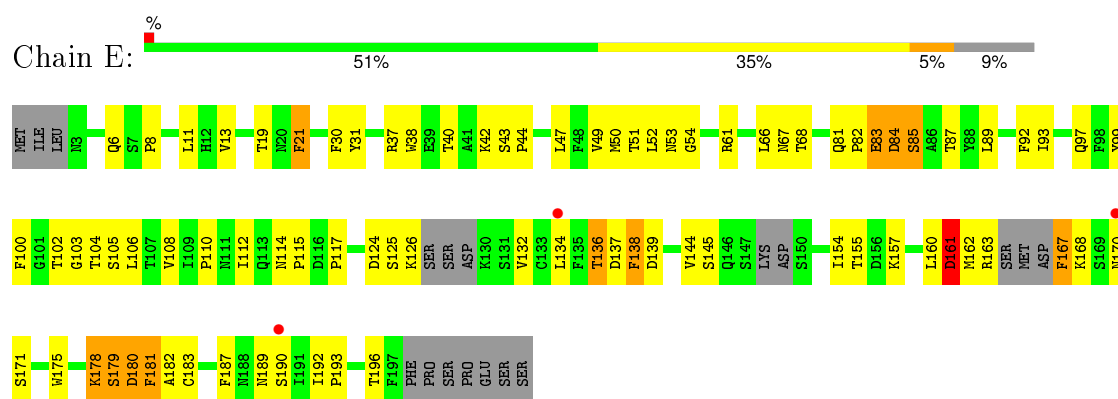
- Molecule 3: C7 TCR alpha chain



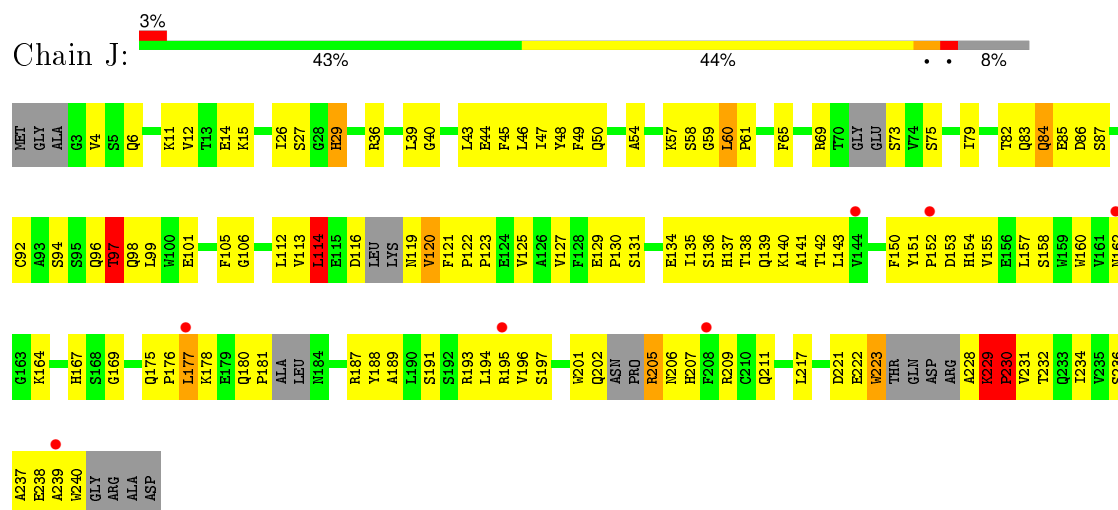
- Molecule 3: C7 TCR alpha chain



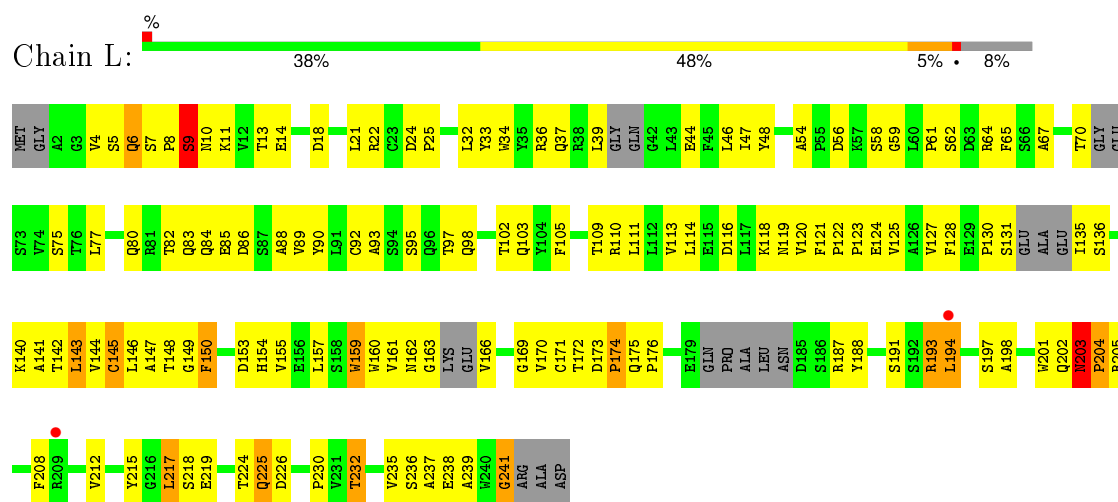
- Molecule 3: C7 TCR alpha chain



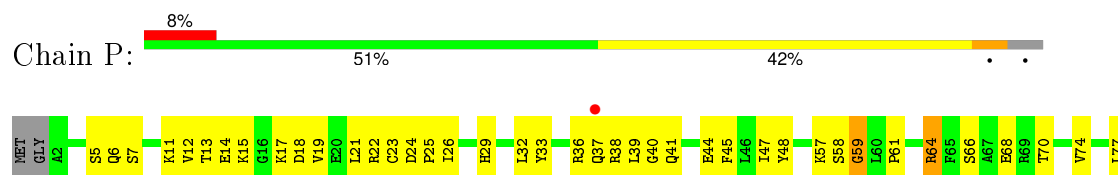
• Molecule 4: C7 TCR beta chain

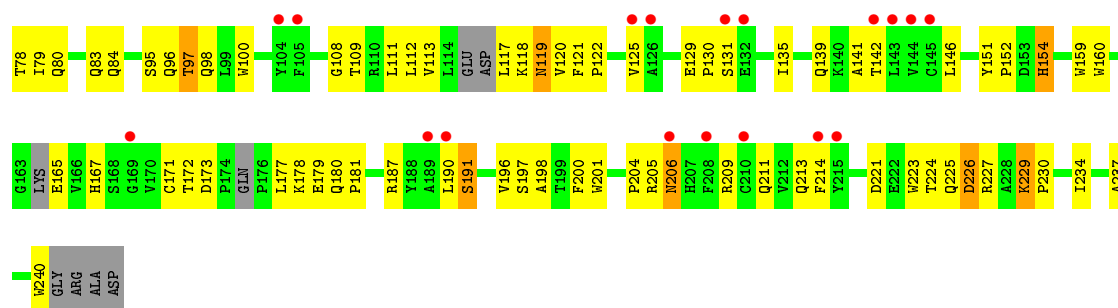


• Molecule 4: C7 TCR beta chain

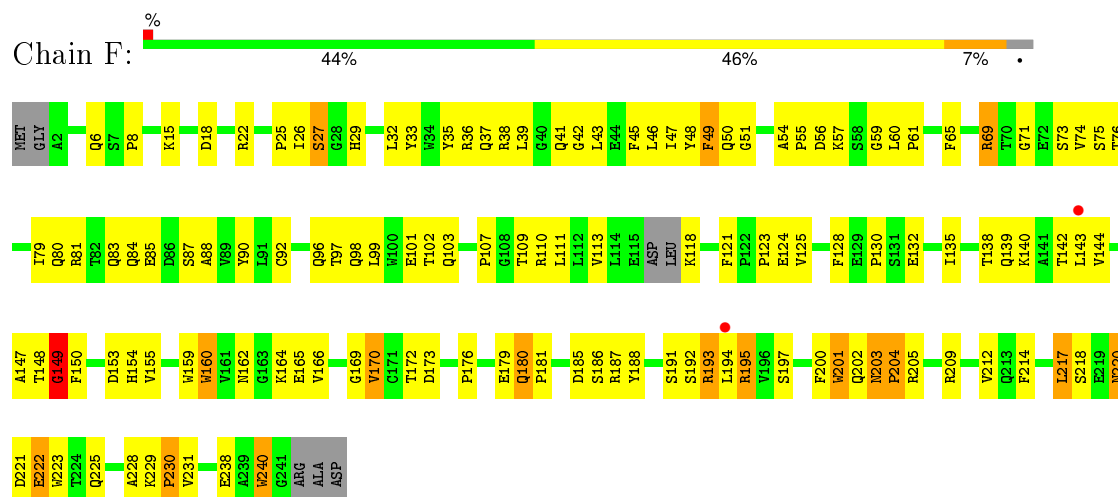


• Molecule 4: C7 TCR beta chain





• Molecule 4: C7 TCR beta chain



• Molecule 5: ASN-LEU-VAL-PRO-MET-VAL-ALA-THR-VAL



• Molecule 5: ASN-LEU-VAL-PRO-MET-VAL-ALA-THR-VAL



• Molecule 5: ASN-LEU-VAL-PRO-MET-VAL-ALA-THR-VAL



• Molecule 5: ASN-LEU-VAL-PRO-MET-VAL-ALA-THR-VAL



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	151.76Å 366.64Å 151.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.51 – 3.51 49.84 – 3.51	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.51-3.51) 91.4 (49.84-3.51)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 3.48Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.270 , 0.355 0.266 , 0.348	Depositor DCC
R_{free} test set	2469 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	81.7	Xtriage
Anisotropy	0.596	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 60.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	1 of 52979 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	25272	wwPDB-VP
Average B, all atoms (Å ²)	80.0	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 26.13 % 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 2.7879e-03. 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.47	0/2307	0.61	1/3132 (0.0%)
1	C	0.46	0/2307	0.59	1/3132 (0.0%)
1	G	0.53	1/2262 (0.0%)	0.72	2/3072 (0.1%)
1	M	0.42	0/2272	0.69	2/3085 (0.1%)
2	B	0.43	0/845	0.66	0/1143
2	D	0.53	0/850	0.68	2/1151 (0.2%)
2	H	0.44	0/798	0.64	0/1083
2	N	0.52	0/848	0.80	0/1150
3	E	0.46	0/1463	0.70	0/1987
3	I	0.54	0/1433	0.80	4/1946 (0.2%)
3	K	0.56	1/1486 (0.1%)	0.85	4/2018 (0.2%)
3	O	0.54	2/1466 (0.1%)	0.82	4/1992 (0.2%)
4	F	0.54	1/1900 (0.1%)	0.77	3/2586 (0.1%)
4	J	0.50	2/1801 (0.1%)	0.76	2/2448 (0.1%)
4	L	0.52	0/1737	0.95	11/2362 (0.5%)
4	P	0.43	0/1829	0.73	2/2494 (0.1%)
5	Q	0.45	0/64	0.72	0/88
5	R	0.42	0/64	0.67	0/88
5	T	0.55	0/64	0.78	0/88
5	U	0.30	0/64	0.50	0/88
All	All	0.49	7/25860 (0.0%)	0.74	38/35133 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	G	0	4
2	H	0	1
2	N	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	E	0	3
3	K	0	5
3	O	0	3
4	F	0	3
4	J	0	2
4	L	0	5
4	P	0	3
All	All	0	32

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	230	PRO	N-CD	5.28	1.55	1.47
1	G	267	PRO	N-CD	5.25	1.55	1.47
3	K	172	ALA	CA-CB	-5.25	1.41	1.52
3	O	82	PRO	N-CD	5.13	1.55	1.47
3	O	117	PRO	N-CD	5.13	1.55	1.47
4	F	230	PRO	N-CD	5.08	1.54	1.47
4	J	61	PRO	N-CD	5.00	1.54	1.47

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	241	GLY	N-CA-C	12.45	144.23	113.10
3	I	7	SER	C-N-CD	-11.91	94.40	120.60
4	L	149	GLY	N-CA-C	10.65	139.73	113.10
1	G	179	LEU	N-CA-C	8.08	132.81	111.00
3	I	192	ILE	C-N-CD	6.94	142.98	128.40
3	K	114	ASN	C-N-CD	-6.57	106.14	120.60
4	P	146	LEU	CA-CB-CG	6.29	129.77	115.30
3	K	190	SER	N-CA-C	-6.21	94.22	111.00
4	L	203	ASN	C-N-CD	6.09	141.20	128.40
2	D	2	GLN	CA-CB-CG	6.07	126.74	113.40
4	L	54	ALA	C-N-CD	6.06	141.13	128.40
4	L	174	PRO	N-CA-CB	6.04	110.55	103.30
3	O	162	MET	CA-CB-CG	6.02	123.54	113.30
3	O	43	SER	C-N-CD	6.00	141.01	128.40
2	D	89	GLN	C-N-CD	6.00	141.00	128.40
3	I	122	LEU	N-CA-C	-5.97	94.88	111.00
4	L	194	LEU	CA-CB-CG	5.97	129.03	115.30
4	J	138	THR	N-CA-C	5.95	127.05	111.00
4	L	56	ASP	N-CA-C	-5.94	94.97	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	180	GLN	C-N-CD	5.93	140.85	128.40
4	L	157	LEU	CA-CB-CG	5.90	128.87	115.30
3	I	193	PRO	CA-N-CD	-5.88	103.27	111.50
1	M	19	GLU	C-N-CD	5.81	140.61	128.40
4	F	229	LYS	C-N-CD	5.80	140.57	128.40
1	M	50	PRO	N-CA-CB	5.71	110.15	103.30
3	O	81	GLN	C-N-CD	5.69	140.35	128.40
3	O	116	ASP	C-N-CD	5.69	140.34	128.40
1	G	266	LEU	C-N-CD	5.65	140.27	128.40
4	F	149	GLY	N-CA-C	-5.58	99.14	113.10
4	L	4	VAL	N-CA-C	5.55	125.99	111.00
3	K	43	SER	C-N-CD	5.47	139.89	128.40
4	F	204	PRO	N-CA-C	5.38	126.08	112.10
1	A	224	GLN	CA-C-N	-5.38	105.37	117.20
4	L	225	GLN	CA-CB-CG	5.35	125.17	113.40
1	C	215	LEU	CA-CB-CG	5.07	126.95	115.30
3	K	157	LYS	N-CA-C	5.06	124.66	111.00
4	J	230	PRO	CA-N-CD	-5.01	104.48	111.50
4	L	86	ASP	N-CA-C	-5.00	97.50	111.00

There are no chirality outliers.

All (32) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	224	GLN	Mainchain
1	C	225	THR	Peptide
3	E	161	ASP	Peptide
3	E	181	PHE	Peptide
3	E	84	ASP	Peptide
4	F	149	GLY	Peptide
4	F	27	SER	Peptide
4	F	69	ARG	Peptide
1	G	105	SER	Peptide
1	G	160	LEU	Mainchain
1	G	186	LYS	Peptide
1	G	56	GLY	Peptide
2	H	17	ASN	Peptide
4	J	229	LYS	Peptide
4	J	97	THR	Peptide
3	K	130	LYS	Peptide
3	K	131	SER	Peptide
3	K	139	ASP	Peptide

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Mol	Chain	Res	Type	Group
3	K	145	SER	Peptide
3	K	54	GLY	Peptide
4	L	136	SER	Peptide
4	L	204	PRO	Peptide
4	L	232	THR	Peptide
4	L	58	SER	Peptide
4	L	9	SER	Peptide
2	N	19	LYS	Peptide
3	O	111	ASN	Peptide
3	O	136	THR	Peptide
3	O	156	ASP	Peptide
4	P	206	ASN	Peptide
4	P	224	THR	Peptide
4	P	59	GLY	Peptide

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	2242	0	2090	131	0
1	C	2242	0	2090	122	0
1	G	2199	0	2039	220	0
1	M	2210	0	2042	163	0
2	B	823	0	787	47	0
2	D	827	0	781	51	0
2	H	777	0	715	63	0
2	N	825	0	770	78	0
3	E	1432	0	1307	102	0
3	I	1404	0	1269	125	1
3	K	1452	0	1320	213	4
3	O	1435	0	1323	107	2
4	F	1852	0	1726	181	0
4	J	1759	0	1634	156	0
4	L	1699	0	1542	201	0
4	P	1784	0	1638	134	2
5	Q	64	0	74	12	0
5	R	64	0	74	12	0
5	T	64	0	74	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	U	64	0	74	27	0
6	A	9	0	0	4	0
6	B	1	0	0	0	0
6	C	8	0	0	1	0
6	D	2	0	0	0	0
6	E	2	0	0	0	0
6	G	7	0	0	3	0
6	I	3	0	0	1	0
6	J	2	0	0	1	0
6	K	2	0	0	0	0
6	M	3	0	0	3	0
6	N	5	0	0	2	0
6	O	5	0	0	0	0
6	P	5	0	0	1	0
All	All	25272	0	23369	1971	5

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 41.

All (1971) 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)
3:I:192:ILE:HG23	3:I:193:PRO:CD	1.42	1.46
1:A:230:LEU:HD21	1:A:243:LYS:NZ	1.27	1.43
3:K:175:TRP:CZ2	4:L:146:LEU:HD22	1.53	1.42
4:L:88:ALA:CB	4:L:110:ARG:HG3	1.46	1.41
3:K:112:ILE:CG2	3:K:139:ASP:HB3	1.48	1.41
3:K:175:TRP:CZ2	4:L:146:LEU:HD13	1.57	1.38
4:L:170:VAL:HA	4:L:194:LEU:CD2	1.51	1.38
3:K:38:TRP:CE3	3:K:44:PRO:HG3	1.59	1.38
4:P:112:LEU:CD1	4:P:154:HIS:CE1	2.05	1.38
1:C:202:ARG:CD	1:C:244:TRP:HE1	1.37	1.35
3:I:192:ILE:CG2	3:I:193:PRO:HD3	1.57	1.35
1:G:98:MET:HE2	1:G:113:TYR:CD1	1.59	1.34
4:J:29:HIS:HD2	4:J:94:SER:CB	1.40	1.34
3:K:61:ARG:HD2	3:K:78:LYS:O	1.25	1.32
4:P:14:GLU:OE2	4:P:117:LEU:CD2	1.76	1.31
1:G:98:MET:CE	1:G:113:TYR:CE1	2.15	1.30
2:N:13:HIS:CE1	4:F:81:ARG:NH2	1.99	1.29
2:D:44:GLU:OE2	2:D:46:ILE:HD11	1.28	1.28
3:K:138:PHE:HE1	3:K:157:LYS:CE	1.45	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:8:PRO:O	3:I:104:THR:HG23	1.23	1.27
1:A:102:ASP:CG	1:A:113:TYR:OH	1.73	1.26
1:G:192:HIS:CD2	1:G:202:ARG:HH21	1.51	1.26
1:G:98:MET:CE	1:G:113:TYR:CD1	2.19	1.26
4:F:170:VAL:CG1	4:F:194:LEU:HD13	1.64	1.26
3:K:175:TRP:CZ2	4:L:146:LEU:CD2	2.19	1.25
1:A:4:SER:HB2	1:A:102:ASP:OD1	1.36	1.25
4:P:7:SER:OG	4:P:22:ARG:HB3	1.35	1.25
1:A:230:LEU:CD2	1:A:243:LYS:NZ	1.98	1.24
4:J:47:ILE:HD11	4:J:60:LEU:CD2	1.66	1.24
3:K:175:TRP:HZ2	4:L:146:LEU:CG	1.52	1.21
1:G:97:ARG:NH1	5:U:6:VAL:CG1	2.01	1.21
4:L:88:ALA:HB3	4:L:110:ARG:CG	1.70	1.20
3:K:175:TRP:CZ2	4:L:146:LEU:CD1	2.23	1.20
3:E:167:PHE:HD2	3:E:168:LYS:N	1.39	1.20
1:G:97:ARG:HH11	5:U:6:VAL:CG1	1.52	1.19
3:O:138:PHE:CE1	3:O:142:THR:HG21	1.75	1.19
1:G:98:MET:HE1	1:G:113:TYR:CE1	1.76	1.19
3:K:136:THR:HG22	3:K:171:SER:HA	1.23	1.19
1:G:97:ARG:HH11	5:U:6:VAL:HG11	1.08	1.19
3:K:112:ILE:CG2	3:K:139:ASP:CB	2.21	1.17
3:K:138:PHE:CE1	3:K:157:LYS:CE	2.27	1.17
4:J:29:HIS:CD2	4:J:94:SER:CB	2.27	1.17
4:P:112:LEU:HD11	4:P:154:HIS:CE1	1.74	1.16
1:G:98:MET:HE2	1:G:113:TYR:CE1	1.80	1.16
1:G:97:ARG:NE	1:G:116:TYR:HE1	1.41	1.16
3:I:122:LEU:CA	3:I:132:VAL:O	1.93	1.15
3:K:161:ASP:CG	3:K:168:LYS:HD3	1.65	1.15
1:A:230:LEU:HD21	1:A:243:LYS:CE	1.77	1.14
3:O:182:ALA:HB1	3:O:185:ASN:HB3	1.24	1.14
4:L:89:VAL:HG12	4:L:110:ARG:CB	1.75	1.14
4:L:89:VAL:HG12	4:L:110:ARG:HB2	1.27	1.14
3:K:148:LYS:HB3	3:K:149:ASP:O	1.46	1.14
3:K:138:PHE:CE1	3:K:157:LYS:HE2	1.84	1.13
1:G:16:GLY:HA3	1:G:17:ARG:HB2	1.29	1.12
1:C:202:ARG:HD3	1:C:244:TRP:HE1	1.01	1.12
2:N:40:LEU:HD23	2:N:43:GLY:HA3	1.13	1.12
4:L:83:GLN:HG3	4:L:84:GLN:H	0.98	1.12
3:K:175:TRP:CE2	4:L:146:LEU:HD22	1.82	1.12
1:A:230:LEU:CD2	1:A:243:LYS:CE	2.28	1.12
4:F:170:VAL:HG13	4:F:194:LEU:CD1	1.78	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:175:TRP:HZ2	4:L:146:LEU:CD2	1.58	1.11
4:J:29:HIS:HD2	4:J:94:SER:HB2	1.07	1.10
4:L:88:ALA:HB1	4:L:89:VAL:HA	1.31	1.09
4:P:112:LEU:HD12	4:P:154:HIS:CE1	1.83	1.09
4:F:54:ALA:HB1	4:F:57:LYS:HE3	1.27	1.09
3:O:53:ASN:HB2	3:O:68:THR:HG23	1.33	1.09
3:K:175:TRP:HZ2	4:L:146:LEU:CD1	1.64	1.09
3:K:138:PHE:HE1	3:K:157:LYS:HE2	0.97	1.08
3:K:138:PHE:CE1	3:K:157:LYS:HE3	1.89	1.08
1:G:192:HIS:CD2	1:G:202:ARG:NH2	2.22	1.08
3:O:138:PHE:CE1	3:O:142:THR:CG2	2.35	1.07
4:J:47:ILE:HD11	4:J:60:LEU:HD21	1.12	1.07
4:F:218:SER:OG	4:F:221:ASP:HB2	1.55	1.07
2:N:73:THR:CG2	2:N:76:ASP:OD1	2.01	1.07
3:E:136:THR:HG23	3:E:171:SER:HB2	1.14	1.07
3:O:138:PHE:HE1	3:O:142:THR:CG2	1.68	1.07
1:G:2:SER:N	1:G:105:SER:HG	1.52	1.07
1:A:4:SER:HB3	1:A:102:ASP:CG	1.75	1.07
4:P:97:THR:HG22	4:P:98:GLN:HG2	1.37	1.07
1:M:78:LEU:HD23	1:M:95:VAL:CG2	1.86	1.06
4:J:141:ALA:HB3	4:J:196:VAL:O	1.55	1.06
3:I:146:GLN:CD	3:I:154:ILE:HG12	1.75	1.06
4:P:223:TRP:CH2	4:P:229:LYS:O	2.09	1.06
1:G:97:ARG:NE	1:G:116:TYR:CE1	2.15	1.06
3:K:112:ILE:HG23	3:K:139:ASP:HB3	1.10	1.05
1:C:202:ARG:CG	1:C:244:TRP:HE1	1.68	1.05
1:C:202:ARG:HD3	1:C:244:TRP:NE1	1.69	1.05
4:L:88:ALA:CB	4:L:110:ARG:CG	2.27	1.05
4:J:29:HIS:CD2	4:J:94:SER:HB2	1.87	1.05
4:P:14:GLU:HG2	4:P:117:LEU:HG	1.06	1.05
3:K:61:ARG:CD	3:K:78:LYS:O	2.04	1.05
2:B:37:VAL:HG12	2:B:82:VAL:HG22	1.10	1.05
1:M:19:GLU:OE1	1:M:19:GLU:N	1.88	1.04
4:J:29:HIS:CD2	4:J:94:SER:OG	2.09	1.04
4:P:14:GLU:HG2	4:P:117:LEU:CG	1.87	1.04
2:N:73:THR:HG22	2:N:76:ASP:OD1	1.56	1.04
4:P:112:LEU:HD11	4:P:154:HIS:HE1	1.10	1.04
1:A:102:ASP:CG	1:A:113:TYR:HH	1.53	1.04
3:I:33:LEU:HD12	3:I:91:ALA:O	1.58	1.04
4:J:113:VAL:O	4:J:114:LEU:HG	1.57	1.03
4:L:170:VAL:CA	4:L:194:LEU:CD2	2.35	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:14:GLU:CG	4:P:117:LEU:HG	1.89	1.03
4:P:14:GLU:OE2	4:P:117:LEU:HD21	0.87	1.03
3:K:185:ASN:O	3:K:188:ASN:ND2	1.91	1.03
1:M:20:PRO:HD2	1:M:75:ARG:CD	1.89	1.03
4:P:14:GLU:CD	4:P:117:LEU:HD21	1.77	1.03
4:J:136:SER:HA	4:J:139:GLN:OE1	1.58	1.03
4:L:170:VAL:CA	4:L:194:LEU:HD23	1.89	1.02
1:C:226:GLN:NE2	1:C:227:ASP:OD1	1.92	1.02
4:J:47:ILE:CD1	4:J:60:LEU:CD2	2.37	1.02
1:C:202:ARG:CD	1:C:244:TRP:NE1	2.21	1.01
3:K:148:LYS:HB3	3:K:149:ASP:C	1.79	1.01
4:L:204:PRO:HG3	4:L:241:GLY:HA3	1.42	1.01
4:F:218:SER:OG	4:F:221:ASP:CB	2.07	1.01
4:J:194:LEU:HD23	4:J:195:ARG:N	1.75	1.01
4:P:223:TRP:CZ2	4:P:229:LYS:O	2.13	1.01
3:E:136:THR:HG23	3:E:171:SER:CB	1.89	1.01
1:M:82:ARG:NH1	1:M:93:HIS:HD2	1.56	1.01
3:E:136:THR:CG2	3:E:171:SER:CB	2.40	1.00
1:A:4:SER:CB	1:A:102:ASP:OD1	2.08	1.00
1:M:78:LEU:HD23	1:M:95:VAL:HG23	1.41	1.00
4:P:196:VAL:HG22	4:P:197:SER:H	1.23	1.00
3:O:53:ASN:HB2	3:O:68:THR:CG2	1.89	1.00
4:J:47:ILE:CD1	4:J:60:LEU:HD23	1.91	0.99
3:E:181:PHE:HB2	3:E:182:ALA:HA	1.44	0.99
1:M:66:LYS:HZ1	3:O:29:ASN:CG	1.66	0.99
1:G:35:ARG:HH21	1:G:48:ARG:CG	1.76	0.99
3:K:175:TRP:HE1	4:L:146:LEU:HD21	1.25	0.98
1:G:116:TYR:HD2	1:G:117:ALA:N	1.61	0.98
4:P:112:LEU:HD12	4:P:154:HIS:NE2	1.78	0.97
1:A:4:SER:CB	1:A:102:ASP:CG	2.32	0.97
2:D:44:GLU:OE2	2:D:46:ILE:CD1	2.10	0.97
3:E:167:PHE:CD2	3:E:168:LYS:N	2.18	0.97
3:E:192:ILE:HG22	3:E:193:PRO:CD	1.94	0.97
4:L:170:VAL:HG22	4:L:194:LEU:HD21	1.44	0.97
1:G:82:ARG:HH21	1:G:89:GLU:N	1.61	0.97
4:L:89:VAL:CG1	4:L:110:ARG:HB2	1.93	0.97
1:M:82:ARG:HH11	1:M:93:HIS:HD2	1.03	0.97
3:E:83:GLU:HA	3:E:84:ASP:OD1	1.64	0.96
3:K:175:TRP:CH2	4:L:146:LEU:HD13	2.00	0.96
1:G:98:MET:CE	1:G:113:TYR:HE1	1.67	0.96
4:F:149:GLY:H	4:F:150:PHE:HD2	1.14	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:125:ALA:O	1:G:134:THR:HG22	1.64	0.95
3:E:136:THR:CG2	3:E:171:SER:HB2	1.93	0.95
1:A:227:ASP:OD2	1:A:248:VAL:HG22	1.65	0.95
1:M:73:THR:HG21	5:T:6:VAL:HG23	1.44	0.95
4:F:54:ALA:HB1	4:F:57:LYS:CE	1.96	0.95
1:A:230:LEU:CD2	1:A:243:LYS:HZ3	1.72	0.95
3:K:49:VAL:HG21	4:L:102:THR:HG22	1.47	0.95
1:G:97:ARG:HG2	1:G:116:TYR:CD1	2.02	0.95
4:F:159:TRP:HE1	4:F:192:SER:HG	1.15	0.95
3:K:185:ASN:CG	3:K:188:ASN:ND2	2.20	0.95
4:L:83:GLN:HG3	4:L:84:GLN:N	1.82	0.95
4:L:97:THR:CB	4:L:98:GLN:OE1	2.15	0.95
2:H:22:PHE:CD2	2:H:68:THR:O	2.20	0.95
4:P:97:THR:CG2	4:P:98:GLN:HG2	1.96	0.94
1:G:97:ARG:NH1	5:U:6:VAL:HG13	1.81	0.94
1:G:2:SER:N	1:G:105:SER:OG	1.98	0.94
2:N:42:ASN:H	2:N:43:GLY:HA2	1.32	0.94
1:G:187:THR:HB	1:G:272:LEU:HD21	1.49	0.94
4:P:223:TRP:CZ2	4:P:225:GLN:NE2	2.34	0.94
3:I:14:GLN:OE1	3:I:14:GLN:N	2.00	0.94
3:K:112:ILE:HG21	3:K:139:ASP:HB3	1.47	0.94
3:K:148:LYS:HB2	3:K:149:ASP:HA	1.48	0.93
2:N:13:HIS:HE1	4:F:81:ARG:NH2	1.60	0.93
3:O:81:GLN:HB3	3:O:82:PRO:HD2	1.48	0.93
4:F:160:TRP:NE1	4:F:165:GLU:HA	1.81	0.93
1:A:35:ARG:HD3	1:A:48:ARG:HE	1.32	0.93
2:N:13:HIS:CE1	4:F:81:ARG:HH22	1.75	0.93
4:P:223:TRP:CH2	4:P:225:GLN:NE2	2.35	0.93
4:L:83:GLN:CG	4:L:84:GLN:H	1.80	0.93
3:K:192:ILE:HG13	3:K:193:PRO:HD2	1.50	0.93
2:N:13:HIS:CE1	4:F:81:ARG:HH21	1.74	0.93
4:L:191:SER:OG	4:L:193:ARG:NH2	2.02	0.93
1:C:231:VAL:HG11	1:C:244:TRP:HE3	1.33	0.92
1:G:16:GLY:CA	1:G:17:ARG:HB2	1.99	0.92
1:M:20:PRO:HD2	1:M:75:ARG:HD3	1.47	0.92
3:I:8:PRO:O	3:I:104:THR:CG2	2.15	0.92
3:K:136:THR:HB	3:K:170:ASN:O	1.69	0.92
1:G:98:MET:HE2	1:G:113:TYR:HD1	1.29	0.91
1:M:219:ARG:HD3	1:M:224:GLN:NE2	1.86	0.91
4:P:160:TRP:HE3	4:P:209:ARG:HD2	1.34	0.91
1:C:4:SER:HB3	1:C:102:ASP:OD1	1.71	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:170:VAL:HA	4:L:194:LEU:HD23	0.93	0.91
4:F:223:TRP:HH2	4:F:228:ALA:O	1.54	0.91
3:K:112:ILE:HG23	3:K:139:ASP:CB	1.95	0.91
4:F:170:VAL:HG13	4:F:194:LEU:HD13	0.94	0.91
4:J:135:ILE:HA	4:J:140:LYS:O	1.71	0.91
3:K:53:ASN:HA	3:K:66:LEU:HD22	1.53	0.91
3:K:136:THR:HG22	3:K:171:SER:CA	2.00	0.91
1:G:98:MET:HE1	1:G:113:TYR:HE1	1.11	0.91
1:C:131:ARG:HH11	1:C:131:ARG:HG3	1.35	0.90
1:G:35:ARG:HH21	1:G:48:ARG:HG2	1.36	0.90
2:N:4:THR:HG23	2:N:86:THR:HG21	1.51	0.90
3:K:175:TRP:CE2	4:L:146:LEU:CD2	2.49	0.90
4:L:202:GLN:CA	4:L:204:PRO:HD2	2.01	0.90
4:F:149:GLY:HA3	4:F:150:PHE:HB3	1.53	0.90
3:O:138:PHE:CD1	3:O:142:THR:HG21	2.06	0.90
1:C:102:ASP:CG	1:C:113:TYR:OH	2.10	0.90
3:I:178:LYS:CG	3:I:179:SER:OG	2.19	0.90
3:K:161:ASP:CG	3:K:168:LYS:CD	2.39	0.90
1:G:162:GLY:O	1:G:166:GLU:HG2	1.72	0.90
4:L:89:VAL:HG12	4:L:110:ARG:CG	1.99	0.89
4:P:112:LEU:CD1	4:P:154:HIS:NE2	2.33	0.89
1:G:17:ARG:HG3	1:G:17:ARG:HH11	1.37	0.89
3:K:38:TRP:HE3	3:K:44:PRO:HG3	1.35	0.89
1:M:10:THR:HG21	2:N:54:LEU:HD22	1.53	0.89
4:F:160:TRP:O	4:F:209:ARG:HG2	1.73	0.89
1:C:100:GLY:O	1:C:113:TYR:HD2	1.56	0.89
2:H:24:ASN:HD21	2:H:65:LEU:HG	1.38	0.89
1:M:188:HIS:HB2	1:M:204:TRP:HB2	1.55	0.89
4:F:193:ARG:HG3	4:F:193:ARG:HH11	1.38	0.89
3:I:138:PHE:HE1	3:I:142:THR:HG1	1.18	0.89
3:K:156:ASP:OD1	3:K:157:LYS:N	2.06	0.88
1:A:230:LEU:HD21	1:A:243:LYS:HZ3	0.84	0.88
3:K:175:TRP:CZ2	4:L:146:LEU:CG	2.45	0.88
2:N:40:LEU:CD2	2:N:43:GLY:HA3	2.02	0.88
1:M:82:ARG:NH1	1:M:93:HIS:CD2	2.41	0.88
3:K:161:ASP:OD1	3:K:168:LYS:CD	2.20	0.88
3:K:144:VAL:HG23	3:K:157:LYS:NZ	1.89	0.88
4:L:88:ALA:HB3	4:L:110:ARG:HG3	0.88	0.87
2:N:54:LEU:HD21	2:N:62:PHE:CD1	2.09	0.87
1:G:98:MET:CE	1:G:113:TYR:HD1	1.75	0.87
1:C:202:ARG:CG	1:C:244:TRP:NE1	2.37	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:88:ALA:HB1	4:L:110:ARG:HG3	1.57	0.87
3:O:138:PHE:CE1	3:O:142:THR:CB	2.56	0.87
3:K:112:ILE:HG22	3:K:139:ASP:OD2	1.75	0.86
1:A:102:ASP:OD2	1:A:113:TYR:OH	1.93	0.86
4:P:151:TYR:O	4:P:214:PHE:CE1	2.27	0.86
3:K:135:PHE:HZ	3:K:192:ILE:CD1	1.88	0.86
2:N:13:HIS:HE1	4:F:81:ARG:HH22	1.12	0.86
1:G:116:TYR:CD2	1:G:117:ALA:N	2.43	0.86
3:I:146:GLN:OE1	3:I:154:ILE:CD1	2.24	0.86
1:G:16:GLY:HA3	1:G:17:ARG:CB	2.05	0.86
3:K:175:TRP:NE1	4:L:146:LEU:HD21	1.90	0.86
1:M:215:LEU:HD21	1:M:261:VAL:HG22	1.55	0.86
1:M:82:ARG:HH11	1:M:93:HIS:CD2	1.93	0.85
1:A:230:LEU:HD23	1:A:243:LYS:CE	2.03	0.85
4:P:7:SER:OG	4:P:22:ARG:CB	2.22	0.85
3:O:80:SER:O	3:O:81:GLN:NE2	2.09	0.85
3:O:61:ARG:NH1	3:O:84:ASP:OD2	2.09	0.85
4:F:121:PHE:CE2	4:F:187:ARG:NH2	2.44	0.85
3:E:178:LYS:O	3:E:179:SER:OG	1.95	0.85
3:I:146:GLN:OE1	3:I:154:ILE:HD11	1.75	0.85
3:E:38:TRP:HD1	3:E:44:PRO:HG3	1.41	0.85
4:F:110:ARG:NH2	4:F:154:HIS:CD2	2.45	0.85
2:N:2:GLN:NE2	2:N:85:VAL:HB	1.91	0.85
3:E:136:THR:CG2	3:E:171:SER:HB3	2.06	0.84
1:C:226:GLN:OE1	1:C:227:ASP:N	2.09	0.84
4:L:127:VAL:HG11	4:L:239:ALA:HB2	1.57	0.84
1:G:225:THR:O	6:G:301:HOH:O	1.95	0.84
4:F:96:GLN:O	4:F:97:THR:OG1	1.94	0.84
1:A:42:SER:OG	1:A:44:ARG:HG2	1.77	0.84
4:F:201:TRP:C	4:F:204:PRO:HD3	1.97	0.84
3:I:15:GLU:OE2	6:I:301:HOH:O	1.94	0.84
3:O:119:VAL:HA	3:O:134:LEU:O	1.77	0.84
1:M:9:PHE:HB2	1:M:97:ARG:HB3	1.60	0.84
3:K:175:TRP:NE1	4:L:146:LEU:CD2	2.40	0.84
4:J:223:TRP:CE3	4:J:223:TRP:HA	2.13	0.83
3:K:120:TYR:HH	4:L:135:ILE:N	1.76	0.83
4:F:54:ALA:CB	4:F:57:LYS:HE3	2.07	0.83
4:L:161:VAL:HG23	4:L:166:VAL:HG11	1.59	0.83
3:O:53:ASN:CB	3:O:68:THR:HG23	2.06	0.83
4:F:160:TRP:HE1	4:F:165:GLU:HA	1.37	0.83
1:C:45:MET:H	1:C:64:THR:HG22	1.41	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:39:LEU:HD12	4:P:39:LEU:O	1.77	0.83
4:F:26:ILE:O	4:F:27:SER:OG	1.96	0.83
2:D:79:ALA:HB1	2:D:92:ILE:HD11	1.59	0.83
1:G:125:ALA:HB3	1:G:134:THR:CG2	2.08	0.83
4:F:197:SER:HB3	4:F:200:PHE:HB2	1.60	0.83
1:G:218:GLN:HB3	1:G:223:ASP:HA	1.59	0.83
4:J:84:GLN:NE2	1:G:177:GLU:OE1	2.11	0.83
4:J:129:GLU:HG3	4:J:130:PRO:HD2	1.59	0.83
3:E:192:ILE:HG22	3:E:193:PRO:HD2	1.60	0.83
4:J:194:LEU:CD2	4:J:196:VAL:HG23	2.08	0.82
1:G:58:GLU:O	1:G:62:GLY:N	2.13	0.82
4:L:150:PHE:CE1	4:L:188:TYR:O	2.33	0.82
2:N:12:ARG:O	2:N:13:HIS:CG	2.32	0.82
3:O:138:PHE:CE1	3:O:142:THR:HB	2.14	0.82
3:I:178:LYS:HG2	3:I:179:SER:HG	1.44	0.82
1:M:66:LYS:NZ	3:O:29:ASN:CG	2.32	0.82
3:E:30:PHE:HD2	3:E:92:PHE:CE2	1.98	0.82
4:F:46:LEU:O	4:F:59:GLY:HA3	1.80	0.82
3:K:38:TRP:CE3	3:K:44:PRO:CG	2.55	0.82
3:E:136:THR:HA	3:E:138:PHE:HE1	1.45	0.82
1:C:100:GLY:O	1:C:113:TYR:CD2	2.32	0.82
2:D:54:LEU:HD21	2:D:62:PHE:CD1	2.13	0.82
4:P:160:TRP:HD1	4:P:165:GLU:HG3	1.44	0.82
1:A:230:LEU:CD2	1:A:243:LYS:HZ1	1.90	0.81
4:L:123:PRO:HG3	4:L:150:PHE:HD2	1.43	0.81
3:K:148:LYS:CB	3:K:149:ASP:C	2.49	0.81
3:E:178:LYS:C	3:E:179:SER:OG	2.11	0.81
3:I:194:GLU:O	3:I:196:THR:CG2	2.28	0.81
1:C:192:HIS:CE1	1:C:202:ARG:HH12	1.98	0.81
3:K:161:ASP:OD1	3:K:168:LYS:HD2	1.81	0.81
1:C:225:THR:O	1:C:228:THR:HG22	1.79	0.81
3:I:178:LYS:C	3:I:179:SER:OG	2.16	0.81
2:B:37:VAL:CG1	2:B:82:VAL:HG22	2.04	0.81
2:B:17:ASN:ND2	2:B:74:GLU:OE1	2.14	0.81
3:I:178:LYS:HG2	3:I:179:SER:OG	1.79	0.80
4:J:160:TRP:CZ3	4:J:211:GLN:CB	2.64	0.80
4:P:112:LEU:CG	4:P:154:HIS:CE1	2.63	0.80
4:P:19:VAL:HG22	4:P:79:ILE:HG12	1.63	0.80
3:E:136:THR:HG22	3:E:171:SER:HB3	1.63	0.80
3:O:122:LEU:HD22	4:P:130:PRO:HA	1.64	0.80
1:G:14:ARG:O	1:G:18:GLY:HA3	1.80	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:SER:CB	1:C:102:ASP:OD1	2.29	0.80
3:E:138:PHE:O	3:E:139:ASP:C	2.16	0.79
1:G:192:HIS:HD2	1:G:202:ARG:NH2	1.69	0.79
1:A:223:ASP:O	1:A:225:THR:HG23	1.82	0.79
3:I:138:PHE:CD1	3:I:142:THR:OG1	2.35	0.79
1:M:220:ASP:OD1	6:M:301:HOH:O	2.01	0.79
4:F:223:TRP:CZ3	4:F:230:PRO:HD2	2.18	0.79
1:C:234:ARG:NH2	1:C:242:GLN:OE1	2.12	0.79
2:H:70:PHE:HE1	2:H:78:TYR:CD1	2.00	0.79
3:K:49:VAL:HG21	4:L:102:THR:CG2	2.13	0.79
3:O:81:GLN:HB3	3:O:82:PRO:CD	2.12	0.78
4:F:110:ARG:NH2	4:F:154:HIS:HD2	1.80	0.78
3:I:146:GLN:CD	3:I:154:ILE:CG1	2.52	0.78
1:G:125:ALA:HB3	1:G:134:THR:HG21	1.64	0.78
4:P:178:LYS:HA	4:P:187:ARG:O	1.81	0.78
4:J:27:SER:OG	6:J:301:HOH:O	2.00	0.78
3:I:192:ILE:HG23	3:I:193:PRO:HD3	0.78	0.78
3:K:38:TRP:CZ3	3:K:42:LYS:O	2.35	0.78
3:K:112:ILE:HG22	3:K:139:ASP:CG	2.05	0.78
4:F:149:GLY:N	4:F:150:PHE:HD2	1.81	0.78
4:L:25:PRO:HG3	4:L:32:LEU:HD13	1.65	0.78
4:L:64:ARG:O	4:L:80:GLN:NE2	2.17	0.78
3:K:175:TRP:HE1	4:L:146:LEU:CD2	1.96	0.78
3:K:144:VAL:HG23	3:K:157:LYS:HZ1	1.46	0.78
2:N:73:THR:HG21	2:N:76:ASP:OD1	1.81	0.78
1:G:133:TRP:CZ3	1:G:147:TRP:CZ3	2.72	0.78
3:E:49:VAL:CG2	4:F:102:THR:HG22	2.13	0.78
3:K:148:LYS:CB	3:K:149:ASP:CA	2.61	0.77
3:I:115:PRO:CB	3:I:137:ASP:OD2	2.32	0.77
3:K:49:VAL:CG2	4:L:102:THR:HG22	2.15	0.77
1:C:93:HIS:ND1	1:C:118:TYR:OH	2.14	0.77
4:J:60:LEU:O	4:J:60:LEU:HD12	1.83	0.77
2:B:37:VAL:HG21	2:B:66:TYR:CE1	2.19	0.77
3:I:178:LYS:HG3	3:I:179:SER:OG	1.83	0.77
1:C:72:GLN:HG3	4:F:55:PRO:HB2	1.66	0.77
1:M:192:HIS:O	1:M:200:THR:OG1	2.02	0.77
1:C:66:LYS:NZ	5:R:1:ASN:OD1	2.18	0.77
3:O:138:PHE:HD1	3:O:142:THR:OG1	1.67	0.77
2:N:42:ASN:O	6:N:101:HOH:O	2.01	0.77
1:M:87:GLN:OE1	1:M:93:HIS:NE2	2.17	0.77
2:N:42:ASN:N	2:N:43:GLY:HA2	1.96	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:97:THR:OG1	4:F:98:GLN:HG2	1.85	0.77
4:L:170:VAL:CG2	4:L:194:LEU:HD21	2.15	0.77
4:J:217:LEU:HD13	4:J:221:ASP:HB3	1.67	0.77
3:K:138:PHE:CZ	3:K:157:LYS:HE3	2.19	0.77
4:F:217:LEU:CD1	4:F:218:SER:H	1.97	0.77
1:M:78:LEU:CD2	1:M:95:VAL:HG23	2.13	0.77
1:A:187:THR:HB	1:A:272:LEU:HD11	1.67	0.77
2:D:87:LEU:HD13	2:D:90:PRO:HA	1.66	0.77
1:G:188:HIS:HB3	1:G:204:TRP:HB2	1.66	0.77
1:G:220:ASP:OD2	1:G:256:ARG:CZ	2.32	0.77
4:J:84:GLN:HA	4:J:113:VAL:HG21	1.67	0.77
3:I:138:PHE:CE1	3:I:142:THR:OG1	2.38	0.76
4:P:14:GLU:H	4:P:17:LYS:HZ1	1.33	0.76
1:G:218:GLN:HB2	1:G:222:GLU:O	1.86	0.76
1:A:4:SER:HB3	1:A:102:ASP:OD2	1.84	0.76
4:P:7:SER:HG	4:P:22:ARG:HB3	1.51	0.76
4:F:132:GLU:HG3	4:F:135:ILE:HG21	1.68	0.76
4:F:159:TRP:O	4:F:166:VAL:HB	1.84	0.76
2:N:30:PHE:CE1	2:N:62:PHE:HB2	2.20	0.76
4:L:143:LEU:HD12	4:L:144:VAL:N	2.00	0.76
1:G:133:TRP:CZ3	1:G:147:TRP:CE3	2.72	0.76
1:C:235:PRO:O	2:D:10:TYR:OH	2.01	0.76
3:K:161:ASP:OD1	3:K:168:LYS:HD3	1.83	0.76
1:A:230:LEU:HD21	1:A:243:LYS:HE2	1.68	0.76
3:K:185:ASN:CG	3:K:188:ASN:HD22	1.89	0.76
4:L:143:LEU:HD12	4:L:144:VAL:H	1.50	0.76
2:N:54:LEU:HD21	2:N:62:PHE:HD1	1.51	0.76
2:D:76:ASP:HB3	2:D:78:TYR:HE1	1.50	0.76
3:O:53:ASN:CB	3:O:68:THR:CG2	2.62	0.75
4:P:223:TRP:HZ2	4:P:225:GLN:HE21	1.30	0.75
2:H:24:ASN:OD1	2:H:65:LEU:HD23	1.86	0.75
2:B:89:GLN:HB2	2:B:90:PRO:HD2	1.68	0.75
3:K:17:ASP:O	3:K:80:SER:OG	2.04	0.75
3:K:135:PHE:CZ	3:K:192:ILE:CD1	2.70	0.75
2:D:44:GLU:HG2	2:D:46:ILE:HG12	1.67	0.75
1:G:97:ARG:NH1	5:U:6:VAL:HG11	1.84	0.75
4:J:223:TRP:HE3	4:J:223:TRP:HA	1.47	0.75
1:A:122:ASP:OD1	2:B:60:TRP:NE1	2.20	0.75
3:K:59:LYS:HD2	3:K:60:GLY:H	1.50	0.75
4:J:113:VAL:O	4:J:114:LEU:CG	2.35	0.75
1:G:17:ARG:HG3	1:G:17:ARG:NH1	1.99	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:151:TYR:O	4:P:214:PHE:CZ	2.40	0.75
1:M:20:PRO:HD2	1:M:75:ARG:HD2	1.67	0.75
4:J:57:LYS:O	4:J:59:GLY:N	2.17	0.75
4:P:122:PRO:HD3	4:P:230:PRO:HG3	1.69	0.75
4:P:14:GLU:HB2	4:P:17:LYS:HE3	1.69	0.75
1:G:97:ARG:HH12	5:U:6:VAL:CG1	1.99	0.75
3:E:84:ASP:HB3	3:E:85:SER:HB2	1.69	0.75
4:F:142:THR:HA	4:F:195:ARG:HB2	1.66	0.75
3:K:31:TYR:HD1	5:U:4:PRO:HB2	1.52	0.75
4:J:29:HIS:CD2	4:J:94:SER:C	2.59	0.75
1:G:192:HIS:CD2	1:G:202:ARG:HD2	2.21	0.75
3:K:185:ASN:C	3:K:188:ASN:HD22	1.90	0.75
3:E:49:VAL:HG21	4:F:102:THR:HG22	1.67	0.75
1:A:96:GLN:OE1	2:B:60:TRP:CE3	2.39	0.75
1:A:230:LEU:CD2	1:A:243:LYS:HE2	2.13	0.74
4:P:112:LEU:CG	4:P:154:HIS:NE2	2.50	0.74
1:A:102:ASP:OD1	1:A:113:TYR:OH	1.93	0.74
4:L:153:ASP:HB2	4:L:188:TYR:CD2	2.22	0.74
1:C:192:HIS:ND1	1:C:202:ARG:NH1	2.30	0.74
3:K:148:LYS:HB2	3:K:149:ASP:CA	2.17	0.74
4:P:112:LEU:HG	4:P:154:HIS:NE2	2.02	0.74
3:E:136:THR:CA	3:E:138:PHE:HE1	2.00	0.74
1:C:131:ARG:HG3	1:C:131:ARG:NH1	1.98	0.74
3:O:53:ASN:HB2	3:O:68:THR:CB	2.17	0.74
3:K:135:PHE:CZ	3:K:192:ILE:HG12	2.23	0.74
4:P:112:LEU:CD1	4:P:154:HIS:HE1	1.71	0.74
4:F:218:SER:OG	4:F:221:ASP:HB3	1.86	0.74
4:F:223:TRP:CH2	4:F:228:ALA:O	2.39	0.74
3:E:97:GLN:NE2	3:E:99:TYR:OH	2.20	0.74
4:L:88:ALA:CB	4:L:89:VAL:HA	2.03	0.74
4:J:47:ILE:CG1	4:J:60:LEU:HD23	2.18	0.74
1:C:66:LYS:HD2	5:R:4:PRO:HA	1.67	0.74
1:A:93:HIS:ND1	1:A:119:ASP:OD1	2.20	0.74
3:K:25:PHE:CZ	3:K:71:GLY:HA2	2.22	0.74
3:K:192:ILE:HG13	3:K:193:PRO:CD	2.17	0.74
3:K:93:ILE:HG22	5:U:5:MET:HE1	1.70	0.74
3:O:138:PHE:CD1	3:O:142:THR:CB	2.71	0.73
1:A:33:PHE:HD1	1:A:52:ILE:HD12	1.52	0.73
3:I:48:PHE:HE1	3:I:59:LYS:HG3	1.52	0.73
4:F:205:ARG:HA	4:F:240:TRP:CH2	2.23	0.73
3:O:138:PHE:HE1	3:O:142:THR:CB	1.96	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:192:ILE:CG2	3:E:193:PRO:HD3	2.17	0.73
1:C:35:ARG:HD2	2:D:53:ASP:CG	2.08	0.73
4:J:178:LYS:HD2	4:J:188:TYR:CE1	2.23	0.73
4:F:201:TRP:O	4:F:204:PRO:CD	2.36	0.73
1:A:202:ARG:HG3	1:A:244:TRP:HE1	1.53	0.73
1:G:192:HIS:HD2	1:G:202:ARG:HH21	0.87	0.73
1:M:259:CYS:HB3	1:M:272:LEU:HB2	1.70	0.73
1:G:186:LYS:O	1:G:186:LYS:HG3	1.87	0.73
2:H:21:ASN:OD1	2:H:22:PHE:N	2.22	0.73
3:I:194:GLU:O	3:I:196:THR:HG23	1.89	0.73
1:G:214:THR:O	1:G:214:THR:HG23	1.89	0.73
3:I:192:ILE:CG2	3:I:193:PRO:CD	2.36	0.73
3:E:192:ILE:CG2	3:E:193:PRO:CD	2.66	0.73
4:P:159:TRP:CD1	4:P:209:ARG:O	2.41	0.73
4:J:129:GLU:CG	4:J:130:PRO:HD2	2.18	0.73
2:B:36:GLU:HB2	2:B:83:ASN:HB3	1.71	0.73
4:L:10:ASN:HB2	4:L:154:HIS:NE2	2.04	0.72
1:C:202:ARG:HE	1:C:244:TRP:HZ2	1.33	0.72
1:G:191:HIS:O	1:G:191:HIS:ND1	2.20	0.72
3:K:138:PHE:O	3:K:139:ASP:OD1	2.07	0.72
3:I:146:GLN:NE2	3:I:154:ILE:HG12	2.04	0.72
4:L:173:ASP:OD2	4:L:191:SER:OG	2.07	0.72
1:C:225:THR:O	1:C:228:THR:N	2.16	0.72
2:H:37:VAL:HG23	2:H:81:ARG:O	1.88	0.72
4:J:116:ASP:HB3	4:J:119:ASN:N	2.05	0.72
4:L:202:GLN:C	4:L:204:PRO:HD2	2.09	0.72
1:A:99:TYR:OH	5:Q:3:VAL:HG12	1.90	0.72
4:P:18:ASP:OD2	2:D:20:SER:OG	2.08	0.72
3:E:42:LYS:HD2	3:E:43:SER:H	1.55	0.72
4:J:194:LEU:HD22	4:J:196:VAL:HG23	1.70	0.72
4:F:160:TRP:O	4:F:209:ARG:CG	2.37	0.72
3:K:34:HIS:HB2	3:K:91:ALA:HB3	1.71	0.72
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.70	0.72
4:F:150:PHE:CE1	4:F:155:VAL:HG11	2.23	0.72
4:L:88:ALA:HB1	4:L:89:VAL:CA	2.15	0.72
1:C:235:PRO:HD2	2:D:10:TYR:OH	1.89	0.72
3:K:2:LEU:HB3	3:K:3:ASN:HA	1.70	0.72
4:L:202:GLN:HA	4:L:204:PRO:HD2	1.70	0.72
4:P:196:VAL:HG22	4:P:197:SER:N	2.02	0.72
3:I:117:PRO:HB2	3:I:196:THR:HB	1.71	0.72
3:K:9:GLN:HA	3:K:104:THR:HA	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:89:GLN:HG3	2:D:90:PRO:HD2	1.72	0.72
4:J:98:GLN:HB2	4:J:101:GLU:OE1	1.90	0.72
1:M:96:GLN:NE2	2:N:31:HIS:HE1	1.87	0.72
1:M:59:TYR:OH	1:M:171:TYR:OH	2.06	0.71
4:J:114:LEU:N	4:J:114:LEU:HD12	2.03	0.71
1:M:197:HIS:O	1:M:198:GLU:HG2	1.90	0.71
1:M:224:GLN:OE1	1:M:227:ASP:HB3	1.90	0.71
4:P:160:TRP:CE3	4:P:209:ARG:HD2	2.22	0.71
3:O:70:GLU:N	3:O:71:GLY:HA2	2.05	0.71
4:J:29:HIS:NE2	4:J:94:SER:O	2.22	0.71
3:E:30:PHE:HD2	3:E:92:PHE:HE2	1.39	0.71
4:J:178:LYS:HD2	4:J:188:TYR:HE1	1.55	0.71
1:M:89:GLU:HG2	1:M:89:GLU:O	1.90	0.71
4:F:170:VAL:HA	4:F:194:LEU:HD12	1.72	0.71
1:M:87:GLN:OE1	1:M:93:HIS:CE1	2.44	0.71
1:A:223:ASP:O	1:A:225:THR:CG2	2.38	0.71
2:N:12:ARG:O	2:N:13:HIS:ND1	2.23	0.71
2:H:24:ASN:HD21	2:H:65:LEU:CG	2.03	0.70
2:H:24:ASN:OD1	2:H:65:LEU:CD2	2.39	0.70
3:K:102:THR:OG1	3:K:103:GLY:N	2.23	0.70
3:E:112:ILE:HG22	3:E:115:PRO:HD3	1.73	0.70
4:F:84:GLN:CD	4:F:85:GLU:H	1.93	0.70
4:P:112:LEU:HG	4:P:154:HIS:CE1	2.26	0.70
3:E:178:LYS:O	3:E:180:ASP:N	2.21	0.70
3:I:194:GLU:O	3:I:196:THR:HG22	1.91	0.70
1:A:230:LEU:HD23	1:A:243:LYS:HE3	1.71	0.70
4:P:151:TYR:O	4:P:214:PHE:HE1	1.75	0.70
4:F:217:LEU:HD13	4:F:218:SER:H	1.54	0.70
4:L:160:TRP:NE1	4:L:163:GLY:O	2.23	0.70
2:D:33:SER:HB3	2:D:62:PHE:CD2	2.25	0.70
1:G:192:HIS:CG	1:G:202:ARG:NH2	2.60	0.70
4:F:121:PHE:HE2	4:F:187:ARG:HH21	1.37	0.70
3:K:112:ILE:CG2	3:K:139:ASP:CG	2.59	0.70
1:M:95:VAL:CG1	1:M:116:TYR:CE1	2.74	0.70
1:M:66:LYS:CE	3:O:29:ASN:ND2	2.54	0.70
4:L:89:VAL:HG12	4:L:110:ARG:HG3	1.73	0.70
1:C:218:GLN:HG2	1:C:260:HIS:CD2	2.27	0.70
1:A:59:TYR:HH	1:A:171:TYR:HH	1.40	0.70
3:O:155:THR:HG23	4:P:173:ASP:OD2	1.91	0.70
4:P:119:ASN:HB3	4:P:151:TYR:CD2	2.27	0.70
1:C:231:VAL:HG11	1:C:244:TRP:CE3	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:204:PRO:CG	4:L:241:GLY:HA3	2.19	0.69
2:N:4:THR:CG2	2:N:86:THR:HG21	2.22	0.69
3:E:136:THR:HA	3:E:138:PHE:CE1	2.27	0.69
3:K:50:MET:HB3	3:K:66:LEU:HD12	1.73	0.69
2:N:57:SER:O	2:N:59:ASP:N	2.24	0.69
4:P:25:PRO:HD3	4:P:32:LEU:HD21	1.74	0.69
4:L:202:GLN:HA	4:L:202:GLN:OE1	1.90	0.69
4:J:160:TRP:HB2	4:J:209:ARG:CB	2.23	0.69
3:K:59:LYS:HD2	3:K:60:GLY:N	2.07	0.69
3:K:35:TRP:HE1	3:K:75:LEU:HD22	1.56	0.69
3:O:34:HIS:HB2	3:O:91:ALA:HB3	1.72	0.69
4:L:9:SER:O	4:L:10:ASN:OD1	2.09	0.69
4:L:127:VAL:CG1	4:L:239:ALA:HB2	2.22	0.69
2:D:24:ASN:HB3	2:D:65:LEU:HD11	1.73	0.69
4:L:88:ALA:HB1	4:L:110:ARG:HA	1.75	0.69
4:L:170:VAL:HA	4:L:194:LEU:HD21	1.69	0.69
3:I:122:LEU:CA	3:I:132:VAL:H	2.05	0.69
3:K:148:LYS:CB	3:K:149:ASP:HA	2.20	0.69
4:F:201:TRP:O	4:F:204:PRO:HD3	1.93	0.69
4:L:33:TYR:HB2	4:L:93:ALA:HB3	1.73	0.69
1:G:24:ALA:HB3	1:G:36:PHE:HB3	1.74	0.69
4:L:125:VAL:HB	4:L:237:ALA:HB2	1.73	0.69
2:B:24:ASN:HB3	2:B:65:LEU:HD11	1.74	0.69
3:O:138:PHE:HD1	3:O:142:THR:HG1	1.37	0.69
4:P:160:TRP:CD1	4:P:165:GLU:HG3	2.27	0.69
1:A:99:TYR:CZ	5:Q:3:VAL:HG12	2.26	0.69
3:I:161:ASP:OD2	3:I:166:ASP:N	2.25	0.69
2:H:71:THR:OG1	2:H:72:PRO:HD3	1.92	0.68
4:J:47:ILE:HG13	4:J:60:LEU:HD23	1.74	0.68
1:M:219:ARG:NH2	1:M:222:GLU:OE1	2.26	0.68
3:I:146:GLN:NE2	3:I:154:ILE:CG1	2.57	0.68
4:J:85:GLU:O	4:J:87:SER:N	2.27	0.68
1:G:35:ARG:HE	1:G:48:ARG:HG3	1.56	0.68
1:G:159:TYR:CD1	1:G:163:THR:OG1	2.46	0.68
4:F:98:GLN:NE2	4:F:98:GLN:HA	2.08	0.68
1:G:192:HIS:HB2	1:G:202:ARG:HH22	1.57	0.68
1:M:22:PHE:H	1:M:38:SER:HB2	1.56	0.68
2:H:22:PHE:HD2	2:H:68:THR:O	1.75	0.68
3:I:117:PRO:O	3:I:196:THR:O	2.12	0.68
3:I:34:HIS:HB2	3:I:91:ALA:HB3	1.73	0.68
1:G:162:GLY:O	1:G:166:GLU:CG	2.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:5:MET:HB3	1:M:168:LEU:HD13	1.75	0.68
4:L:10:ASN:HB2	4:L:154:HIS:CE1	2.28	0.68
4:L:36:ARG:HB3	4:L:89:VAL:O	1.94	0.68
3:K:112:ILE:HG22	3:K:139:ASP:CB	2.21	0.68
4:L:114:LEU:HD23	4:L:116:ASP:H	1.59	0.68
4:L:90:TYR:N	4:L:109:THR:O	2.22	0.68
1:G:98:MET:HE3	1:G:99:TYR:HA	1.76	0.68
1:M:200:THR:HG22	1:M:248:VAL:HA	1.75	0.68
3:K:131:SER:HG	4:L:128:PHE:HD1	1.41	0.68
1:C:27:TYR:CE2	1:C:32:GLN:HB2	2.28	0.68
4:J:153:ASP:O	4:J:155:VAL:N	2.26	0.67
3:O:53:ASN:CB	3:O:68:THR:OG1	2.43	0.67
3:I:146:GLN:HE22	3:I:154:ILE:HD13	1.57	0.67
4:L:123:PRO:HG3	4:L:150:PHE:CD2	2.27	0.67
1:M:21:ARG:HG3	1:M:38:SER:HB3	1.76	0.67
1:C:10:THR:HG21	2:D:54:LEU:HD22	1.75	0.67
3:E:50:MET:HB3	3:E:66:LEU:HD12	1.75	0.67
4:L:62:SER:CA	4:L:65:PHE:CE2	2.78	0.67
1:G:6:ARG:HB3	1:G:8:PHE:HE2	1.60	0.67
3:K:148:LYS:CB	3:K:149:ASP:O	2.34	0.67
4:J:113:VAL:C	4:J:114:LEU:HG	2.14	0.67
3:O:117:PRO:HB2	3:O:196:THR:HA	1.77	0.67
4:L:47:ILE:HD11	4:L:67:ALA:HB3	1.77	0.67
4:F:98:GLN:HB2	4:F:101:GLU:OE1	1.95	0.67
3:O:134:LEU:HD13	3:O:173:VAL:HG12	1.75	0.67
3:K:123:ARG:HA	3:K:131:SER:OG	1.94	0.67
1:G:55:GLU:O	1:G:59:TYR:HB3	1.95	0.67
1:A:121:LYS:HE3	2:B:1:ILE:HD13	1.77	0.67
3:K:11:LEU:HB3	3:K:106:LEU:HD13	1.76	0.67
3:O:160:LEU:O	3:O:168:LYS:HA	1.95	0.67
3:E:132:VAL:HG22	3:E:175:TRP:HB3	1.75	0.67
4:P:14:GLU:OE2	4:P:117:LEU:CG	2.40	0.67
1:A:42:SER:OG	1:A:44:ARG:CG	2.42	0.67
3:K:112:ILE:HG21	3:K:139:ASP:CB	2.13	0.66
1:G:143:THR:HB	5:U:9:VAL:HG23	1.76	0.66
2:N:47:GLU:HG3	2:N:47:GLU:O	1.94	0.66
1:M:66:LYS:HZ2	3:O:29:ASN:HB2	1.60	0.66
1:G:66:LYS:HD2	5:U:4:PRO:HA	1.76	0.66
4:P:204:PRO:HB2	4:P:205:ARG:HA	1.78	0.66
4:F:170:VAL:CG1	4:F:194:LEU:CD1	2.53	0.66
1:M:78:LEU:HD23	1:M:95:VAL:HG21	1.74	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:135:PHE:HZ	3:K:192:ILE:CG1	2.08	0.66
3:K:144:VAL:CG2	3:K:157:LYS:NZ	2.57	0.66
3:O:138:PHE:CD1	3:O:142:THR:OG1	2.48	0.66
4:P:26:ILE:HB	4:P:29:HIS:CD2	2.30	0.66
1:M:133:TRP:HB2	1:M:144:LYS:HG3	1.77	0.66
3:I:178:LYS:C	3:I:179:SER:HG	1.98	0.66
4:J:206:ASN:OD1	4:J:207:HIS:N	2.28	0.66
3:E:181:PHE:CB	3:E:182:ALA:HA	2.20	0.66
3:O:53:ASN:HB2	3:O:68:THR:OG1	1.96	0.66
3:E:84:ASP:HA	3:E:85:SER:OG	1.95	0.66
4:F:79:ILE:O	4:F:79:ILE:HG13	1.96	0.66
3:E:84:ASP:HB3	3:E:85:SER:O	1.95	0.66
4:J:223:TRP:CZ2	4:J:228:ALA:O	2.49	0.66
1:G:35:ARG:CG	1:G:46:GLU:HB3	2.26	0.65
4:F:165:GLU:O	4:F:166:VAL:HG23	1.95	0.65
3:I:13:VAL:C	3:I:14:GLN:OE1	2.33	0.65
3:K:135:PHE:HZ	3:K:192:ILE:HD11	1.62	0.65
4:L:170:VAL:HG22	4:L:194:LEU:CD2	2.21	0.65
4:F:98:GLN:HE21	4:F:98:GLN:HA	1.61	0.65
1:A:255:GLN:NE2	6:A:301:HOH:O	2.11	0.65
3:E:124:ASP:HB3	4:F:128:PHE:HA	1.75	0.65
1:M:77:ASP:OD2	5:T:8:THR:HB	1.97	0.65
4:P:100:TRP:HH2	5:T:7:ALA:HB2	1.61	0.65
3:O:15:GLU:OE1	3:O:168:LYS:NZ	2.29	0.65
4:J:65:PHE:HA	4:J:79:ILE:HG22	1.78	0.65
3:I:160:LEU:HD12	3:I:169:SER:HB2	1.77	0.65
4:F:6:GLN:HB3	4:F:107:PRO:HD2	1.77	0.65
3:K:151:ASP:CG	3:K:177:ASN:H	1.99	0.65
3:K:185:ASN:O	3:K:188:ASN:CB	2.44	0.65
3:E:82:PRO:O	3:E:85:SER:OG	2.08	0.65
3:O:17:ASP:O	3:O:80:SER:OG	2.15	0.65
1:M:237:GLY:O	1:M:238:ASP:HB2	1.94	0.65
2:B:29:GLY:HA2	2:B:61:SER:HB2	1.79	0.65
1:G:97:ARG:CG	1:G:116:TYR:CD1	2.80	0.65
1:M:87:GLN:OE1	1:M:93:HIS:CD2	2.50	0.65
3:O:138:PHE:CD1	3:O:142:THR:CG2	2.75	0.65
2:N:81:ARG:HG3	2:N:92:ILE:HG13	1.76	0.65
4:L:159:TRP:CZ2	4:L:194:LEU:HG	2.32	0.65
4:F:195:ARG:HG2	4:F:195:ARG:HH11	1.61	0.65
4:F:160:TRP:CD1	4:F:165:GLU:HA	2.31	0.65
1:C:202:ARG:NE	1:C:244:TRP:HZ2	1.94	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:2:GLN:NE2	2:N:85:VAL:CG2	2.60	0.65
4:L:5:SER:HB2	4:L:24:ASP:HB3	1.79	0.65
1:G:98:MET:HE1	1:G:99:TYR:C	2.18	0.64
2:H:17:ASN:OD1	2:H:97:ARG:NH1	2.30	0.64
1:G:137:ASP:OD1	1:G:138:MET:N	2.25	0.64
3:I:192:ILE:HG23	3:I:193:PRO:N	2.13	0.64
1:M:95:VAL:CG1	1:M:116:TYR:HE1	2.10	0.64
3:I:178:LYS:O	3:I:180:ASP:N	2.25	0.64
4:P:11:LYS:NZ	4:P:19:VAL:HB	2.12	0.64
4:J:26:ILE:HG22	4:J:27:SER:H	1.63	0.64
3:O:118:ALA:HB1	3:O:120:TYR:CE1	2.32	0.64
1:M:35:ARG:HD3	1:M:48:ARG:HH11	1.61	0.64
1:M:37:ASP:HB3	1:M:40:ALA:HB2	1.80	0.64
1:C:187:THR:C	1:C:188:HIS:ND1	2.50	0.64
4:L:90:TYR:HB2	4:L:109:THR:HG23	1.79	0.64
3:I:132:VAL:CG1	3:I:173:VAL:HG13	2.28	0.64
4:J:194:LEU:HD23	4:J:195:ARG:H	1.61	0.64
2:B:37:VAL:HG21	2:B:66:TYR:CZ	2.32	0.64
3:E:82:PRO:HA	3:E:108:VAL:HG21	1.78	0.64
1:M:219:ARG:HG3	1:M:257:TYR:CE2	2.32	0.64
2:H:72:PRO:HB2	2:H:78:TYR:OH	1.98	0.64
3:I:160:LEU:CD2	4:J:169:GLY:O	2.46	0.64
1:M:58:GLU:HA	1:M:61:ASP:HB3	1.79	0.64
3:I:146:GLN:CD	3:I:154:ILE:CD1	2.66	0.64
1:G:27:TYR:OH	2:H:63:TYR:OH	2.12	0.64
4:L:103:GLN:HG2	4:L:105:PHE:HE1	1.63	0.64
3:I:7:SER:CB	3:I:8:PRO:HD3	2.28	0.64
4:L:97:THR:CB	4:L:98:GLN:CD	2.66	0.64
4:F:170:VAL:HG12	4:F:194:LEU:HD13	1.76	0.64
4:L:161:VAL:HG23	4:L:166:VAL:CG1	2.27	0.64
1:A:81:LEU:HG	5:Q:9:VAL:HG21	1.80	0.64
4:J:127:VAL:HG11	4:J:239:ALA:HB2	1.79	0.64
3:I:138:PHE:HE1	3:I:142:THR:O	1.81	0.64
4:L:161:VAL:CG2	4:L:166:VAL:HG11	2.27	0.64
3:K:16:GLY:N	3:K:80:SER:O	2.31	0.64
3:E:53:ASN:HB2	3:E:68:THR:HB	1.79	0.64
3:K:135:PHE:CE1	3:K:138:PHE:HB3	2.33	0.63
1:A:35:ARG:HD2	2:B:53:ASP:OD1	1.98	0.63
4:F:121:PHE:CD2	4:F:187:ARG:NH2	2.66	0.63
2:H:70:PHE:CE1	2:H:78:TYR:CE1	2.86	0.63
1:G:234:ARG:HG3	1:G:242:GLN:HB2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:120:GLY:O	2:D:3:ARG:NH2	2.32	0.63
3:I:141:GLN:HG3	3:I:141:GLN:O	1.98	0.63
1:C:202:ARG:NE	1:C:244:TRP:CZ2	2.66	0.63
4:J:129:GLU:CD	4:J:130:PRO:CD	2.66	0.63
1:G:97:ARG:NH1	5:U:6:VAL:HG12	2.10	0.63
3:O:140:SER:C	3:O:142:THR:H	2.02	0.63
3:O:138:PHE:HE1	3:O:142:THR:HB	1.58	0.63
4:L:191:SER:CB	4:L:193:ARG:HH21	2.12	0.63
4:L:150:PHE:CE1	4:L:188:TYR:C	2.72	0.63
3:I:194:GLU:C	3:I:196:THR:HG23	2.18	0.63
4:J:97:THR:HB	4:J:98:GLN:HG2	1.80	0.63
1:A:80:THR:HG23	5:Q:9:VAL:HG23	1.79	0.63
4:F:159:TRP:NE1	4:F:192:SER:OG	2.19	0.63
4:F:200:PHE:O	4:F:204:PRO:HB3	1.99	0.63
4:F:173:ASP:OD2	4:F:191:SER:OG	2.17	0.63
4:J:83:GLN:HG2	4:J:84:GLN:H	1.63	0.63
2:H:5:PRO:HB3	2:H:30:PHE:HB3	1.78	0.63
4:L:218:SER:OG	4:L:218:SER:O	2.12	0.63
1:M:146:LYS:HZ2	4:P:97:THR:HG1	1.47	0.63
2:N:2:GLN:NE2	2:N:85:VAL:CB	2.60	0.63
1:G:77:ASP:OD1	1:G:97:ARG:NH2	2.32	0.63
4:L:201:TRP:C	4:L:204:PRO:CD	2.67	0.63
3:I:196:THR:OG1	3:I:197:PHE:N	2.32	0.63
4:J:238:GLU:HG3	4:J:239:ALA:N	2.14	0.63
1:G:192:HIS:HB2	1:G:202:ARG:NH2	2.12	0.62
3:O:123:ARG:HG2	3:O:124:ASP:H	1.64	0.62
3:O:180:ASP:OD1	3:O:182:ALA:HB2	1.98	0.62
4:F:230:PRO:O	4:F:231:VAL:CG2	2.47	0.62
2:H:11:SER:HB2	2:H:95:TRP:HZ2	1.63	0.62
1:M:12:VAL:HG22	1:M:94:THR:HG23	1.81	0.62
3:I:10:SER:O	3:I:11:LEU:HD23	1.99	0.62
3:K:38:TRP:HZ3	3:K:42:LYS:O	1.81	0.62
3:I:33:LEU:CD1	3:I:91:ALA:O	2.42	0.62
4:F:165:GLU:O	4:F:166:VAL:CG2	2.46	0.62
4:F:193:ARG:CG	4:F:193:ARG:HH11	2.09	0.62
2:H:70:PHE:CE1	2:H:78:TYR:CD1	2.87	0.62
3:O:33:LEU:HB3	3:O:50:MET:HB2	1.81	0.62
4:F:195:ARG:CG	4:F:195:ARG:HH11	2.13	0.62
3:K:161:ASP:CB	3:K:168:LYS:HD3	2.29	0.62
4:P:21:LEU:HB2	4:P:77:LEU:HB3	1.82	0.62
1:G:126:LEU:HD11	1:G:130:LEU:HA	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:20:PRO:CD	1:M:75:ARG:HD2	2.29	0.62
4:F:47:ILE:HG22	4:F:48:TYR:N	2.13	0.62
3:K:115:PRO:HB3	3:K:139:ASP:OD2	2.00	0.62
1:C:102:ASP:OD1	1:C:113:TYR:OH	2.10	0.62
3:E:38:TRP:CD1	3:E:44:PRO:HG3	2.29	0.62
1:A:96:GLN:OE1	2:B:60:TRP:HE3	1.83	0.62
2:H:24:ASN:CG	2:H:65:LEU:HD21	2.20	0.62
1:G:73:THR:HG21	5:U:6:VAL:HG12	1.82	0.62
3:I:146:GLN:NE2	3:I:154:ILE:HD13	2.15	0.62
4:L:119:ASN:OD1	4:L:187:ARG:NH2	2.33	0.62
3:I:15:GLU:O	3:I:15:GLU:HG3	1.99	0.61
4:L:161:VAL:HG13	4:L:208:PHE:HA	1.81	0.61
3:O:183:CYS:O	3:O:186:ALA:HB2	2.00	0.61
4:L:153:ASP:HB2	4:L:188:TYR:HD2	1.64	0.61
1:G:133:TRP:CE3	1:G:147:TRP:HE3	2.18	0.61
4:P:64:ARG:HH11	4:P:64:ARG:CG	2.13	0.61
1:C:213:ILE:HG13	1:C:263:HIS:HB2	1.82	0.61
1:A:22:PHE:H	1:A:38:SER:HB3	1.65	0.61
2:N:73:THR:HG23	2:N:75:LYS:H	1.64	0.61
3:K:185:ASN:ND2	3:K:188:ASN:ND2	2.48	0.61
4:F:132:GLU:CG	4:F:135:ILE:HG21	2.31	0.61
4:J:234:ILE:HD12	4:J:234:ILE:O	1.99	0.61
3:K:185:ASN:O	3:K:188:ASN:N	2.30	0.61
3:E:181:PHE:HB2	3:E:182:ALA:CA	2.25	0.61
1:M:103:VAL:HA	1:M:108:ARG:O	2.01	0.61
3:K:185:ASN:O	3:K:188:ASN:HB3	2.01	0.61
1:C:197:HIS:ND1	1:C:198:GLU:HG3	2.16	0.61
2:N:59:ASP:HB3	2:N:61:SER:OG	2.01	0.61
2:B:36:GLU:CB	2:B:83:ASN:HB3	2.29	0.61
2:N:81:ARG:HD3	2:N:92:ILE:HG12	1.83	0.61
4:P:14:GLU:CD	4:P:117:LEU:CD2	2.53	0.61
2:D:89:GLN:HG3	2:D:90:PRO:CD	2.31	0.61
3:E:126:LYS:N	3:E:126:LYS:HD2	2.16	0.61
1:M:47:PRO:HB3	1:M:60:TRP:CH2	2.36	0.61
4:F:25:PRO:HG2	4:F:73:SER:HB2	1.81	0.60
4:L:161:VAL:HG12	4:L:162:ASN:N	2.16	0.60
1:G:27:TYR:CD1	1:G:32:GLN:NE2	2.66	0.60
2:N:81:ARG:HD3	2:N:92:ILE:CG1	2.30	0.60
2:H:44:GLU:OE1	4:F:71:GLY:HA2	2.00	0.60
1:G:218:GLN:OE1	1:G:221:GLY:HA2	2.01	0.60
2:D:87:LEU:HD13	2:D:89:GLN:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:THR:HG23	3:I:96:ASN:HD21	1.67	0.60
3:I:13:VAL:HG23	3:I:15:GLU:H	1.66	0.60
1:G:99:TYR:CZ	5:U:3:VAL:HG12	2.37	0.60
4:L:150:PHE:O	4:L:150:PHE:HD1	1.84	0.60
2:D:82:VAL:O	2:D:90:PRO:HB2	2.02	0.60
1:G:207:SER:HA	1:G:240:THR:HB	1.83	0.60
3:I:87:THR:HA	3:I:105:SER:HA	1.83	0.60
1:M:195:SER:O	1:M:197:HIS:ND1	2.34	0.60
1:C:187:THR:HB	1:C:272:LEU:HD11	1.81	0.60
1:A:231:VAL:O	1:A:231:VAL:HG23	2.00	0.60
1:M:95:VAL:HG13	1:M:116:TYR:CE1	2.37	0.60
2:D:30:PHE:HE1	2:D:62:PHE:HB2	1.66	0.60
1:G:6:ARG:HB2	1:G:27:TYR:HB2	1.83	0.60
1:G:56:GLY:HA2	1:G:60:TRP:CE2	2.36	0.60
1:G:35:ARG:NH2	1:G:48:ARG:CG	2.58	0.60
1:G:159:TYR:HD1	1:G:163:THR:OG1	1.84	0.60
4:J:129:GLU:CG	4:J:130:PRO:CD	2.79	0.60
1:A:93:HIS:HB3	1:A:119:ASP:OD1	2.02	0.60
3:K:68:THR:HG22	3:K:68:THR:O	2.02	0.60
4:F:222:GLU:HG2	4:F:223:TRP:N	2.15	0.60
1:G:123:TYR:CE2	1:G:143:THR:HG21	2.37	0.60
4:F:170:VAL:CA	4:F:194:LEU:HD12	2.32	0.59
2:N:2:GLN:HE21	2:N:85:VAL:HB	1.65	0.59
4:F:197:SER:CB	4:F:200:PHE:HB2	2.30	0.59
4:J:129:GLU:CD	4:J:130:PRO:HD2	2.22	0.59
4:F:88:ALA:HB3	4:F:90:TYR:CE1	2.37	0.59
2:H:70:PHE:CZ	2:H:78:TYR:CE2	2.90	0.59
1:G:195:SER:CB	1:G:196:ASP:HA	2.32	0.59
4:J:12:VAL:HG22	4:J:154:HIS:CE1	2.37	0.59
4:F:125:VAL:HG22	4:F:147:ALA:HA	1.84	0.59
1:G:97:ARG:CG	1:G:116:TYR:CE1	2.85	0.59
1:C:81:LEU:HG	5:R:9:VAL:HG21	1.83	0.59
2:D:45:ARG:O	2:D:45:ARG:HG2	2.00	0.59
3:K:135:PHE:CZ	3:K:192:ILE:CG1	2.85	0.59
2:N:41:LYS:O	2:N:42:ASN:OD1	2.20	0.59
4:J:223:TRP:HZ2	4:J:228:ALA:O	1.86	0.59
3:I:74:TYR:HB3	3:I:76:TYR:HE1	1.66	0.59
3:K:135:PHE:HE1	3:K:138:PHE:HB3	1.66	0.59
1:M:146:LYS:NZ	4:P:97:THR:OG1	2.31	0.59
4:J:113:VAL:C	4:J:114:LEU:CG	2.69	0.59
1:G:220:ASP:OD2	1:G:256:ARG:NH1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:209:TYR:CD1	1:G:210:PRO:HA	2.37	0.59
1:A:37:ASP:HB3	1:A:40:ALA:HB2	1.84	0.59
1:G:192:HIS:CE1	2:H:98:ASP:HB3	2.37	0.59
1:G:259:CYS:HB3	1:G:272:LEU:HB2	1.84	0.59
1:M:103:VAL:HB	1:M:107:TRP:HA	1.83	0.59
1:A:203:CYS:HB2	1:A:217:TRP:CZ3	2.38	0.59
4:J:194:LEU:HD21	4:J:196:VAL:CG2	2.33	0.59
4:L:201:TRP:C	4:L:204:PRO:HD3	2.23	0.59
4:J:129:GLU:CD	4:J:130:PRO:HD3	2.23	0.59
3:K:136:THR:CG2	3:K:171:SER:CB	2.80	0.59
3:K:192:ILE:CG1	3:K:193:PRO:HD2	2.29	0.59
4:F:223:TRP:CE3	4:F:230:PRO:HD2	2.37	0.59
1:C:35:ARG:HH11	2:D:53:ASP:CG	2.06	0.59
1:M:197:HIS:N	1:M:197:HIS:HD1	2.01	0.59
3:I:115:PRO:HB3	3:I:137:ASP:OD2	2.01	0.59
1:M:213:ILE:HG13	1:M:263:HIS:HB2	1.85	0.59
3:K:21:PHE:HB2	3:K:75:LEU:HB3	1.85	0.59
4:P:66:SER:HG	4:P:78:THR:HG1	1.49	0.59
1:A:170:ARG:O	1:A:174:ASN:ND2	2.32	0.59
4:J:69:ARG:HA	4:J:75:SER:HB2	1.84	0.59
3:K:144:VAL:HG23	3:K:157:LYS:HZ2	1.67	0.59
4:P:23:CYS:SG	4:P:24:ASP:N	2.76	0.59
3:K:20:ASN:HA	3:K:75:LEU:O	2.03	0.59
1:M:255:GLN:NE2	1:M:255:GLN:O	2.35	0.59
4:F:110:ARG:HH21	4:F:154:HIS:CD2	2.20	0.58
1:G:133:TRP:CE3	1:G:147:TRP:CE3	2.90	0.58
1:M:270:LEU:HD13	1:M:272:LEU:CD2	2.32	0.58
2:B:92:ILE:O	2:B:92:ILE:HG23	2.03	0.58
3:K:136:THR:HG21	3:K:171:SER:CB	2.33	0.58
1:M:197:HIS:O	1:M:198:GLU:CG	2.50	0.58
4:J:26:ILE:HG22	4:J:27:SER:N	2.18	0.58
1:M:198:GLU:HA	1:M:251:SER:H	1.67	0.58
2:H:35:ILE:HG13	2:H:83:ASN:O	2.03	0.58
1:M:203:CYS:HB2	1:M:217:TRP:HE1	1.68	0.58
3:K:138:PHE:HZ	3:K:157:LYS:HG2	1.68	0.58
4:P:160:TRP:CH2	4:P:211:GLN:HG3	2.38	0.58
3:O:118:ALA:HB1	3:O:120:TYR:CZ	2.39	0.58
4:P:47:ILE:HG22	4:P:57:LYS:HA	1.85	0.58
1:C:238:ASP:HB3	1:C:240:THR:HG22	1.84	0.58
4:L:204:PRO:HG3	4:L:241:GLY:CA	2.25	0.58
1:M:253:GLN:HG3	1:M:256:ARG:HE	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:229:LYS:CB	4:J:230:PRO:HA	2.33	0.58
1:M:13:SER:HB3	1:M:78:LEU:HD13	1.85	0.58
1:C:216:THR:HG23	1:C:260:HIS:HB2	1.85	0.58
2:N:81:ARG:CG	2:N:92:ILE:HG13	2.33	0.58
1:G:178:THR:O	1:G:181:ARG:HB3	2.02	0.58
1:G:73:THR:HG23	5:U:8:THR:HG22	1.85	0.58
1:C:72:GLN:CG	4:F:55:PRO:HB2	2.34	0.58
1:C:35:ARG:HD2	2:D:53:ASP:OD2	2.04	0.58
4:L:147:ALA:HB2	4:L:212:VAL:HG21	1.84	0.58
4:J:135:ILE:O	4:J:139:GLN:OE1	2.20	0.58
4:F:153:ASP:O	4:F:155:VAL:N	2.37	0.58
4:J:162:ASN:HA	4:J:207:HIS:CE1	2.39	0.58
1:A:89:GLU:OE2	1:C:86:ASN:ND2	2.32	0.58
4:P:14:GLU:CG	4:P:117:LEU:CG	2.66	0.58
3:E:82:PRO:HA	3:E:108:VAL:CG2	2.33	0.58
1:M:10:THR:HG21	2:N:54:LEU:CD2	2.29	0.58
4:F:97:THR:OG1	4:F:98:GLN:N	2.35	0.58
3:K:61:ARG:CB	3:K:78:LYS:O	2.51	0.58
3:O:182:ALA:CB	3:O:185:ASN:HB3	2.15	0.58
1:G:35:ARG:HH21	1:G:48:ARG:CD	2.17	0.58
4:P:211:GLN:HE21	4:P:234:ILE:HG13	1.68	0.58
4:F:50:GLN:NE2	4:F:97:THR:O	2.36	0.58
1:G:133:TRP:CZ3	1:G:147:TRP:HZ3	2.20	0.58
3:E:82:PRO:O	3:E:84:ASP:HA	2.03	0.57
1:G:123:TYR:CE2	5:U:9:VAL:HG21	2.39	0.57
1:M:170:ARG:O	1:M:174:ASN:ND2	2.37	0.57
3:E:134:LEU:HD11	4:F:144:VAL:HG21	1.86	0.57
3:K:175:TRP:HZ2	4:L:146:LEU:CB	2.15	0.57
4:J:83:GLN:CG	4:J:84:GLN:H	2.17	0.57
4:L:201:TRP:O	4:L:204:PRO:CD	2.52	0.57
3:E:192:ILE:HG23	3:E:193:PRO:HD3	1.84	0.57
3:E:84:ASP:CB	3:E:85:SER:HB2	2.34	0.57
4:L:147:ALA:CB	4:L:212:VAL:HG21	2.35	0.57
1:A:66:LYS:HE2	3:I:29:ASN:CG	2.25	0.57
3:E:145:SER:HB2	3:E:189:ASN:HB3	1.86	0.57
2:N:70:PHE:CZ	2:N:72:PRO:HB3	2.39	0.57
3:I:121:GLN:O	3:I:132:VAL:O	2.23	0.57
1:M:74:HIS:O	1:M:77:ASP:N	2.36	0.57
4:J:217:LEU:HD13	4:J:221:ASP:CB	2.34	0.57
4:F:143:LEU:HB2	4:F:194:LEU:O	2.03	0.57
3:O:140:SER:C	3:O:142:THR:N	2.56	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:121:PHE:O	4:L:150:PHE:HA	2.04	0.57
4:L:95:SER:OG	4:L:103:GLN:HB3	2.05	0.57
1:A:266:LEU:HD13	1:A:270:LEU:HD13	1.87	0.57
3:O:27:SER:HB2	3:O:69:LYS:HD2	1.86	0.57
3:I:122:LEU:N	3:I:132:VAL:O	2.37	0.57
4:J:194:LEU:HD21	4:J:196:VAL:HG23	1.84	0.57
1:G:35:ARG:HG2	1:G:46:GLU:HB3	1.86	0.57
2:D:5:PRO:HB3	2:D:30:PHE:HB3	1.86	0.57
1:A:163:THR:HA	1:A:166:GLU:HB2	1.86	0.57
4:P:226:ASP:OD1	4:P:226:ASP:N	2.36	0.57
4:F:118:LYS:CD	4:F:217:LEU:HD21	2.35	0.57
1:M:139:ALA:O	1:M:142:THR:OG1	2.22	0.57
4:J:14:GLU:HB2	4:J:114:LEU:O	2.04	0.57
1:G:220:ASP:OD1	1:G:256:ARG:HG3	2.05	0.57
3:I:2:LEU:HD21	3:I:26:PRO:HB3	1.87	0.57
3:O:53:ASN:ND2	3:O:68:THR:OG1	2.38	0.57
1:G:35:ARG:NH2	1:G:48:ARG:NE	2.53	0.57
1:C:113:TYR:N	1:C:113:TYR:CD2	2.73	0.57
1:M:58:GLU:O	1:M:62:GLY:N	2.30	0.57
3:I:2:LEU:HD13	3:I:26:PRO:HG3	1.87	0.57
4:J:6:GLN:NE2	4:J:92:CYS:HB3	2.20	0.57
3:O:187:PHE:N	3:O:187:PHE:CD2	2.73	0.57
4:P:197:SER:HB3	4:P:200:PHE:CD2	2.40	0.56
1:M:5:MET:HB2	1:M:28:VAL:HG12	1.87	0.56
1:G:12:VAL:HG11	2:H:33:SER:HB3	1.86	0.56
3:K:135:PHE:CE1	3:K:138:PHE:CD2	2.93	0.56
3:K:35:TRP:O	3:K:47:LEU:HB3	2.05	0.56
2:B:84:HIS:ND1	2:B:85:VAL:O	2.39	0.56
4:F:87:SER:HB3	4:F:113:VAL:HG12	1.87	0.56
4:P:7:SER:OG	4:P:22:ARG:HD3	2.05	0.56
3:E:157:LYS:NZ	3:E:170:ASN:HD21	2.03	0.56
3:I:146:GLN:NE2	3:I:154:ILE:CD1	2.69	0.56
1:A:204:TRP:CZ3	1:A:244:TRP:HB2	2.41	0.56
1:C:73:THR:HG21	5:R:6:VAL:HG23	1.86	0.56
4:P:37:GLN:HG3	4:P:41:GLN:OE1	2.05	0.56
4:L:170:VAL:CA	4:L:194:LEU:HD21	2.30	0.56
2:B:20:SER:OG	4:L:18:ASP:OD2	2.23	0.56
1:C:10:THR:HG21	2:D:54:LEU:CD2	2.35	0.56
1:A:96:GLN:NE2	2:B:62:PHE:CE1	2.67	0.56
1:G:124:ILE:HD12	1:G:143:THR:HG23	1.87	0.56
4:L:145:CYS:SG	4:L:146:LEU:N	2.77	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:243:LYS:HG2	1:C:244:TRP:H	1.70	0.56
3:I:50:MET:HB3	3:I:66:LEU:HD22	1.88	0.56
3:K:185:ASN:CB	3:K:188:ASN:HD22	2.18	0.56
1:M:133:TRP:HB2	1:M:144:LYS:CG	2.36	0.56
1:C:5:MET:HB2	1:C:168:LEU:HD13	1.88	0.56
4:P:223:TRP:CZ3	4:P:229:LYS:O	2.57	0.56
4:F:150:PHE:CD1	4:F:155:VAL:HG11	2.40	0.56
1:G:234:ARG:HB3	2:H:8:GLN:HE21	1.71	0.56
3:K:62:ILE:HG22	3:K:75:LEU:HD11	1.88	0.56
4:J:29:HIS:HD2	4:J:94:SER:CA	2.13	0.56
4:F:230:PRO:O	4:F:231:VAL:HG22	2.06	0.56
4:F:179:GLU:HB2	4:F:187:ARG:O	2.06	0.56
1:G:199:ALA:N	1:G:249:VAL:O	2.39	0.56
1:A:89:GLU:HG2	1:C:86:ASN:OD1	2.05	0.55
1:C:122:ASP:OD1	2:D:60:TRP:NE1	2.36	0.55
2:D:74:GLU:HA	2:D:97:ARG:NH2	2.21	0.55
3:K:138:PHE:CZ	3:K:157:LYS:CE	2.82	0.55
1:M:256:ARG:HD3	6:M:301:HOH:O	2.05	0.55
1:G:133:TRP:CZ3	1:G:147:TRP:HE3	2.21	0.55
2:D:76:ASP:HB3	2:D:78:TYR:CE1	2.36	0.55
1:A:33:PHE:CD1	1:A:52:ILE:HD12	2.38	0.55
1:M:253:GLN:O	1:M:256:ARG:HG3	2.06	0.55
2:H:24:ASN:ND2	2:H:65:LEU:HD21	2.21	0.55
4:J:160:TRP:CE3	4:J:211:GLN:CB	2.90	0.55
4:J:207:HIS:HB3	4:J:240:TRP:CZ3	2.41	0.55
3:K:180:ASP:N	3:K:180:ASP:OD1	2.38	0.55
1:A:131:ARG:NH2	1:A:157:ARG:NH2	2.54	0.55
1:C:131:ARG:HH11	1:C:131:ARG:CG	2.12	0.55
4:J:129:GLU:HG3	4:J:130:PRO:CD	2.34	0.55
2:D:56:PHE:HA	2:D:62:PHE:HA	1.86	0.55
1:M:14:ARG:NH2	1:M:21:ARG:HB2	2.21	0.55
4:F:150:PHE:CE1	4:F:155:VAL:CG1	2.90	0.55
3:I:42:LYS:NZ	3:I:43:SER:OG	2.40	0.55
4:L:88:ALA:HB1	4:L:89:VAL:HG12	1.89	0.55
3:K:136:THR:CB	3:K:170:ASN:O	2.51	0.55
4:L:170:VAL:CB	4:L:194:LEU:HD21	2.35	0.55
4:L:82:THR:HG22	4:L:83:GLN:N	2.21	0.55
1:M:66:LYS:HE3	3:O:29:ASN:ND2	2.21	0.55
2:N:83:ASN:OD1	2:N:84:HIS:N	2.40	0.55
4:J:157:LEU:HD23	4:J:158:SER:N	2.22	0.55
3:E:93:ILE:HG22	5:R:5:MET:HE1	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:17:LYS:NZ	4:P:221:ASP:OD1	2.29	0.55
3:O:138:PHE:CD2	3:O:138:PHE:N	2.74	0.55
1:M:219:ARG:O	1:M:222:GLU:N	2.40	0.55
2:H:37:VAL:CG2	2:H:82:VAL:HG12	2.36	0.55
4:L:124:GLU:HA	4:L:235:VAL:HG11	1.87	0.55
1:G:192:HIS:CB	1:G:202:ARG:NH2	2.70	0.55
4:J:131:SER:HB2	4:J:134:GLU:HB3	1.89	0.55
3:I:34:HIS:CE1	3:I:93:ILE:HD11	2.42	0.55
3:K:122:LEU:HD13	4:L:144:VAL:HG23	1.88	0.55
4:J:127:VAL:HG23	4:J:237:ALA:HB3	1.89	0.55
4:L:59:GLY:O	4:L:61:PRO:HD3	2.06	0.55
1:C:231:VAL:HG23	1:C:232:GLU:O	2.06	0.55
3:O:123:ARG:HG2	3:O:124:ASP:N	2.22	0.55
1:M:133:TRP:CB	1:M:144:LYS:HG3	2.36	0.55
4:P:83:GLN:O	4:P:113:VAL:HG11	2.06	0.55
2:D:90:PRO:HG2	2:D:90:PRO:O	2.07	0.55
2:B:18:GLY:HA2	2:B:71:THR:HG22	1.88	0.55
1:G:81:LEU:HG	5:U:9:VAL:HG11	1.88	0.54
5:T:7:ALA:O	5:T:8:THR:HG23	2.06	0.54
3:I:14:GLN:O	3:I:15:GLU:HB3	2.07	0.54
1:M:163:THR:HA	1:M:166:GLU:HB2	1.89	0.54
1:M:268:LYS:HB2	1:M:269:PRO:HD2	1.89	0.54
1:G:98:MET:CE	1:G:99:TYR:CA	2.85	0.54
3:K:185:ASN:CB	3:K:188:ASN:ND2	2.69	0.54
4:L:201:TRP:C	4:L:204:PRO:HD2	2.28	0.54
4:F:36:ARG:HB3	4:F:46:LEU:HD11	1.89	0.54
4:F:125:VAL:HG21	4:F:212:VAL:HG21	1.89	0.54
1:A:88:SER:OG	1:A:89:GLU:N	2.40	0.54
3:E:136:THR:HG22	3:E:171:SER:CB	2.24	0.54
2:N:83:ASN:HB2	2:N:90:PRO:HG3	1.89	0.54
4:P:141:ALA:HB2	4:P:198:ALA:HA	1.89	0.54
3:E:138:PHE:CD1	3:E:138:PHE:N	2.72	0.54
4:J:221:ASP:CG	4:J:222:GLU:H	2.11	0.54
2:H:11:SER:HB2	2:H:95:TRP:CZ2	2.42	0.54
1:A:103:VAL:HG12	1:A:108:ARG:C	2.28	0.54
3:K:52:LEU:O	3:K:52:LEU:HD12	2.07	0.54
3:K:144:VAL:CG2	3:K:157:LYS:HZ1	2.15	0.54
4:F:54:ALA:CB	4:F:57:LYS:CE	2.78	0.54
1:G:82:ARG:HH21	1:G:88:SER:C	2.08	0.54
3:K:66:LEU:HD23	3:K:67:ASN:N	2.23	0.54
4:F:98:GLN:CA	4:F:98:GLN:HE21	2.19	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:7:SER:O	4:L:22:ARG:HB3	2.08	0.54
3:O:87:THR:HA	3:O:105:SER:HA	1.89	0.54
4:J:123:PRO:HA	4:J:150:PHE:HB3	1.88	0.54
1:M:128:GLU:OE1	1:M:128:GLU:N	2.36	0.54
4:P:223:TRP:CE2	4:P:229:LYS:O	2.61	0.54
4:F:155:VAL:HG12	4:F:214:PHE:HD1	1.71	0.54
3:K:47:LEU:O	3:K:48:PHE:HD1	1.91	0.54
1:G:143:THR:CB	5:U:9:VAL:HG23	2.38	0.54
1:A:12:VAL:HG22	1:A:94:THR:HG22	1.90	0.54
1:M:66:LYS:NZ	3:O:29:ASN:CB	2.71	0.54
3:I:160:LEU:HD22	4:J:169:GLY:O	2.07	0.54
1:G:91:GLY:HA3	1:G:93:HIS:CE1	2.43	0.54
1:G:218:GLN:CD	1:G:221:GLY:HA2	2.27	0.54
2:H:71:THR:O	2:H:72:PRO:O	2.26	0.54
4:L:7:SER:OG	4:L:8:PRO:HA	2.08	0.54
4:L:13:THR:OG1	4:L:14:GLU:N	2.40	0.54
1:C:159:TYR:CD1	1:C:163:THR:HB	2.43	0.54
2:N:46:ILE:O	2:N:49:VAL:HG23	2.08	0.54
2:H:24:ASN:CG	2:H:65:LEU:CD2	2.77	0.53
1:M:175:GLY:O	1:M:179:LEU:N	2.41	0.53
3:I:9:GLN:HA	3:I:104:THR:HA	1.90	0.53
2:H:70:PHE:HE1	2:H:78:TYR:CG	2.26	0.53
4:J:98:GLN:NE2	4:J:98:GLN:HA	2.23	0.53
4:J:177:LEU:HB3	4:J:189:ALA:HB3	1.91	0.53
1:C:195:SER:OG	1:C:196:ASP:N	2.39	0.53
4:L:203:ASN:N	4:L:204:PRO:HD2	2.22	0.53
4:F:160:TRP:CD1	4:F:165:GLU:CA	2.91	0.53
1:M:219:ARG:O	1:M:220:ASP:C	2.46	0.53
1:G:138:MET:N	1:G:138:MET:SD	2.82	0.53
3:E:8:PRO:O	3:E:104:THR:HB	2.08	0.53
2:B:21:ASN:OD1	2:B:22:PHE:N	2.33	0.53
2:D:30:PHE:CE1	2:D:62:PHE:HB2	2.44	0.53
4:J:160:TRP:CH2	4:J:211:GLN:CB	2.91	0.53
1:M:110:LEU:HD23	1:M:111:ARG:HG2	1.91	0.53
1:G:58:GLU:O	1:G:61:ASP:N	2.42	0.53
4:J:122:PRO:HG3	4:J:230:PRO:HB2	1.90	0.53
1:M:191:HIS:NE2	1:M:193:ALA:HB2	2.24	0.53
3:E:84:ASP:HB3	3:E:85:SER:CB	2.39	0.53
4:P:159:TRP:O	4:P:165:GLU:HB2	2.07	0.53
4:J:130:PRO:HG3	4:J:142:THR:O	2.09	0.53
2:B:57:SER:O	2:B:60:TRP:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:85:VAL:O	2:B:86:THR:OG1	2.19	0.53
1:M:154:GLU:HB3	3:O:52:LEU:HD11	1.90	0.53
3:O:4:VAL:HG21	3:O:99:TYR:O	2.08	0.53
3:E:136:THR:CA	3:E:138:PHE:CE1	2.86	0.53
4:L:191:SER:CB	4:L:193:ARG:NH2	2.70	0.53
1:A:2:SER:HB3	1:A:103:VAL:O	2.08	0.53
2:N:58:LYS:NZ	6:N:102:HOH:O	2.40	0.53
1:A:4:SER:CB	1:A:102:ASP:OD2	2.53	0.53
3:K:185:ASN:O	3:K:188:ASN:CG	2.46	0.53
4:F:26:ILE:HG22	4:F:26:ILE:O	2.09	0.53
1:C:59:TYR:O	1:C:63:GLU:HG2	2.09	0.53
3:I:160:LEU:HD23	4:J:169:GLY:O	2.09	0.53
3:K:52:LEU:H	3:K:52:LEU:HD12	1.73	0.53
3:O:182:ALA:O	3:O:186:ALA:N	2.40	0.53
4:F:123:PRO:HB3	4:F:150:PHE:CD2	2.43	0.53
3:K:59:LYS:CD	3:K:60:GLY:H	2.21	0.53
3:I:115:PRO:CA	3:I:137:ASP:OD2	2.56	0.53
1:A:131:ARG:NH1	6:A:302:HOH:O	2.31	0.53
1:G:99:TYR:OH	5:U:3:VAL:HG12	2.09	0.52
4:F:118:LYS:HD2	4:F:217:LEU:HD21	1.91	0.52
4:F:217:LEU:HD12	4:F:218:SER:H	1.73	0.52
3:O:29:ASN:HB2	5:T:4:PRO:HG3	1.91	0.52
4:L:191:SER:HB2	4:L:193:ARG:HH21	1.74	0.52
1:G:218:GLN:CB	1:G:223:ASP:HA	2.37	0.52
1:M:63:GLU:OE1	5:T:2:LEU:HD12	2.08	0.52
3:I:74:TYR:HB3	3:I:76:TYR:CE1	2.44	0.52
3:E:157:LYS:HZ2	3:E:170:ASN:HD21	1.56	0.52
2:H:70:PHE:CZ	2:H:78:TYR:CD2	2.97	0.52
3:K:25:PHE:CE1	3:K:71:GLY:HA2	2.44	0.52
1:M:67:VAL:O	1:M:70:HIS:HB2	2.09	0.52
4:F:140:LYS:CD	4:F:197:SER:HA	2.39	0.52
3:I:117:PRO:O	3:I:196:THR:C	2.48	0.52
4:P:11:LYS:HZ3	4:P:19:VAL:HB	1.72	0.52
4:P:70:THR:O	4:P:74:VAL:HB	2.09	0.52
4:J:135:ILE:CA	4:J:140:LYS:O	2.52	0.52
4:L:203:ASN:N	4:L:204:PRO:CD	2.72	0.52
1:M:97:ARG:HH22	1:M:147:TRP:HH2	1.56	0.52
1:G:192:HIS:HD2	1:G:202:ARG:HD2	1.73	0.52
4:F:193:ARG:HG3	4:F:193:ARG:NH1	2.18	0.52
3:E:49:VAL:HG21	4:F:102:THR:CG2	2.36	0.52
2:D:37:VAL:HG22	2:D:82:VAL:HG12	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:15:LYS:HZ2	4:P:83:GLN:HG3	1.75	0.52
3:O:44:PRO:O	3:O:44:PRO:HG2	2.10	0.52
4:L:125:VAL:HG21	4:L:236:SER:O	2.10	0.52
2:D:74:GLU:HA	2:D:97:ARG:HH22	1.75	0.52
4:L:217:LEU:HB2	4:L:230:PRO:O	2.09	0.52
4:P:61:PRO:O	6:P:301:HOH:O	2.19	0.52
1:C:74:HIS:CD2	1:C:97:ARG:HH21	2.27	0.52
3:E:89:LEU:HD21	3:E:100:PHE:CD1	2.43	0.52
3:I:155:THR:HG21	4:J:191:SER:OG	2.09	0.52
4:J:11:LYS:NZ	4:J:217:LEU:CD2	2.73	0.52
2:N:60:TRP:CE3	2:N:60:TRP:HA	2.42	0.52
4:J:36:ARG:HB3	4:J:46:LEU:HD11	1.92	0.52
4:J:96:GLN:O	4:J:98:GLN:N	2.40	0.52
2:H:55:SER:OG	2:H:56:PHE:N	2.43	0.52
1:G:12:VAL:HA	1:G:94:THR:HA	1.92	0.52
2:N:41:LYS:O	2:N:77:GLU:O	2.27	0.52
3:I:146:GLN:CG	3:I:154:ILE:HG12	2.40	0.52
3:E:181:PHE:CB	3:E:182:ALA:CA	2.86	0.52
1:M:219:ARG:N	1:M:222:GLU:O	2.41	0.52
4:F:6:GLN:HG3	4:F:22:ARG:O	2.10	0.52
1:C:155:GLN:HE21	3:E:51:THR:HG21	1.75	0.52
3:I:182:ALA:O	3:I:186:ALA:HB2	2.10	0.52
4:L:36:ARG:HD2	4:L:90:TYR:CG	2.45	0.51
3:E:157:LYS:CE	3:E:170:ASN:OD1	2.58	0.51
4:L:130:PRO:HG2	4:L:201:TRP:CE2	2.45	0.51
3:O:61:ARG:NH1	3:O:81:GLN:HB2	2.25	0.51
2:H:37:VAL:HG21	2:H:82:VAL:HG12	1.93	0.51
3:I:158:CYS:SG	4:J:193:ARG:NH1	2.83	0.51
1:M:230:LEU:HD12	1:M:230:LEU:C	2.30	0.51
1:G:131:ARG:NH2	6:G:303:HOH:O	2.27	0.51
2:N:12:ARG:O	2:N:12:ARG:HG2	2.09	0.51
1:G:200:THR:HG21	1:G:202:ARG:NH2	2.26	0.51
4:P:97:THR:CG2	4:P:98:GLN:N	2.73	0.51
4:J:141:ALA:CB	4:J:196:VAL:O	2.45	0.51
4:J:6:GLN:HE21	4:J:92:CYS:HB3	1.74	0.51
2:D:73:THR:HG22	2:D:74:GLU:H	1.74	0.51
1:G:168:LEU:O	1:G:172:LEU:HG	2.11	0.51
3:E:30:PHE:CD2	3:E:92:PHE:HE2	2.23	0.51
3:O:52:LEU:O	3:O:55:ASP:N	2.42	0.51
3:O:140:SER:O	3:O:142:THR:N	2.43	0.51
3:K:50:MET:HB3	3:K:66:LEU:CD1	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:134:LEU:HD12	3:O:135:PHE:H	1.74	0.51
4:F:37:GLN:NE2	4:F:38:ARG:O	2.44	0.51
2:D:54:LEU:HD21	2:D:62:PHE:HD1	1.72	0.51
4:J:113:VAL:HG22	4:J:114:LEU:N	2.26	0.51
2:H:24:ASN:OD1	2:H:66:TYR:O	2.28	0.51
4:F:121:PHE:HE2	4:F:187:ARG:NH2	1.92	0.51
4:L:62:SER:CA	4:L:65:PHE:HE2	2.24	0.51
1:G:249:VAL:HG22	1:G:257:TYR:CZ	2.46	0.51
3:I:81:GLN:HG2	3:I:82:PRO:HD2	1.92	0.51
2:N:11:SER:C	2:N:13:HIS:H	2.13	0.51
3:O:181:PHE:O	3:O:182:ALA:HB3	2.11	0.51
3:E:157:LYS:NZ	3:E:170:ASN:OD1	2.44	0.51
2:B:37:VAL:CG2	2:B:66:TYR:CZ	2.94	0.51
4:L:161:VAL:O	4:L:162:ASN:CB	2.59	0.51
3:K:59:LYS:CD	3:K:60:GLY:N	2.73	0.51
3:K:21:PHE:HE1	3:K:88:TYR:CD2	2.28	0.51
4:F:73:SER:OG	4:F:74:VAL:N	2.43	0.51
3:K:152:VAL:HG13	3:K:153:TYR:N	2.26	0.51
3:E:161:ASP:OD1	3:E:161:ASP:N	2.43	0.51
3:I:34:HIS:O	3:I:90:CYS:HA	2.10	0.51
3:K:185:ASN:HB2	3:K:188:ASN:HB3	1.92	0.51
1:C:226:GLN:OE1	1:C:227:ASP:HB2	2.10	0.51
1:M:188:HIS:HD2	1:M:204:TRP:HE3	1.59	0.51
1:G:101:CYS:N	1:G:164:CYS:SG	2.84	0.51
1:C:6:ARG:HA	1:C:100:GLY:HA3	1.92	0.51
3:O:134:LEU:HD12	3:O:135:PHE:N	2.26	0.51
2:B:1:ILE:HG13	2:B:2:GLN:N	2.26	0.51
2:D:70:PHE:HE1	2:D:72:PRO:HB3	1.75	0.51
3:E:21:PHE:N	3:E:21:PHE:CD2	2.79	0.51
1:M:9:PHE:HE2	1:M:99:TYR:CE2	2.28	0.51
4:F:29:HIS:ND1	4:F:96:GLN:HG2	2.26	0.51
4:P:135:ILE:HG13	4:P:141:ALA:HA	1.92	0.51
3:I:113:GLN:OE1	3:I:113:GLN:N	2.24	0.51
4:L:215:TYR:HA	4:L:232:THR:OG1	2.11	0.51
3:E:187:PHE:O	3:E:192:ILE:HD12	2.11	0.51
3:E:83:GLU:OE1	3:E:162:MET:CE	2.58	0.51
4:L:123:PRO:CG	4:L:150:PHE:HD2	2.18	0.51
1:A:143:THR:HG21	5:Q:9:VAL:HG12	1.92	0.51
3:I:81:GLN:N	3:I:84:ASP:OD2	2.40	0.51
4:F:47:ILE:CG2	4:F:48:TYR:N	2.73	0.50
3:I:44:PRO:HG2	4:J:105:PHE:CD2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:35:TYR:OH	4:F:103:GLN:OE1	2.20	0.50
4:P:160:TRP:HA	4:P:165:GLU:HB3	1.92	0.50
4:F:135:ILE:CD1	4:F:201:TRP:HZ3	2.24	0.50
2:B:1:ILE:HG13	2:B:2:GLN:H	1.75	0.50
4:F:83:GLN:HA	4:F:113:VAL:HG21	1.93	0.50
1:A:207:SER:O	1:A:207:SER:OG	2.22	0.50
4:F:170:VAL:HA	4:F:194:LEU:CD1	2.40	0.50
4:F:123:PRO:HA	4:F:149:GLY:HA3	1.92	0.50
2:N:33:SER:O	2:N:35:ILE:HD12	2.11	0.50
2:N:2:GLN:HE22	2:N:85:VAL:HB	1.76	0.50
4:L:150:PHE:CD1	4:L:150:PHE:C	2.85	0.50
3:I:2:LEU:HD23	3:I:3:ASN:H	1.77	0.50
3:O:96:ASN:H	5:T:5:MET:HE2	1.75	0.50
1:G:37:ASP:HB3	1:G:40:ALA:HB2	1.93	0.50
2:N:38:ASP:OD2	2:N:45:ARG:HB3	2.12	0.50
1:G:98:MET:CE	1:G:99:TYR:HA	2.41	0.50
4:P:130:PRO:HB3	4:P:142:THR:O	2.11	0.50
4:L:46:LEU:O	4:L:47:ILE:HG22	2.12	0.50
3:K:30:PHE:HD1	3:K:92:PHE:HE1	1.57	0.50
3:I:154:ILE:HD12	3:I:155:THR:N	2.26	0.50
1:M:66:LYS:NZ	3:O:29:ASN:HB2	2.25	0.50
1:M:249:VAL:HG22	1:M:257:TYR:CD1	2.46	0.50
4:F:203:ASN:N	4:F:204:PRO:CD	2.75	0.50
4:P:64:ARG:NH1	4:P:64:ARG:CG	2.73	0.50
1:C:13:SER:HB3	1:C:78:LEU:HD13	1.93	0.50
1:G:102:ASP:HB2	1:G:111:ARG:HG3	1.93	0.50
4:L:10:ASN:OD1	4:L:109:THR:HA	2.12	0.50
4:L:89:VAL:CG1	4:L:110:ARG:CG	2.83	0.50
3:K:144:VAL:CG2	3:K:157:LYS:HZ2	2.23	0.50
4:J:29:HIS:CD2	4:J:94:SER:O	2.64	0.50
4:F:170:VAL:CA	4:F:194:LEU:CD1	2.90	0.50
3:K:161:ASP:HA	3:K:168:LYS:HB3	1.93	0.50
4:L:204:PRO:HB2	4:L:205:ARG:HA	1.93	0.50
3:E:84:ASP:HA	3:E:85:SER:HG	1.76	0.50
4:F:110:ARG:HH21	4:F:154:HIS:HA	1.77	0.50
4:L:67:ALA:HB2	4:L:77:LEU:HD13	1.93	0.50
2:N:20:SER:HB3	4:F:18:ASP:CG	2.32	0.50
1:A:131:ARG:NH2	6:A:302:HOH:O	2.19	0.50
1:G:189:MET:CE	1:G:274:TRP:N	2.75	0.50
4:L:146:LEU:O	4:L:146:LEU:HD12	2.12	0.50
2:H:70:PHE:CE1	2:H:78:TYR:CZ	3.00	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:188:HIS:ND1	1:C:188:HIS:N	2.60	0.50
4:P:37:GLN:HG3	4:P:41:GLN:CD	2.32	0.50
4:J:150:PHE:O	4:J:187:ARG:HB2	2.12	0.50
3:K:135:PHE:CZ	3:K:192:ILE:HD11	2.44	0.49
1:M:227:ASP:OD1	1:M:248:VAL:HG12	2.12	0.49
4:L:150:PHE:CD1	4:L:188:TYR:O	2.65	0.49
2:B:18:GLY:N	2:B:72:PRO:O	2.37	0.49
1:A:147:TRP:HB3	1:A:152:VAL:HB	1.92	0.49
2:H:96:ASP:HB3	2:H:99:MET:HB2	1.94	0.49
3:I:36:TYR:O	3:I:88:TYR:HA	2.12	0.49
3:K:61:ARG:HH21	3:K:84:ASP:CG	2.15	0.49
1:G:97:ARG:HH22	5:U:8:THR:HA	1.77	0.49
4:P:11:LYS:O	4:P:111:LEU:HD12	2.13	0.49
3:K:135:PHE:C	3:K:135:PHE:CD1	2.85	0.49
1:G:195:SER:HB2	1:G:196:ASP:HA	1.93	0.49
1:A:98:MET:C	1:A:98:MET:HE2	2.33	0.49
1:C:202:ARG:HG3	1:C:244:TRP:NE1	2.26	0.49
2:B:89:GLN:CB	2:B:90:PRO:HD2	2.42	0.49
3:K:48:PHE:HD2	3:K:64:ALA:HB2	1.77	0.49
4:F:162:ASN:O	4:F:164:LYS:HG3	2.13	0.49
3:E:6:GLN:OE1	3:E:103:GLY:HA2	2.11	0.49
1:C:99:TYR:OH	5:R:3:VAL:HG12	2.12	0.49
4:F:69:ARG:HB2	4:F:75:SER:HB2	1.94	0.49
4:J:131:SER:HB2	4:J:134:GLU:CB	2.42	0.49
4:L:202:GLN:N	4:L:204:PRO:HD2	2.27	0.49
3:K:35:TRP:C	3:K:36:TYR:HD1	2.16	0.49
2:B:52:SER:OG	2:B:65:LEU:N	2.43	0.49
1:C:25:VAL:HG21	1:C:32:GLN:HE21	1.77	0.49
1:A:203:CYS:HB2	1:A:217:TRP:HZ3	1.75	0.49
1:G:185:PRO:HB3	1:G:208:PHE:HB3	1.93	0.49
1:M:8:PHE:HB2	1:M:25:VAL:HG13	1.92	0.49
4:L:170:VAL:CG2	4:L:194:LEU:CD2	2.87	0.49
4:P:129:GLU:HG3	4:P:201:TRP:CZ2	2.48	0.49
3:K:119:VAL:HA	3:K:134:LEU:O	2.13	0.49
4:J:162:ASN:HB2	4:J:164:LYS:NZ	2.28	0.49
4:P:21:LEU:HD22	4:P:109:THR:HG21	1.95	0.49
4:P:38:ARG:O	4:P:40:GLY:HA2	2.12	0.49
1:G:142:THR:O	1:G:146:LYS:HG3	2.13	0.49
3:K:72:TYR:C	3:K:72:TYR:CD1	2.85	0.49
4:L:36:ARG:HD2	4:L:90:TYR:HA	1.94	0.49
4:L:150:PHE:C	4:L:150:PHE:HD1	2.16	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:11:LYS:O	4:L:111:LEU:HA	2.13	0.49
1:M:73:THR:HG22	5:T:8:THR:HG21	1.95	0.49
1:A:9:PHE:HB2	1:A:97:ARG:HB3	1.95	0.49
1:M:49:ALA:HB3	1:M:52:ILE:HG22	1.94	0.49
2:H:54:LEU:HA	2:H:64:LEU:HD21	1.93	0.49
4:J:113:VAL:O	4:J:114:LEU:CB	2.60	0.49
3:K:159:VAL:N	4:L:171:CYS:SG	2.85	0.49
1:M:21:ARG:NH2	1:M:37:ASP:OD2	2.38	0.49
1:G:142:THR:OG1	6:G:302:HOH:O	2.20	0.49
3:K:133:CYS:SG	3:K:183:CYS:N	2.86	0.49
4:F:218:SER:HG	4:F:221:ASP:CB	2.22	0.49
4:J:154:HIS:N	4:J:154:HIS:CD2	2.80	0.49
4:J:49:PHE:CE1	4:J:54:ALA:HB2	2.47	0.49
1:A:219:ARG:HD2	1:A:257:TYR:CZ	2.47	0.49
3:K:175:TRP:CZ2	4:L:146:LEU:CB	2.95	0.48
1:G:98:MET:HE3	1:G:99:TYR:CA	2.40	0.48
4:F:217:LEU:CD1	4:F:218:SER:N	2.72	0.48
4:P:196:VAL:CG2	4:P:197:SER:H	2.06	0.48
2:N:3:ARG:O	2:N:30:PHE:HA	2.13	0.48
3:K:2:LEU:CB	3:K:3:ASN:HA	2.39	0.48
4:L:125:VAL:HG22	4:L:235:VAL:HG12	1.95	0.48
1:M:37:ASP:OD1	1:M:38:SER:N	2.46	0.48
4:J:153:ASP:OD2	4:J:176:PRO:HG3	2.12	0.48
4:F:35:TYR:CD1	4:F:43:LEU:HD21	2.48	0.48
1:M:197:HIS:N	1:M:197:HIS:ND1	2.60	0.48
2:D:89:GLN:HG3	2:D:90:PRO:N	2.28	0.48
2:H:7:ILE:HG23	2:H:93:VAL:HG21	1.95	0.48
3:K:63:SER:O	3:K:75:LEU:HA	2.12	0.48
3:E:31:TYR:C	3:E:31:TYR:CD2	2.86	0.48
3:I:7:SER:HB2	3:I:8:PRO:HD3	1.96	0.48
3:I:134:LEU:HB3	3:I:173:VAL:HA	1.94	0.48
1:C:102:ASP:OD2	1:C:113:TYR:OH	2.29	0.48
1:M:259:CYS:HB3	1:M:272:LEU:CB	2.43	0.48
1:M:270:LEU:HD13	1:M:272:LEU:HD21	1.95	0.48
3:K:48:PHE:HE2	3:K:63:SER:HA	1.77	0.48
4:L:141:ALA:H	4:L:198:ALA:H	1.61	0.48
2:N:12:ARG:O	2:N:13:HIS:CE1	2.67	0.48
1:G:192:HIS:CB	1:G:202:ARG:HH22	2.23	0.48
1:G:35:ARG:NH2	1:G:48:ARG:CD	2.76	0.48
1:M:73:THR:HG22	5:T:8:THR:CG2	2.43	0.48
2:H:24:ASN:ND2	2:H:65:LEU:CD2	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:178:LYS:HG2	3:E:179:SER:OG	2.13	0.48
4:L:62:SER:CA	4:L:65:PHE:CD2	2.97	0.48
1:M:203:CYS:HB2	1:M:217:TRP:NE1	2.28	0.48
1:C:145:HIS:HD2	6:C:305:HOH:O	1.95	0.48
1:C:24:ALA:HB3	1:C:36:PHE:HB3	1.96	0.48
1:M:225:THR:OG1	1:M:226:GLN:N	2.47	0.48
4:L:88:ALA:CB	4:L:110:ARG:HA	2.42	0.48
3:K:136:THR:HG21	3:K:171:SER:HB3	1.95	0.48
4:P:14:GLU:OE2	4:P:117:LEU:HD11	2.13	0.48
2:B:37:VAL:HG21	2:B:66:TYR:CD1	2.49	0.48
4:F:160:TRP:H	4:F:209:ARG:HG3	1.78	0.48
2:N:54:LEU:HD23	2:N:54:LEU:C	2.34	0.48
2:N:63:TYR:C	2:N:63:TYR:CD1	2.87	0.48
2:B:10:TYR:HE2	2:B:26:TYR:HB3	1.79	0.48
3:O:123:ARG:HB2	3:O:131:SER:HB3	1.95	0.48
2:H:70:PHE:HZ	2:H:78:TYR:CD2	2.31	0.48
3:O:120:TYR:HB3	4:P:131:SER:OG	2.14	0.48
3:E:87:THR:HA	3:E:105:SER:HA	1.96	0.48
3:I:152:VAL:HA	3:I:176:SER:OG	2.13	0.48
1:A:70:HIS:HD2	5:Q:6:VAL:HG22	1.77	0.48
3:K:138:PHE:HD2	3:K:138:PHE:H	1.61	0.48
3:I:121:GLN:HG3	4:J:131:SER:HA	1.95	0.48
3:O:79:GLY:C	3:O:81:GLN:OE1	2.51	0.48
1:G:163:THR:HA	1:G:166:GLU:HG2	1.95	0.48
1:A:225:THR:OG1	1:A:226:GLN:HB2	2.14	0.48
1:A:59:TYR:OH	1:A:171:TYR:OH	2.16	0.48
1:M:102:ASP:HB2	1:M:111:ARG:HG2	1.95	0.48
4:L:82:THR:CG2	4:L:83:GLN:N	2.77	0.48
4:L:130:PRO:HD2	4:L:201:TRP:CZ2	2.49	0.48
3:E:84:ASP:CA	3:E:85:SER:CB	2.91	0.48
4:F:123:PRO:HA	4:F:149:GLY:CA	2.44	0.48
4:P:160:TRP:HH2	4:P:234:ILE:HD11	1.78	0.48
2:N:30:PHE:CE1	2:N:35:ILE:HD11	2.48	0.48
4:F:201:TRP:O	4:F:204:PRO:CG	2.62	0.48
1:G:10:THR:HG22	2:H:56:PHE:CE2	2.48	0.48
4:J:45:PHE:HZ	4:J:48:TYR:HB3	1.78	0.48
1:C:22:PHE:H	1:C:38:SER:HB3	1.78	0.48
3:O:131:SER:OG	3:O:181:PHE:HE2	1.97	0.48
4:F:130:PRO:HB3	4:F:142:THR:O	2.14	0.48
2:D:74:GLU:N	2:D:74:GLU:OE1	2.47	0.48
3:K:118:ALA:HB2	3:K:197:PHE:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:GLU:CG	1:A:178:THR:N	2.77	0.48
4:F:33:TYR:O	4:F:92:CYS:HA	2.14	0.48
3:I:33:LEU:O	3:I:50:MET:N	2.41	0.47
4:L:161:VAL:HG12	4:L:162:ASN:H	1.78	0.47
4:L:150:PHE:HE1	4:L:188:TYR:C	2.15	0.47
1:C:103:VAL:HG12	1:C:109:PHE:HA	1.96	0.47
4:J:14:GLU:HA	4:J:114:LEU:O	2.14	0.47
4:L:150:PHE:CZ	4:L:155:VAL:HG11	2.49	0.47
1:G:234:ARG:CG	1:G:242:GLN:HB2	2.43	0.47
1:M:11:SER:HA	1:M:21:ARG:O	2.14	0.47
3:K:124:ASP:CA	4:L:128:PHE:HA	2.45	0.47
2:H:3:ARG:HH21	2:H:61:SER:HB2	1.78	0.47
1:M:217:TRP:HZ3	1:M:247:VAL:HG22	1.79	0.47
1:C:159:TYR:HD1	1:C:163:THR:HB	1.78	0.47
1:G:98:MET:SD	1:G:99:TYR:N	2.87	0.47
4:F:201:TRP:O	4:F:204:PRO:HG3	2.14	0.47
1:C:66:LYS:HE3	5:R:2:LEU:HB2	1.95	0.47
4:P:173:ASP:N	4:P:173:ASP:OD1	2.47	0.47
3:O:155:THR:CG2	4:P:173:ASP:OD2	2.60	0.47
4:F:60:LEU:HD22	4:F:65:PHE:HB3	1.94	0.47
2:B:49:VAL:HG12	2:B:50:GLU:O	2.15	0.47
4:L:131:SER:HB2	4:L:135:ILE:HG21	1.96	0.47
1:G:66:LYS:NZ	5:U:2:LEU:O	2.45	0.47
1:C:27:TYR:CD2	1:C:32:GLN:HB2	2.49	0.47
4:L:103:GLN:N	4:L:103:GLN:OE1	2.48	0.47
1:A:66:LYS:HE2	3:I:29:ASN:OD1	2.14	0.47
1:A:202:ARG:HG3	1:A:244:TRP:NE1	2.26	0.47
4:F:84:GLN:CG	4:F:85:GLU:H	2.27	0.47
1:M:14:ARG:HH21	1:M:21:ARG:HB2	1.78	0.47
2:D:55:SER:O	2:D:63:TYR:N	2.46	0.47
1:G:68:LYS:O	1:G:72:GLN:HG2	2.15	0.47
3:K:135:PHE:HZ	3:K:192:ILE:HG12	1.67	0.47
4:J:191:SER:OG	4:J:191:SER:O	2.33	0.47
1:M:213:ILE:HD11	1:M:261:VAL:CG1	2.44	0.47
1:M:203:CYS:HB2	1:M:217:TRP:CZ2	2.50	0.47
1:C:155:GLN:HG2	3:E:51:THR:HG21	1.96	0.47
4:L:140:LYS:HA	4:L:197:SER:HA	1.95	0.47
2:B:40:LEU:HD23	2:B:43:GLY:HA2	1.96	0.47
4:L:36:ARG:HB2	4:L:44:GLU:OE2	2.15	0.47
4:P:154:HIS:N	4:P:154:HIS:ND1	2.60	0.47
1:G:98:MET:C	1:G:98:MET:SD	2.93	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:117:ALA:HB2	2:H:60:TRP:CE2	2.50	0.47
3:E:138:PHE:CE1	3:E:170:ASN:O	2.68	0.47
4:J:223:TRP:NE1	4:J:228:ALA:O	2.47	0.47
1:G:218:GLN:HB2	1:G:222:GLU:C	2.35	0.47
1:A:49:ALA:O	1:A:52:ILE:HG22	2.15	0.47
4:P:172:THR:HG22	4:P:173:ASP:H	1.80	0.47
3:O:118:ALA:CB	3:O:120:TYR:CZ	2.98	0.47
3:I:61:ARG:NH1	3:I:84:ASP:OD2	2.48	0.47
3:I:89:LEU:HD22	3:I:100:PHE:HD2	1.79	0.47
1:C:9:PHE:HE2	1:C:99:TYR:CE2	2.33	0.47
4:P:118:LYS:O	4:P:120:VAL:N	2.48	0.47
1:G:42:SER:HB3	1:G:44:ARG:HG3	1.97	0.47
3:O:153:TYR:HB3	4:P:177:LEU:HD21	1.97	0.47
4:J:86:ASP:N	4:J:86:ASP:OD1	2.48	0.47
3:K:115:PRO:HG3	3:K:139:ASP:OD2	2.14	0.47
4:P:223:TRP:CZ2	4:P:225:GLN:CG	2.97	0.47
4:J:175:GLN:HG3	4:J:176:PRO:HD2	1.96	0.47
3:O:168:LYS:HB3	3:O:168:LYS:HE2	1.67	0.47
4:F:83:GLN:CA	4:F:113:VAL:HG21	2.45	0.47
4:P:84:GLN:HA	4:P:113:VAL:HG13	1.96	0.47
3:O:137:ASP:HB3	3:O:169:SER:HA	1.97	0.47
4:L:224:THR:OG1	4:L:225:GLN:N	2.48	0.47
4:P:190:LEU:HD12	4:P:191:SER:H	1.80	0.47
1:C:231:VAL:CG1	1:C:244:TRP:HE3	2.17	0.47
4:F:155:VAL:HG12	4:F:214:PHE:CD1	2.50	0.47
1:A:35:ARG:HD3	1:A:48:ARG:NE	2.14	0.47
4:F:201:TRP:HA	4:F:204:PRO:HG3	1.96	0.47
3:K:33:LEU:HD23	3:K:91:ALA:O	2.15	0.47
3:I:42:LYS:HG2	3:I:43:SER:N	2.30	0.47
4:J:123:PRO:CA	4:J:150:PHE:HB3	2.45	0.47
1:C:22:PHE:H	1:C:38:SER:CB	2.27	0.47
3:O:112:ILE:HG22	3:O:114:ASN:H	1.80	0.47
1:C:172:LEU:HD23	1:C:179:LEU:HD13	1.97	0.47
3:K:175:TRP:NE1	4:L:146:LEU:HD22	2.12	0.47
3:K:137:ASP:N	3:K:137:ASP:OD1	2.47	0.47
3:E:13:VAL:O	3:E:108:VAL:HA	2.15	0.47
1:G:125:ALA:C	1:G:134:THR:HG22	2.34	0.47
4:P:33:TYR:OH	4:P:95:SER:OG	2.13	0.47
3:E:138:PHE:O	3:E:139:ASP:O	2.33	0.46
3:E:84:ASP:HB3	3:E:85:SER:C	2.35	0.46
1:G:187:THR:HB	1:G:272:LEU:CD2	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:26:TYR:CE2	2:B:28:SER:HB2	2.51	0.46
4:F:56:ASP:OD1	4:F:57:LYS:N	2.48	0.46
1:G:163:THR:HA	1:G:166:GLU:CG	2.45	0.46
1:G:159:TYR:CE1	1:G:163:THR:OG1	2.68	0.46
4:L:150:PHE:CE2	4:L:155:VAL:HG11	2.50	0.46
2:N:22:PHE:HD2	2:N:67:TYR:HB2	1.80	0.46
1:C:147:TRP:CD1	1:C:147:TRP:N	2.83	0.46
4:L:89:VAL:HG11	4:L:110:ARG:HB2	1.91	0.46
3:K:38:TRP:CZ3	3:K:44:PRO:HG3	2.38	0.46
4:P:196:VAL:CG2	4:P:197:SER:N	2.73	0.46
4:F:36:ARG:HE	4:F:38:ARG:NH1	2.13	0.46
2:H:7:ILE:HD11	2:H:25:CYS:SG	2.56	0.46
3:E:114:ASN:HA	3:E:115:PRO:HD2	1.57	0.46
3:K:151:ASP:OD2	3:K:181:PHE:HB3	2.15	0.46
4:F:15:LYS:NZ	4:F:83:GLN:HE21	2.14	0.46
1:C:243:LYS:CG	1:C:244:TRP:H	2.28	0.46
2:H:3:ARG:NH2	2:H:59:ASP:O	2.43	0.46
1:M:266:LEU:HD12	1:M:266:LEU:N	2.31	0.46
4:J:11:LYS:HZ1	4:J:217:LEU:CD2	2.29	0.46
1:C:136:ALA:O	1:C:137:ASP:HB3	2.16	0.46
3:O:7:SER:HB3	3:O:22:THR:HB	1.98	0.46
4:L:159:TRP:CE3	4:L:170:VAL:HG13	2.50	0.46
1:G:97:ARG:HH12	5:U:6:VAL:HG12	1.74	0.46
3:O:53:ASN:CA	3:O:68:THR:HG23	2.46	0.46
1:M:188:HIS:CD2	1:M:204:TRP:HE3	2.33	0.46
4:J:217:LEU:CD1	4:J:221:ASP:HB3	2.41	0.46
1:G:234:ARG:HB3	2:H:8:GLN:NE2	2.31	0.46
1:A:93:HIS:CG	1:A:119:ASP:OD1	2.68	0.46
4:P:24:ASP:HA	4:P:25:PRO:HD2	1.76	0.46
2:D:96:ASP:HB3	2:D:99:MET:HB3	1.97	0.46
4:P:130:PRO:HD2	4:P:201:TRP:CZ2	2.51	0.46
4:F:176:PRO:HB2	4:F:188:TYR:HB3	1.97	0.46
3:I:15:GLU:OE1	3:I:110:PRO:HA	2.15	0.46
1:M:187:THR:HB	1:M:272:LEU:HD11	1.98	0.46
1:A:84:TYR:OH	1:A:146:LYS:NZ	2.26	0.46
1:C:33:PHE:O	1:C:52:ILE:HG21	2.15	0.46
1:C:189:MET:HG3	1:C:202:ARG:O	2.16	0.46
1:G:97:ARG:CD	1:G:116:TYR:CE1	2.98	0.46
4:F:165:GLU:C	4:F:166:VAL:HG23	2.36	0.46
1:G:154:GLU:O	1:G:157:ARG:HG2	2.16	0.46
4:J:202:GLN:O	4:J:205:ARG:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:129:ASP:N	1:M:129:ASP:OD1	2.46	0.46
1:C:106:ASP:N	1:C:106:ASP:OD1	2.47	0.46
1:A:106:ASP:OD1	1:A:106:ASP:N	2.48	0.46
1:M:78:LEU:CD2	1:M:95:VAL:CG2	2.74	0.46
1:M:198:GLU:HB3	1:M:249:VAL:O	2.16	0.46
3:I:137:ASP:CG	3:I:138:PHE:H	2.19	0.46
4:F:202:GLN:C	4:F:204:PRO:HD3	2.36	0.46
2:B:3:ARG:NH1	2:B:59:ASP:O	2.29	0.46
3:I:159:VAL:HA	3:I:169:SER:O	2.15	0.46
1:A:217:TRP:CD1	1:A:247:VAL:HG11	2.51	0.46
1:M:135:ALA:HB1	1:M:140:ALA:HB1	1.97	0.46
1:G:99:TYR:CE2	5:U:3:VAL:HG12	2.51	0.46
3:K:81:GLN:O	3:K:108:VAL:HG21	2.16	0.46
3:E:11:LEU:HD13	3:E:19:THR:HG21	1.97	0.46
4:P:14:GLU:OE2	4:P:117:LEU:CD1	2.63	0.45
4:J:84:GLN:O	4:J:87:SER:OG	2.33	0.45
2:H:21:ASN:OD1	2:H:22:PHE:O	2.34	0.45
3:K:158:CYS:SG	4:L:172:THR:N	2.84	0.45
2:H:70:PHE:CE1	2:H:78:TYR:CG	3.04	0.45
4:F:195:ARG:CG	4:F:195:ARG:NH1	2.73	0.45
1:C:35:ARG:HD3	1:C:48:ARG:HD3	1.98	0.45
1:M:96:GLN:HE22	2:N:31:HIS:HE1	1.62	0.45
1:M:14:ARG:HB3	1:M:17:ARG:HB2	1.98	0.45
3:O:50:MET:HB3	3:O:66:LEU:HD22	1.98	0.45
4:F:180:GLN:CA	4:F:186:SER:OG	2.63	0.45
2:B:5:PRO:HA	2:B:30:PHE:HB3	1.97	0.45
1:G:98:MET:HE3	1:G:113:TYR:HD1	1.73	0.45
2:H:7:ILE:HD12	2:H:82:VAL:HG11	1.97	0.45
2:N:59:ASP:O	2:N:60:TRP:HB2	2.17	0.45
1:G:6:ARG:CB	1:G:8:PHE:HE2	2.27	0.45
4:P:38:ARG:HH11	4:P:38:ARG:HG2	1.81	0.45
2:H:40:LEU:HD12	2:H:79:ALA:HB3	1.98	0.45
4:J:180:GLN:HA	4:J:181:PRO:HA	1.72	0.45
3:E:154:ILE:HG22	3:E:155:THR:N	2.31	0.45
3:E:157:LYS:HE2	3:E:170:ASN:OD1	2.16	0.45
3:E:82:PRO:HG3	3:E:110:PRO:HB3	1.98	0.45
3:I:138:PHE:O	3:I:138:PHE:CD1	2.70	0.45
3:K:124:ASP:H	3:K:131:SER:CB	2.29	0.45
1:G:59:TYR:O	1:G:63:GLU:HG2	2.17	0.45
3:I:21:PHE:CE2	3:I:77:ILE:HD11	2.51	0.45
1:G:69:ALA:O	1:G:73:THR:OG1	2.26	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:97:ARG:NH2	1:M:147:TRP:HH2	2.13	0.45
4:F:202:GLN:C	4:F:204:PRO:CD	2.85	0.45
3:K:31:TYR:CD1	5:U:4:PRO:HB2	2.42	0.45
4:J:151:TYR:HB2	4:J:187:ARG:HB3	1.97	0.45
3:O:112:ILE:HB	3:O:115:PRO:HG3	1.98	0.45
3:K:190:SER:O	3:K:190:SER:OG	2.34	0.45
1:M:220:ASP:HB3	1:M:221:GLY:H	1.64	0.45
4:P:160:TRP:HA	4:P:165:GLU:CB	2.46	0.45
2:B:89:GLN:HB2	2:B:90:PRO:CD	2.44	0.45
1:A:22:PHE:H	1:A:38:SER:CB	2.29	0.45
1:G:102:ASP:HB2	1:G:111:ARG:CG	2.47	0.45
1:A:98:MET:C	1:A:98:MET:CE	2.85	0.45
1:A:9:PHE:HZ	5:Q:2:LEU:HD23	1.82	0.45
1:C:67:VAL:HA	1:C:70:HIS:HD2	1.82	0.45
2:N:2:GLN:HE21	2:N:85:VAL:CB	2.27	0.45
4:L:46:LEU:C	4:L:47:ILE:CG2	2.85	0.45
1:G:124:ILE:HG12	1:G:135:ALA:HA	1.99	0.45
4:F:138:THR:O	4:F:139:GLN:HB2	2.16	0.45
3:O:102:THR:HA	3:O:103:GLY:HA3	1.74	0.45
2:H:7:ILE:HB	2:H:27:VAL:HG12	1.99	0.45
1:C:99:TYR:CZ	5:R:3:VAL:HG12	2.52	0.45
3:I:53:ASN:HA	3:I:54:GLY:HA2	1.57	0.45
3:E:84:ASP:HA	3:E:85:SER:CB	2.47	0.45
4:P:159:TRP:HD1	4:P:209:ARG:O	1.99	0.45
1:G:235:PRO:HA	1:G:241:PHE:HA	1.98	0.45
2:B:3:ARG:NH1	2:B:60:TRP:O	2.50	0.45
1:G:179:LEU:HD12	1:G:179:LEU:N	2.31	0.45
3:K:136:THR:CG2	3:K:171:SER:CA	2.83	0.45
4:L:169:GLY:C	4:L:194:LEU:HD22	2.37	0.45
3:K:38:TRP:CE3	3:K:42:LYS:O	2.69	0.45
4:J:29:HIS:HD2	4:J:94:SER:C	2.13	0.45
4:J:194:LEU:HD23	4:J:195:ARG:C	2.37	0.45
1:G:81:LEU:HG	5:U:9:VAL:CG1	2.47	0.45
2:N:5:PRO:HD3	2:N:84:HIS:CD2	2.51	0.45
1:G:179:LEU:CD1	1:G:179:LEU:N	2.80	0.45
2:D:13:HIS:HB2	2:D:21:ASN:OD1	2.17	0.45
1:G:234:ARG:NH2	1:G:244:TRP:HE1	2.15	0.45
3:I:48:PHE:CE1	3:I:59:LYS:HG3	2.41	0.45
1:C:8:PHE:HB2	1:C:25:VAL:HG13	1.99	0.45
1:G:81:LEU:CG	5:U:9:VAL:HG11	2.46	0.45
1:A:103:VAL:HG12	1:A:108:ARG:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:70:PHE:CE1	2:D:72:PRO:HB3	2.52	0.45
3:K:72:TYR:O	3:K:72:TYR:CD1	2.70	0.45
4:J:120:VAL:O	4:J:121:PHE:CG	2.70	0.45
3:O:161:ASP:O	3:O:162:MET:HB3	2.16	0.45
4:L:154:HIS:CD2	4:L:215:TYR:CB	3.01	0.44
2:N:75:LYS:O	2:N:76:ASP:C	2.54	0.44
4:P:97:THR:HG22	4:P:98:GLN:N	2.32	0.44
4:J:84:GLN:CD	1:G:177:GLU:OE1	2.56	0.44
3:I:138:PHE:HD1	3:I:142:THR:OG1	1.95	0.44
2:N:2:GLN:HE21	2:N:85:VAL:CG2	2.30	0.44
4:F:26:ILE:HB	4:F:29:HIS:CD2	2.52	0.44
1:A:259:CYS:HB3	1:A:272:LEU:HB2	2.00	0.44
1:G:188:HIS:HB3	1:G:204:TRP:CB	2.41	0.44
1:G:185:PRO:CA	1:G:208:PHE:HB3	2.46	0.44
4:L:70:THR:N	4:L:75:SER:OG	2.44	0.44
2:B:46:ILE:HG13	2:B:47:GLU:N	2.31	0.44
2:N:39:LEU:HA	2:N:39:LEU:HD23	1.80	0.44
3:K:175:TRP:CZ2	4:L:146:LEU:HB2	2.52	0.44
4:L:83:GLN:CG	4:L:84:GLN:N	2.54	0.44
4:F:29:HIS:CE1	4:F:96:GLN:HG2	2.52	0.44
1:A:223:ASP:O	1:A:225:THR:HG22	2.16	0.44
2:H:72:PRO:HB2	2:H:78:TYR:HH	1.81	0.44
1:C:66:LYS:CD	5:R:4:PRO:HA	2.42	0.44
2:H:3:ARG:NH2	2:H:61:SER:HB2	2.32	0.44
4:J:48:TYR:CD1	4:J:99:LEU:HD11	2.52	0.44
3:O:1:ILE:HG13	3:O:1:ILE:O	2.17	0.44
3:I:146:GLN:OE1	3:I:154:ILE:HG12	2.14	0.44
4:L:130:PRO:HB3	4:L:142:THR:O	2.16	0.44
1:M:66:LYS:HZ1	3:O:29:ASN:ND2	2.14	0.44
1:G:82:ARG:NH2	1:G:89:GLU:N	2.46	0.44
4:P:211:GLN:HE22	4:P:213:GLN:HB2	1.83	0.44
4:J:119:ASN:N	4:J:119:ASN:OD1	2.50	0.44
3:K:47:LEU:O	3:K:48:PHE:CD1	2.70	0.44
4:J:177:LEU:CD1	4:J:177:LEU:C	2.86	0.44
2:N:22:PHE:CE1	4:F:80:GLN:NE2	2.85	0.44
1:G:157:ARG:HG3	1:G:158:ALA:N	2.31	0.44
4:F:41:GLN:O	4:F:42:GLY:C	2.55	0.44
4:L:10:ASN:HB3	4:L:110:ARG:O	2.17	0.44
5:T:3:VAL:O	5:T:4:PRO:C	2.55	0.44
2:H:24:ASN:ND2	2:H:65:LEU:CG	2.77	0.44
4:P:58:SER:HA	4:P:59:GLY:HA2	1.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:51:HIS:HB3	2:N:66:TYR:CE1	2.52	0.44
1:A:274:TRP:CE3	1:A:275:GLU:HB2	2.53	0.44
4:L:171:CYS:HB2	4:L:193:ARG:O	2.17	0.44
3:I:115:PRO:HA	3:I:137:ASP:CG	2.38	0.44
3:E:49:VAL:HG23	4:F:102:THR:HG22	1.97	0.44
1:G:204:TRP:CE3	1:G:244:TRP:HB3	2.51	0.44
1:M:189:MET:SD	1:M:274:TRP:CZ3	3.10	0.44
2:H:9:VAL:CG2	2:H:80:CYS:HB2	2.47	0.44
1:G:156:LEU:HA	1:G:156:LEU:HD23	1.77	0.44
3:E:102:THR:OG1	3:E:102:THR:O	2.34	0.44
3:K:135:PHE:CZ	3:K:192:ILE:HD13	2.51	0.44
3:K:192:ILE:O	3:K:193:PRO:C	2.56	0.44
1:G:116:TYR:C	1:G:116:TYR:CD2	2.85	0.44
3:I:66:LEU:HD12	3:I:67:ASN:N	2.32	0.44
1:A:49:ALA:HA	1:A:50:PRO:HD2	1.77	0.44
4:J:125:VAL:O	4:J:237:ALA:HB2	2.17	0.44
1:A:98:MET:HE2	1:A:98:MET:HB3	1.49	0.44
3:K:113:GLN:O	3:K:114:ASN:C	2.53	0.44
4:L:37:GLN:HG2	4:L:89:VAL:H	1.82	0.44
1:M:195:SER:O	1:M:197:HIS:CE1	2.70	0.44
4:F:230:PRO:C	4:F:231:VAL:HG23	2.37	0.44
3:I:137:ASP:O	3:I:138:PHE:CD2	2.70	0.44
2:B:86:THR:O	2:B:87:LEU:HD23	2.18	0.44
1:M:231:VAL:HG13	1:M:244:TRP:HE3	1.83	0.44
1:A:47:PRO:HB3	1:A:60:TRP:CH2	2.53	0.44
4:J:39:LEU:HA	4:J:40:GLY:HA2	1.68	0.44
4:J:196:VAL:HG12	4:J:197:SER:N	2.33	0.44
3:O:31:TYR:HB2	5:T:4:PRO:HB2	2.00	0.44
4:F:172:THR:HG22	4:F:192:SER:HB2	2.00	0.44
3:E:160:LEU:HD23	4:F:169:GLY:O	2.18	0.44
1:C:37:ASP:HB3	1:C:40:ALA:HB2	2.00	0.44
4:P:45:PHE:HZ	4:P:48:TYR:HB3	1.83	0.44
3:K:136:THR:O	3:K:137:ASP:HB2	2.18	0.43
4:P:14:GLU:HG2	4:P:117:LEU:CD1	2.45	0.43
1:G:16:GLY:CA	1:G:17:ARG:CB	2.77	0.43
1:G:133:TRP:HZ3	1:G:147:TRP:HZ3	1.65	0.43
3:K:21:PHE:O	3:K:74:TYR:HA	2.17	0.43
1:C:25:VAL:CG2	1:C:32:GLN:HE21	2.31	0.43
1:C:117:ALA:HB2	2:D:60:TRP:CE2	2.53	0.43
1:G:189:MET:HE3	1:G:274:TRP:N	2.33	0.43
4:J:120:VAL:C	4:J:121:PHE:CG	2.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:220:ASN:OD1	4:F:220:ASN:N	2.51	0.43
3:K:160:LEU:O	3:K:168:LYS:HB3	2.18	0.43
4:J:84:GLN:O	4:J:113:VAL:HG11	2.18	0.43
4:L:130:PRO:HG2	4:L:201:TRP:NE1	2.32	0.43
4:F:135:ILE:HD13	4:F:201:TRP:HZ3	1.83	0.43
4:J:11:LYS:HZ1	4:J:217:LEU:HD22	1.83	0.43
1:M:59:TYR:O	1:M:63:GLU:HG2	2.18	0.43
3:K:131:SER:HA	4:L:128:PHE:HE1	1.83	0.43
3:E:124:ASP:CG	3:E:125:SER:HA	2.37	0.43
1:A:247:VAL:HG23	1:A:249:VAL:HG23	1.99	0.43
4:J:49:PHE:CE2	4:J:69:ARG:HB2	2.53	0.43
3:O:123:ARG:O	4:P:129:GLU:HB3	2.19	0.43
3:O:176:SER:CB	3:O:181:PHE:O	2.66	0.43
2:N:63:TYR:O	2:N:63:TYR:CD1	2.70	0.43
2:N:81:ARG:CD	2:N:92:ILE:CG1	2.96	0.43
4:F:33:TYR:OH	4:F:99:LEU:HA	2.19	0.43
4:J:120:VAL:O	4:J:121:PHE:CD1	2.70	0.43
2:D:40:LEU:HD13	2:D:81:ARG:H	1.83	0.43
1:G:127:LYS:HA	1:G:127:LYS:HD2	1.66	0.43
1:G:228:THR:HG23	1:G:228:THR:O	2.18	0.43
4:J:131:SER:O	4:J:135:ILE:HG23	2.19	0.43
4:F:149:GLY:CA	4:F:150:PHE:HB3	2.35	0.43
4:L:160:TRP:C	4:L:161:VAL:CG2	2.85	0.43
1:G:191:HIS:ND1	1:G:191:HIS:C	2.72	0.43
3:K:63:SER:O	3:K:75:LEU:HD12	2.19	0.43
1:C:188:HIS:O	1:C:204:TRP:N	2.42	0.43
3:E:53:ASN:HA	3:E:54:GLY:HA2	1.63	0.43
4:P:64:ARG:HH11	4:P:64:ARG:HG2	1.80	0.43
1:A:73:THR:HB	5:Q:8:THR:HG22	2.01	0.43
1:M:162:GLY:O	1:M:166:GLU:HG3	2.17	0.43
4:L:39:LEU:HD12	4:L:39:LEU:HA	1.76	0.43
1:M:177:GLU:OE1	1:M:177:GLU:N	2.51	0.43
3:O:131:SER:OG	3:O:181:PHE:CE2	2.72	0.43
4:F:218:SER:CB	4:F:221:ASP:HB2	2.44	0.43
4:P:223:TRP:CE2	4:P:225:GLN:HG2	2.52	0.43
4:J:223:TRP:CE2	4:J:228:ALA:O	2.72	0.43
1:A:124:ILE:HG13	1:A:134:THR:O	2.19	0.43
3:O:123:ARG:HG3	3:O:130:LYS:O	2.18	0.43
4:P:160:TRP:CH2	4:P:234:ILE:HD11	2.53	0.43
4:P:11:LYS:HG3	4:P:12:VAL:N	2.33	0.43
2:H:23:LEU:HD13	2:H:70:PHE:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:11:LEU:O	3:K:12:HIS:ND1	2.51	0.43
4:L:34:TRP:CZ3	4:L:92:CYS:HB2	2.54	0.43
4:L:120:VAL:O	4:L:230:PRO:HG3	2.19	0.43
1:M:231:VAL:HG22	1:M:244:TRP:H	1.84	0.43
4:L:88:ALA:CB	4:L:110:ARG:HG2	2.39	0.43
3:E:157:LYS:HB3	3:E:157:LYS:HE2	1.75	0.43
1:G:58:GLU:HA	1:G:61:ASP:HB2	2.00	0.43
1:G:214:THR:O	1:G:214:THR:CG2	2.60	0.43
3:K:21:PHE:HZ	3:K:106:LEU:HD22	1.84	0.43
4:J:164:LYS:HE2	4:J:164:LYS:HB2	1.87	0.43
4:F:22:ARG:HG2	4:F:76:THR:HG22	2.01	0.43
3:I:20:ASN:HA	3:I:75:LEU:O	2.19	0.43
1:C:160:LEU:O	1:C:165:VAL:HG23	2.18	0.43
3:K:29:ASN:O	3:K:94:THR:OG1	2.21	0.43
3:E:163:ARG:HA	3:E:163:ARG:HD3	1.63	0.43
1:G:97:ARG:HE	1:G:116:TYR:HE1	0.61	0.43
1:G:17:ARG:HH11	1:G:17:ARG:CG	2.14	0.43
4:J:84:GLN:OE1	1:G:177:GLU:OE1	2.37	0.43
3:K:47:LEU:HD12	3:K:47:LEU:HA	1.77	0.43
1:A:66:LYS:CD	5:Q:4:PRO:HA	2.48	0.43
2:N:89:GLN:O	2:N:90:PRO:C	2.56	0.43
1:A:237:GLY:C	1:A:239:GLY:H	2.22	0.43
3:E:37:ARG:HB2	3:E:47:LEU:HD11	2.01	0.43
1:M:92:SER:OG	1:M:92:SER:O	2.25	0.43
4:L:159:TRP:CE2	4:L:194:LEU:HG	2.54	0.43
4:F:194:LEU:HA	4:F:194:LEU:HD12	1.81	0.43
1:G:97:ARG:NH1	5:U:7:ALA:O	2.46	0.43
3:I:34:HIS:ND1	3:I:93:ILE:HD11	2.34	0.43
4:F:153:ASP:CG	4:F:176:PRO:HG3	2.39	0.43
2:D:82:VAL:O	2:D:90:PRO:CB	2.65	0.43
3:O:34:HIS:NE2	3:O:93:ILE:HD11	2.33	0.43
1:M:53:GLU:HA	1:M:60:TRP:HZ2	1.84	0.43
3:I:25:PHE:HB2	3:I:26:PRO:HD2	2.01	0.43
3:I:2:LEU:HD23	3:I:3:ASN:N	2.33	0.43
4:L:82:THR:HG21	4:L:113:VAL:HG22	2.00	0.43
3:O:53:ASN:HA	3:O:54:GLY:HA2	1.66	0.43
1:M:256:ARG:HB3	6:M:301:HOH:O	2.19	0.43
4:F:193:ARG:CG	4:F:193:ARG:NH1	2.72	0.43
1:A:231:VAL:O	1:A:232:GLU:C	2.57	0.43
3:K:4:VAL:HG11	3:K:92:PHE:HB3	2.00	0.43
4:F:32:LEU:O	4:F:49:PHE:N	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:LEU:HD23	1:A:179:LEU:HD13	2.01	0.43
1:M:78:LEU:HB3	1:M:82:ARG:NH2	2.33	0.42
3:K:122:LEU:HG	4:L:130:PRO:HA	2.00	0.42
3:K:134:LEU:CD2	4:L:142:THR:HG21	2.49	0.42
4:J:211:GLN:HA	4:J:236:SER:HB3	2.00	0.42
4:J:217:LEU:O	4:J:231:VAL:HG12	2.19	0.42
1:M:59:TYR:HH	1:M:171:TYR:HH	1.36	0.42
1:A:228:THR:HA	1:A:247:VAL:HG12	2.01	0.42
3:O:111:ASN:OD1	3:O:112:ILE:N	2.43	0.42
3:O:63:SER:O	3:O:75:LEU:HD12	2.19	0.42
1:C:154:GLU:HB3	3:E:52:LEU:HD11	2.01	0.42
2:B:25:CYS:HB2	2:B:39:LEU:HD21	1.99	0.42
1:M:233:THR:HG22	1:M:243:LYS:HD3	2.00	0.42
4:L:88:ALA:HB1	4:L:89:VAL:CG1	2.49	0.42
3:K:111:ASN:OD1	3:K:112:ILE:N	2.52	0.42
1:A:46:GLU:HG3	1:A:47:PRO:HD2	2.00	0.42
1:A:77:ASP:OD1	5:Q:9:VAL:HG22	2.18	0.42
4:P:6:GLN:OE1	4:P:108:GLY:N	2.52	0.42
4:F:217:LEU:HD12	4:F:218:SER:N	2.34	0.42
1:G:162:GLY:C	1:G:166:GLU:OE2	2.58	0.42
1:G:162:GLY:O	1:G:166:GLU:CD	2.58	0.42
1:G:218:GLN:CB	1:G:222:GLU:O	2.62	0.42
1:C:63:GLU:OE2	1:C:66:LYS:NZ	2.49	0.42
4:J:231:VAL:O	4:J:232:THR:C	2.57	0.42
1:G:49:ALA:HB1	1:G:51:TRP:NE1	2.35	0.42
1:A:69:ALA:HB1	3:I:96:ASN:ND2	2.34	0.42
3:K:96:ASN:ND2	4:L:48:TYR:OH	2.52	0.42
1:C:31:THR:HG23	1:C:209:TYR:CE1	2.54	0.42
4:L:175:GLN:HG2	4:L:175:GLN:H	1.59	0.42
4:J:58:SER:OG	4:J:58:SER:O	2.32	0.42
2:N:57:SER:C	2:N:59:ASP:H	2.15	0.42
1:G:32:GLN:O	1:G:49:ALA:HB2	2.19	0.42
4:J:151:TYR:HA	4:J:152:PRO:HA	1.84	0.42
4:J:4:VAL:HG11	4:J:105:PHE:O	2.19	0.42
1:M:25:VAL:HG11	2:N:55:SER:OG	2.20	0.42
1:C:201:LEU:O	1:C:246:ALA:HA	2.19	0.42
4:L:170:VAL:CB	4:L:194:LEU:CD2	2.95	0.42
4:L:83:GLN:O	4:L:84:GLN:C	2.57	0.42
3:I:146:GLN:HB3	3:I:147:SER:H	1.39	0.42
3:I:177:ASN:OD1	3:I:178:LYS:N	2.51	0.42
3:I:11:LEU:HD12	3:I:21:PHE:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:36:TYR:N	3:I:89:LEU:O	2.48	0.42
1:M:225:THR:O	1:M:228:THR:HG22	2.20	0.42
3:E:11:LEU:HD12	3:E:106:LEU:HD13	2.01	0.42
1:A:107:TRP:CZ2	1:A:172:LEU:HD13	2.54	0.42
1:M:4:SER:OG	1:M:6:ARG:NH1	2.52	0.42
1:A:128:GLU:HG2	1:A:128:GLU:H	1.39	0.42
3:E:167:PHE:HD2	3:E:168:LYS:H	0.61	0.42
1:M:73:THR:HG21	5:T:6:VAL:CG2	2.32	0.42
2:N:30:PHE:CE2	2:N:63:TYR:HA	2.55	0.42
1:G:70:HIS:O	1:G:74:HIS:N	2.49	0.42
4:P:26:ILE:HB	4:P:29:HIS:HD2	1.82	0.42
1:A:76:VAL:O	1:A:80:THR:HG22	2.20	0.42
3:O:187:PHE:HD2	3:O:187:PHE:H	1.66	0.42
4:J:43:LEU:HD23	4:J:44:GLU:N	2.34	0.42
1:A:209:TYR:CD1	1:A:210:PRO:HA	2.54	0.42
3:K:115:PRO:CG	3:K:139:ASP:OD2	2.68	0.42
3:K:193:PRO:C	3:K:195:ASP:N	2.72	0.42
1:C:192:HIS:CE1	1:C:202:ARG:NH1	2.78	0.42
1:C:35:ARG:HD2	2:D:53:ASP:OD1	2.19	0.42
1:C:259:CYS:HB3	1:C:272:LEU:HB2	2.00	0.42
1:C:73:THR:HG23	5:R:8:THR:CG2	2.49	0.42
1:A:150:ALA:HB3	1:A:152:VAL:HG23	2.01	0.42
1:G:64:THR:O	1:G:68:LYS:HG3	2.20	0.42
3:K:94:THR:HG23	3:K:95:GLY:N	2.35	0.42
4:J:15:LYS:HA	4:J:82:THR:O	2.19	0.42
1:A:75:ARG:HB2	1:A:75:ARG:HE	1.74	0.42
3:K:61:ARG:CG	3:K:78:LYS:O	2.65	0.42
2:N:11:SER:O	2:N:13:HIS:N	2.53	0.42
2:N:40:LEU:HB3	2:N:43:GLY:CA	2.49	0.42
2:B:17:ASN:HD22	2:B:74:GLU:CD	2.23	0.42
4:P:64:ARG:HB3	4:P:80:GLN:O	2.20	0.42
1:A:66:LYS:HD3	5:Q:4:PRO:HA	2.02	0.42
4:P:38:ARG:O	4:P:41:GLN:NE2	2.52	0.42
1:A:152:VAL:HA	1:A:155:GLN:OE1	2.19	0.42
1:C:217:TRP:HZ3	1:C:257:TYR:HB3	1.85	0.42
1:M:114:HIS:HB3	1:M:126:LEU:HB3	2.02	0.42
4:J:47:ILE:CD1	4:J:60:LEU:HD21	2.05	0.42
3:O:80:SER:N	3:O:81:GLN:NE2	2.68	0.42
1:G:61:ASP:O	1:G:65:ARG:HG3	2.20	0.42
4:J:238:GLU:HG3	4:J:239:ALA:H	1.80	0.42
3:O:52:LEU:HD23	3:O:52:LEU:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:117:PRO:HB2	3:E:196:THR:HA	2.02	0.42
1:A:173:GLU:HA	1:A:176:LYS:HD3	2.02	0.42
3:I:47:LEU:HD12	3:I:47:LEU:HA	1.90	0.42
4:J:46:LEU:HD22	4:J:60:LEU:HA	2.02	0.42
3:O:176:SER:HB2	3:O:181:PHE:O	2.20	0.42
1:M:142:THR:O	1:M:146:LYS:HG3	2.19	0.42
1:M:69:ALA:O	1:M:73:THR:OG1	2.29	0.42
1:G:218:GLN:HB3	1:G:223:ASP:OD1	2.20	0.42
4:L:122:PRO:HA	4:L:123:PRO:HD3	1.87	0.42
4:P:121:PHE:HA	4:P:122:PRO:HD3	1.81	0.42
4:L:218:SER:O	4:L:219:GLU:HB2	2.20	0.42
4:F:45:PHE:HZ	4:F:48:TYR:HD2	1.67	0.42
3:I:63:SER:OG	3:I:76:TYR:HB2	2.19	0.42
3:K:152:VAL:CG1	3:K:153:TYR:N	2.83	0.42
2:B:55:SER:OG	2:B:56:PHE:N	2.52	0.42
3:K:115:PRO:CB	3:K:139:ASP:OD2	2.67	0.41
1:C:202:ARG:HG2	1:C:244:TRP:NE1	2.28	0.41
1:G:200:THR:HG21	1:G:202:ARG:CZ	2.49	0.41
4:J:143:LEU:HB3	4:J:194:LEU:HB3	2.02	0.41
3:K:158:CYS:SG	3:K:159:VAL:N	2.93	0.41
1:M:219:ARG:CD	1:M:224:GLN:NE2	2.70	0.41
3:K:131:SER:OG	3:K:132:VAL:N	2.47	0.41
1:G:8:PHE:HB2	1:G:25:VAL:HG13	2.01	0.41
4:L:141:ALA:N	4:L:198:ALA:H	2.18	0.41
2:D:84:HIS:CG	2:D:85:VAL:H	2.38	0.41
4:L:6:GLN:HE21	4:L:6:GLN:HB2	1.64	0.41
4:L:88:ALA:HB1	4:L:110:ARG:CA	2.46	0.41
3:I:132:VAL:HG12	3:I:173:VAL:HG13	2.01	0.41
1:M:197:HIS:C	1:M:198:GLU:CG	2.89	0.41
4:F:230:PRO:O	4:F:231:VAL:HG23	2.19	0.41
4:P:119:ASN:HB3	4:P:151:TYR:CE2	2.55	0.41
4:F:203:ASN:N	4:F:204:PRO:HD3	2.35	0.41
2:B:74:GLU:HA	2:B:74:GLU:OE1	2.20	0.41
1:G:70:HIS:CD2	5:U:2:LEU:HD23	2.55	0.41
2:D:28:SER:OG	2:D:29:GLY:N	2.53	0.41
3:K:135:PHE:HD1	3:K:135:PHE:C	2.23	0.41
4:J:112:LEU:HG	4:J:113:VAL:O	2.20	0.41
1:A:11:SER:HA	1:A:22:PHE:HA	2.02	0.41
1:A:73:THR:HG23	3:I:96:ASN:ND2	2.35	0.41
1:G:72:GLN:HG2	1:G:72:GLN:H	1.57	0.41
1:C:52:ILE:HD12	1:C:52:ILE:HA	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:175:GLN:HA	4:L:176:PRO:HD3	1.83	0.41
4:P:125:VAL:HG12	4:P:237:ALA:HB2	2.01	0.41
4:P:36:ARG:O	4:P:44:GLU:HB2	2.21	0.41
3:K:135:PHE:CE1	3:K:138:PHE:CG	3.08	0.41
1:C:243:LYS:HG2	1:C:244:TRP:N	2.33	0.41
1:G:98:MET:CE	1:G:99:TYR:N	2.84	0.41
3:K:188:ASN:O	3:K:189:ASN:HB2	2.19	0.41
1:M:99:TYR:OH	5:T:3:VAL:HG12	2.20	0.41
4:P:160:TRP:HD1	4:P:165:GLU:CG	2.23	0.41
1:G:211:ALA:HB2	1:G:241:PHE:HE2	1.84	0.41
1:A:13:SER:HB3	1:A:93:HIS:H	1.85	0.41
1:C:218:GLN:HG2	1:C:260:HIS:HD2	1.79	0.41
2:N:10:TYR:HE2	2:N:26:TYR:HB3	1.85	0.41
4:L:21:LEU:HD12	4:L:21:LEU:N	2.35	0.41
3:K:193:PRO:C	3:K:195:ASP:H	2.23	0.41
4:J:134:GLU:HA	4:J:137:HIS:HB2	2.01	0.41
3:O:30:PHE:CD2	3:O:68:THR:HG22	2.55	0.41
3:O:80:SER:C	3:O:81:GLN:NE2	2.73	0.41
4:F:230:PRO:C	4:F:231:VAL:CG2	2.88	0.41
4:F:96:GLN:C	4:F:97:THR:HG1	2.11	0.41
4:L:33:TYR:O	4:L:92:CYS:HA	2.21	0.41
1:M:203:CYS:CB	1:M:217:TRP:HE1	2.31	0.41
1:M:128:GLU:H	1:M:128:GLU:CD	2.15	0.41
4:F:51:GLY:O	4:F:69:ARG:NH1	2.52	0.41
3:E:144:VAL:HG21	3:E:155:THR:O	2.19	0.41
3:O:85:SER:OG	3:O:108:VAL:HG22	2.20	0.41
1:G:11:SER:O	1:G:95:VAL:N	2.53	0.41
1:G:268:LYS:O	1:G:269:PRO:C	2.58	0.41
1:M:234:ARG:HE	1:M:234:ARG:HB2	1.62	0.41
1:G:266:LEU:HD23	1:G:266:LEU:HA	1.77	0.41
4:L:154:HIS:O	4:L:215:TYR:HD2	2.02	0.41
3:E:136:THR:N	3:E:138:PHE:HE1	2.18	0.41
4:F:140:LYS:HD3	4:F:197:SER:HA	2.02	0.41
1:A:52:ILE:HD13	1:A:60:TRP:CH2	2.55	0.41
1:M:96:GLN:HE21	2:N:31:HIS:HE1	1.66	0.41
3:E:125:SER:HB3	3:E:126:LYS:HD2	2.03	0.41
1:G:64:THR:HG22	1:G:68:LYS:CE	2.51	0.41
1:G:157:ARG:CG	1:G:158:ALA:N	2.83	0.41
1:G:262:GLN:HA	1:G:269:PRO:HB3	2.01	0.41
1:A:242:GLN:NE2	2:B:12:ARG:O	2.46	0.41
1:C:185:PRO:HD2	1:C:266:LEU:HG	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:13:THR:HB	4:P:17:LYS:HZ2	1.85	0.41
1:M:95:VAL:HG22	1:M:118:TYR:HD1	1.84	0.41
4:P:29:HIS:ND1	4:P:96:GLN:HA	2.36	0.41
2:H:3:ARG:O	2:H:30:PHE:HA	2.20	0.41
1:M:102:ASP:HB2	1:M:111:ARG:CG	2.51	0.41
3:K:95:GLY:O	3:K:96:ASN:HB3	2.20	0.41
2:N:7:ILE:HA	2:N:27:VAL:HG12	2.03	0.41
3:K:155:THR:O	3:K:172:ALA:HB1	2.20	0.41
3:I:188:ASN:ND2	3:I:192:ILE:CD1	2.83	0.41
3:K:136:THR:HA	3:K:138:PHE:CE2	2.55	0.41
1:C:92:SER:O	1:C:93:HIS:HD2	2.04	0.41
3:K:11:LEU:HG	3:K:21:PHE:HE2	1.85	0.41
3:I:76:TYR:CD1	3:I:76:TYR:N	2.88	0.41
4:F:60:LEU:HA	4:F:61:PRO:HD3	1.97	0.41
4:L:225:GLN:HB3	4:L:226:ASP:H	1.67	0.41
1:C:82:ARG:HD3	1:C:89:GLU:HA	2.03	0.41
1:G:33:PHE:CD1	1:G:34:VAL:HG13	2.56	0.41
4:F:124:GLU:N	4:F:148:THR:O	2.48	0.41
4:L:90:TYR:HB2	4:L:109:THR:CG2	2.49	0.41
3:K:116:ASP:OD1	3:K:137:ASP:OD2	2.39	0.41
1:G:192:HIS:HD2	1:G:202:ARG:CD	2.34	0.41
1:G:97:ARG:CZ	1:G:116:TYR:HE1	2.21	0.41
3:I:121:GLN:C	3:I:132:VAL:O	2.59	0.41
1:G:82:ARG:HH21	1:G:89:GLU:CA	2.31	0.41
1:G:134:THR:HG23	1:G:134:THR:O	2.20	0.41
1:A:248:VAL:HG21	6:A:303:HOH:O	2.21	0.41
1:G:259:CYS:C	1:G:260:HIS:HD1	2.23	0.41
4:F:154:HIS:CD2	4:F:154:HIS:N	2.88	0.41
5:R:2:LEU:N	5:R:2:LEU:HD12	2.36	0.41
3:K:35:TRP:O	3:K:47:LEU:CB	2.69	0.41
4:J:4:VAL:CG1	4:J:106:GLY:HA2	2.51	0.41
1:M:49:ALA:HB1	1:M:51:TRP:NE1	2.36	0.41
2:N:22:PHE:HE1	4:F:80:GLN:NE2	2.19	0.41
3:K:79:GLY:O	3:K:81:GLN:HG2	2.21	0.41
4:P:45:PHE:CZ	4:P:48:TYR:HB3	2.56	0.41
1:C:200:THR:HA	1:C:247:VAL:O	2.21	0.41
1:G:230:LEU:HA	1:G:230:LEU:HD12	1.83	0.41
1:A:23:ILE:HD12	2:B:54:LEU:HB3	2.02	0.41
4:P:200:PHE:HA	4:P:200:PHE:HD1	1.74	0.41
1:M:66:LYS:CE	3:O:29:ASN:CG	2.88	0.41
1:M:222:GLU:H	1:M:222:GLU:HG3	1.70	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:235:PRO:HG2	2:H:65:LEU:HD12	2.03	0.41
1:A:93:HIS:CB	1:A:119:ASP:OD1	2.67	0.41
1:M:22:PHE:CD1	1:M:71:SER:HA	2.56	0.41
3:I:133:CYS:SG	3:I:182:ALA:O	2.79	0.41
4:F:35:TYR:HB3	4:F:43:LEU:HD21	2.02	0.41
4:F:8:PRO:O	4:F:109:THR:HG22	2.20	0.41
1:A:45:MET:HG2	1:A:67:VAL:HG11	2.03	0.41
4:P:206:ASN:HD22	4:P:240:TRP:C	2.24	0.41
1:C:231:VAL:O	1:C:243:LYS:HE2	2.22	0.40
3:K:185:ASN:HB2	3:K:188:ASN:CB	2.50	0.40
1:G:35:ARG:HH21	1:G:48:ARG:NE	2.18	0.40
4:L:97:THR:CB	4:L:98:GLN:NE2	2.84	0.40
2:H:65:LEU:HD23	2:H:66:TYR:N	2.36	0.40
4:J:129:GLU:HA	4:J:130:PRO:HD3	1.89	0.40
2:D:27:VAL:HG23	2:D:30:PHE:HE2	1.86	0.40
2:H:7:ILE:HD12	2:H:82:VAL:CG1	2.51	0.40
4:J:50:GLN:NE2	4:J:97:THR:O	2.54	0.40
4:J:69:ARG:NH1	4:J:73:SER:O	2.55	0.40
1:M:167:TRP:CZ3	1:M:170:ARG:HD3	2.56	0.40
4:F:87:SER:HA	4:F:111:LEU:O	2.21	0.40
2:N:37:VAL:HG21	2:N:66:TYR:CD2	2.56	0.40
1:A:31:THR:HG23	1:A:209:TYR:CE1	2.56	0.40
3:O:121:GLN:HA	3:O:132:VAL:O	2.21	0.40
4:L:88:ALA:HB2	4:L:111:LEU:N	2.37	0.40
1:C:202:ARG:HG2	1:C:244:TRP:CD1	2.56	0.40
3:K:161:ASP:OD1	3:K:168:LYS:HB3	2.21	0.40
3:I:146:GLN:NE2	3:I:154:ILE:HG21	2.37	0.40
1:C:35:ARG:NH1	2:D:53:ASP:OD1	2.45	0.40
4:L:124:GLU:O	4:L:147:ALA:HA	2.20	0.40
1:A:177:GLU:HG2	1:A:178:THR:N	2.36	0.40
3:O:166:ASP:O	3:O:167:PHE:C	2.58	0.40
3:K:87:THR:HA	3:K:105:SER:HA	2.03	0.40
1:C:121:LYS:HD2	1:C:121:LYS:HA	1.73	0.40
2:N:11:SER:HB3	2:N:95:TRP:CZ2	2.56	0.40
3:O:53:ASN:HB2	3:O:68:THR:H	1.87	0.40
1:G:2:SER:HA	1:G:103:VAL:O	2.21	0.40
1:M:79:GLY:O	1:M:82:ARG:HB2	2.22	0.40
4:L:161:VAL:CG1	4:L:162:ASN:N	2.84	0.40
2:D:54:LEU:C	2:D:54:LEU:HD23	2.41	0.40
2:H:71:THR:OG1	2:H:72:PRO:CD	2.66	0.40
1:C:73:THR:HG23	5:R:8:THR:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:PHE:N	1:A:97:ARG:O	2.48	0.40
1:A:70:HIS:NE2	5:Q:6:VAL:HG13	2.35	0.40
3:K:187:PHE:O	3:K:190:SER:OG	2.37	0.40
3:K:136:THR:HG22	3:K:171:SER:CB	2.43	0.40
3:E:136:THR:C	3:E:138:PHE:CD1	2.95	0.40
2:B:33:SER:HB3	2:B:62:PHE:CD2	2.56	0.40
1:A:13:SER:HB3	1:A:93:HIS:N	2.36	0.40
4:J:98:GLN:NE2	4:J:98:GLN:CA	2.82	0.40
3:K:35:TRP:O	3:K:36:TYR:HD1	2.04	0.40
1:A:69:ALA:O	3:I:96:ASN:ND2	2.54	0.40
1:A:216:THR:OG1	1:A:217:TRP:N	2.54	0.40
1:M:217:TRP:CZ3	1:M:247:VAL:HG22	2.56	0.40
1:M:185:PRO:HD2	1:M:266:LEU:HD11	2.03	0.40
1:A:29:ASP:HB3	1:A:30:ASP:H	1.61	0.40
3:E:61:ARG:HH12	3:E:81:GLN:HB3	1.86	0.40
2:H:57:SER:O	2:H:58:LYS:C	2.60	0.40
3:K:136:THR:CG2	3:K:171:SER:HB3	2.50	0.40
1:C:231:VAL:CG1	1:C:244:TRP:CE3	3.00	0.40
1:G:187:THR:CB	1:G:272:LEU:HD21	2.35	0.40
4:P:151:TYR:CD1	4:P:152:PRO:HA	2.57	0.40
4:F:36:ARG:HD2	4:F:90:TYR:CZ	2.56	0.40
4:F:36:ARG:HH11	4:F:46:LEU:HD21	1.87	0.40
3:E:66:LEU:HD23	3:E:67:ASN:N	2.36	0.40
1:G:27:TYR:HE2	2:H:55:SER:HG	1.64	0.40
1:G:4:SER:O	1:G:29:ASP:N	2.42	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:12:HIS:ND1	3:O:10:SER:OG[1_556]	1.92	0.28
3:K:12:HIS:CG	3:O:10:SER:OG[1_556]	2.00	0.20
3:K:189:ASN:OD1	4:P:181:PRO:CG[1_556]	2.09	0.11
3:I:10:SER:OG	3:I:12:HIS:ND1[3_655]	2.14	0.06
3:K:189:ASN:OD1	4:P:181:PRO:CD[1_556]	2.17	0.03

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	272/276 (99%)	255 (94%)	17 (6%)	0	100	100
1	C	272/276 (99%)	248 (91%)	23 (8%)	1 (0%)	39	80
1	G	264/276 (96%)	239 (90%)	25 (10%)	0	100	100
1	M	271/276 (98%)	242 (89%)	29 (11%)	0	100	100
2	B	97/100 (97%)	84 (87%)	13 (13%)	0	100	100
2	D	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
2	H	92/100 (92%)	82 (89%)	9 (10%)	1 (1%)	17	63
2	N	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
3	E	179/205 (87%)	152 (85%)	26 (14%)	1 (1%)	30	74
3	I	175/205 (85%)	137 (78%)	37 (21%)	1 (1%)	30	74
3	K	188/205 (92%)	158 (84%)	26 (14%)	4 (2%)	9	49
3	O	181/205 (88%)	160 (88%)	20 (11%)	1 (1%)	30	74
4	F	234/245 (96%)	197 (84%)	34 (14%)	3 (1%)	15	59
4	J	214/245 (87%)	185 (86%)	28 (13%)	1 (0%)	34	77
4	L	214/245 (87%)	183 (86%)	29 (14%)	2 (1%)	21	67
4	P	227/245 (93%)	192 (85%)	32 (14%)	3 (1%)	15	59
5	Q	7/9 (78%)	5 (71%)	2 (29%)	0	100	100
5	R	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
5	T	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
5	U	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	3104/3340 (93%)	2707 (87%)	379 (12%)	18 (1%)	30	74

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	I	122	LEU

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Mol	Chain	Res	Type
4	J	114	LEU
3	K	147	SER
3	K	150	SER
4	L	174	PRO
4	P	229	LYS
4	F	181	PRO
3	K	153	TYR
3	O	178	LYS
3	E	190	SER
4	P	139	GLN
2	H	71	THR
3	K	115	PRO
4	P	119	ASN
4	L	203	ASN
1	C	235	PRO
4	F	203	ASN
4	F	180	GLN

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	231/232 (100%)	226 (98%)	5 (2%)	60	86
1	C	231/232 (100%)	221 (96%)	10 (4%)	35	74
1	G	226/232 (97%)	216 (96%)	10 (4%)	35	73
1	M	225/232 (97%)	216 (96%)	9 (4%)	38	75
2	B	93/95 (98%)	92 (99%)	1 (1%)	80	92
2	D	93/95 (98%)	88 (95%)	5 (5%)	27	67
2	H	86/95 (90%)	83 (96%)	3 (4%)	43	78
2	N	92/95 (97%)	90 (98%)	2 (2%)	60	86
3	E	158/185 (85%)	145 (92%)	13 (8%)	14	51
3	I	155/185 (84%)	145 (94%)	10 (6%)	21	62
3	K	158/185 (85%)	140 (89%)	18 (11%)	7	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	O	159/185 (86%)	145 (91%)	14 (9%)	12	48
4	F	198/212 (93%)	184 (93%)	14 (7%)	18	58
4	J	189/212 (89%)	176 (93%)	13 (7%)	19	59
4	L	174/212 (82%)	162 (93%)	12 (7%)	19	59
4	P	189/212 (89%)	178 (94%)	11 (6%)	25	65
5	Q	8/8 (100%)	7 (88%)	1 (12%)	6	29
5	R	8/8 (100%)	8 (100%)	0	100	100
5	T	8/8 (100%)	7 (88%)	1 (12%)	6	29
5	U	8/8 (100%)	8 (100%)	0	100	100
All	All	2689/2928 (92%)	2537 (94%)	152 (6%)	25	66

All (152) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ARG
1	A	98	MET
1	A	113	TYR
1	A	119	ASP
1	A	230	LEU
2	B	54	LEU
3	I	14	GLN
3	I	15	GLU
3	I	39	GLU
3	I	78	LYS
3	I	80	SER
3	I	81	GLN
3	I	131	SER
3	I	133	CYS
3	I	138	PHE
3	I	179	SER
4	J	29	HIS
4	J	60	LEU
4	J	84	GLN
4	J	97	THR
4	J	114	LEU
4	J	120	VAL
4	J	167	HIS
4	J	177	LEU
4	J	201	TRP

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Mol	Chain	Res	Type
4	J	205	ARG
4	J	223	TRP
4	J	229	LYS
4	J	230	PRO
5	Q	5	MET
1	G	29	ASP
1	G	48	ARG
1	G	58	GLU
1	G	98	MET
1	G	116	TYR
1	G	160	LEU
1	G	161	GLU
1	G	186	LYS
1	G	191	HIS
1	G	268	LYS
2	H	23	LEU
2	H	80	CYS
2	H	81	ARG
3	K	43	SER
3	K	52	LEU
3	K	61	ARG
3	K	70	GLU
3	K	80	SER
3	K	102	THR
3	K	112	ILE
3	K	135	PHE
3	K	137	ASP
3	K	145	SER
3	K	148	LYS
3	K	149	ASP
3	K	155	THR
3	K	157	LYS
3	K	168	LYS
3	K	169	SER
3	K	178	LYS
3	K	180	ASP
4	L	6	GLN
4	L	9	SER
4	L	85	GLU
4	L	118	LYS
4	L	143	LEU
4	L	145	CYS

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Mol	Chain	Res	Type
4	L	148	THR
4	L	150	PHE
4	L	159	TRP
4	L	193	ARG
4	L	217	LEU
4	L	238	GLU
1	M	17	ARG
1	M	88	SER
1	M	155	GLN
1	M	196	ASP
1	M	197	HIS
1	M	222	GLU
1	M	266	LEU
1	M	272	LEU
1	M	274	TRP
2	N	59	ASP
2	N	70	PHE
3	O	69	LYS
3	O	80	SER
3	O	116	ASP
3	O	134	LEU
3	O	138	PHE
3	O	140	SER
3	O	156	ASP
3	O	164	SER
3	O	166	ASP
3	O	168	LYS
3	O	170	ASN
3	O	179	SER
3	O	187	PHE
3	O	188	ASN
4	P	5	SER
4	P	64	ARG
4	P	68	GLU
4	P	97	THR
4	P	154	HIS
4	P	167	HIS
4	P	171	CYS
4	P	179	GLU
4	P	191	SER
4	P	226	ASP
4	P	227	ARG

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Mol	Chain	Res	Type
5	T	2	LEU
1	C	35	ARG
1	C	48	ARG
1	C	61	ASP
1	C	113	TYR
1	C	119	ASP
1	C	131	ARG
1	C	188	HIS
1	C	192	HIS
1	C	226	GLN
1	C	227	ASP
2	D	45	ARG
2	D	53	ASP
2	D	89	GLN
2	D	90	PRO
2	D	91	LYS
3	E	21	PHE
3	E	40	THR
3	E	83	GLU
3	E	85	SER
3	E	136	THR
3	E	137	ASP
3	E	138	PHE
3	E	161	ASP
3	E	167	PHE
3	E	178	LYS
3	E	179	SER
3	E	180	ASP
3	E	183	CYS
4	F	39	LEU
4	F	49	PHE
4	F	160	TRP
4	F	170	VAL
4	F	185	ASP
4	F	193	ARG
4	F	195	ARG
4	F	201	TRP
4	F	217	LEU
4	F	220	ASN
4	F	222	GLU
4	F	225	GLN
4	F	238	GLU

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Mol	Chain	Res	Type
4	F	240	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
3	I	96	ASN
3	I	188	ASN
4	J	29	HIS
4	J	119	ASN
4	J	154	HIS
1	G	93	HIS
1	G	192	HIS
3	K	188	ASN
4	L	220	ASN
1	M	93	HIS
1	M	96	GLN
2	N	2	GLN
2	N	13	HIS
2	N	31	HIS
4	P	83	GLN
4	P	225	GLN
1	C	70	HIS
3	E	97	GLN
4	F	29	HIS
4	F	83	GLN
4	F	98	GLN
4	F	154	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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	274/276 (99%)	-0.18	0 100 100	33, 56, 82, 107	0
1	C	274/276 (99%)	-0.21	1 (0%) 93 90	35, 51, 83, 100	0
1	G	270/276 (97%)	0.06	6 (2%) 65 55	57, 80, 102, 122	0
1	M	273/276 (98%)	0.05	4 (1%) 76 68	51, 77, 111, 119	0
2	B	99/100 (99%)	0.05	3 (3%) 54 43	45, 72, 108, 123	0
2	D	100/100 (100%)	-0.07	0 100 100	40, 66, 90, 113	0
2	H	96/100 (96%)	0.19	2 (2%) 67 58	59, 88, 110, 115	0
2	N	100/100 (100%)	0.17	2 (2%) 68 59	57, 87, 107, 116	0
3	E	187/205 (91%)	-0.06	3 (1%) 74 66	36, 63, 114, 131	0
3	I	185/205 (90%)	-0.05	3 (1%) 74 66	41, 72, 115, 126	0
3	K	192/205 (93%)	0.35	16 (8%) 14 12	55, 89, 129, 140	0
3	O	187/205 (91%)	0.13	8 (4%) 39 30	58, 91, 134, 151	0
4	F	238/245 (97%)	0.05	2 (0%) 87 80	38, 80, 125, 132	0
4	J	226/245 (92%)	0.16	7 (3%) 52 43	25, 88, 129, 141	0
4	L	226/245 (92%)	0.30	2 (0%) 85 78	74, 106, 127, 136	0
4	P	235/245 (95%)	0.32	19 (8%) 15 12	50, 95, 133, 154	0
5	Q	9/9 (100%)	0.09	0 100 100	43, 48, 51, 53	0
5	R	9/9 (100%)	-0.18	0 100 100	40, 41, 44, 46	0
5	T	9/9 (100%)	0.03	0 100 100	59, 63, 71, 72	0
5	U	9/9 (100%)	0.16	0 100 100	63, 67, 72, 73	0
All	All	3198/3340 (95%)	0.07	78 (2%) 62 52	25, 79, 122, 154	0

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	K	134	LEU	6.4
3	K	127	SER	6.1
3	K	128	SER	5.0
4	P	190	LEU	5.0
3	K	172	ALA	4.7
3	K	129	ASP	4.3
4	P	144	VAL	4.0
4	P	206	ASN	3.8
4	L	194	LEU	3.7
3	O	136	THR	3.7
4	P	215	TYR	3.7
3	K	135	PHE	3.6
4	J	239	ALA	3.5
3	K	133	CYS	3.5
3	K	143	ASN	3.4
3	E	190	SER	3.4
4	J	144	VAL	3.3
3	O	173	VAL	3.3
3	K	173	VAL	3.2
3	O	134	LEU	3.2
4	P	169	GLY	3.2
1	M	188	HIS	3.1
3	O	114	ASN	3.1
4	J	162	ASN	3.1
4	P	126	ALA	3.0
2	H	71	THR	3.0
3	I	118	ALA	2.9
4	P	142	THR	2.9
4	J	208	PHE	2.9
3	K	118	ALA	2.8
3	K	174	ALA	2.8
3	K	126	LYS	2.7
4	P	208	PHE	2.7
2	B	40	LEU	2.7
3	E	134	LEU	2.7
1	G	190	THR	2.6
3	O	121	GLN	2.5
4	P	131	SER	2.5
4	F	194	LEU	2.5
4	P	132	GLU	2.5
1	M	270	LEU	2.5
3	I	134	LEU	2.5
4	J	195	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	205	ALA	2.4
3	I	172	ALA	2.4
1	G	274	TRP	2.4
4	P	37	GLN	2.4
4	P	104	TYR	2.3
1	G	92	SER	2.3
3	O	133	CYS	2.3
4	P	189	ALA	2.3
4	P	145	CYS	2.3
1	M	224	GLN	2.3
2	N	83	ASN	2.3
4	P	214	PHE	2.3
3	O	170	ASN	2.2
4	J	152	PRO	2.2
4	F	143	LEU	2.2
4	L	209	ARG	2.2
4	P	210	CYS	2.2
3	E	170	ASN	2.2
2	B	16	GLU	2.2
3	K	91	ALA	2.2
2	H	66	TYR	2.2
1	G	272	LEU	2.2
4	J	177	LEU	2.1
4	P	105	PHE	2.1
2	N	2	GLN	2.1
4	P	125	VAL	2.1
2	B	15	ALA	2.1
1	M	187	THR	2.0
1	G	185	PRO	2.0
3	K	180	ASP	2.0
1	C	17	ARG	2.0
3	K	192	ILE	2.0
3	K	175	TRP	2.0
3	O	175	TRP	2.0
4	P	143	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.