



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:04 PM GMT

PDB ID : 4H1L
Title : TCR interaction with peptide mimics of nickel offers structural insights in nickel contact allergy
Authors : Kappler, J.W.; Yin, L.; Dai, S.; Marrack, P.
Deposited on : 2012-09-10
Resolution : 3.30 Å(reported)

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

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

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

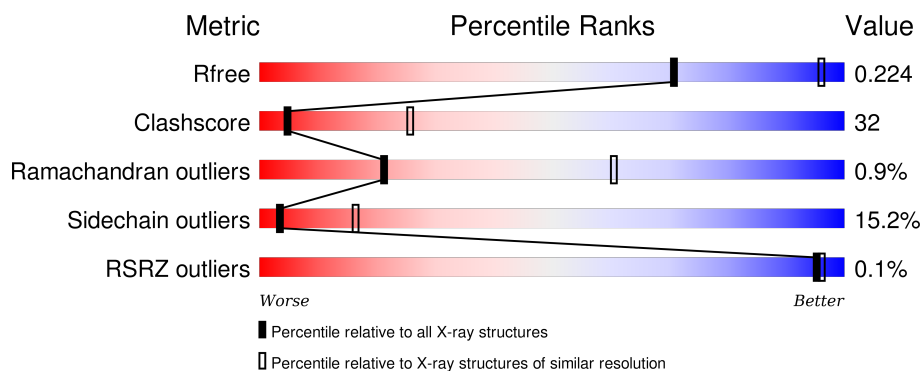
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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.



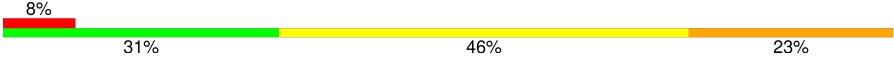
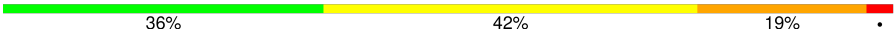



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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	178	<div> <div>52%</div> <div>41%</div> <div>7%</div> </div>
1	D	178	<div> <div>51%</div> <div>43%</div> <div>6%</div> </div>
2	B	187	<div> <div>49%</div> <div>42%</div> <div>5%</div> <div>.</div> </div>
2	E	187	<div> <div>49%</div> <div>42%</div> <div>.</div> <div>.</div> </div>
3	C	13	<div> <div>23%</div> <div>46%</div> <div>31%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	13	 8% 31% 46% 23%
4	G	113	 36% 42% 19% •
4	I	113	 39% 39% 19% •
5	H	111	 54% 34% 9% •
5	J	111	 56% 32% 9% •

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9630 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 II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	178	Total	C	N	O	S	0	0	0
			1465	950	238	272	5			
1	D	178	Total	C	N	O	S	0	0	0
			1465	950	238	272	5			

- Molecule 2 is a protein called MHC class II antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	179	Total	C	N	O	S	0	0	0
			1475	933	264	273	5			
2	E	179	Total	C	N	O	S	0	0	0
			1475	933	264	273	5			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	4	ARG	-	EXPRESSION TAG	UNP D0AB36
B	5	PRO	-	EXPRESSION TAG	UNP D0AB36
B	74	GLN	ARG	SEE REMARK 999	UNP D0AB36
B	86	VAL	GLY	SEE REMARK 999	UNP D0AB36
B	189	ARG	-	EXPRESSION TAG	UNP D0AB36
B	190	ALA	-	EXPRESSION TAG	UNP D0AB36
E	4	ARG	-	EXPRESSION TAG	UNP D0AB36
E	5	PRO	-	EXPRESSION TAG	UNP D0AB36
E	74	GLN	ARG	SEE REMARK 999	UNP D0AB36
E	86	VAL	GLY	SEE REMARK 999	UNP D0AB36
E	189	ARG	-	EXPRESSION TAG	UNP D0AB36
E	190	ALA	-	EXPRESSION TAG	UNP D0AB36

- Molecule 3 is a protein called mimotope peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	S	0	0	0
			107	65	24	17	1			
3	F	13	Total	C	N	O	S	0	0	0
			107	65	24	17	1			

- Molecule 4 is a protein called Ani2.3 TCR A chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	113	Total	C	N	O	S	15	0	0
			878	564	146	166	2			
4	I	113	Total	C	N	O	S	15	0	0
			878	564	146	166	2			

- Molecule 5 is a protein called Ani2.3 TCR B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	H	111	Total	C	N	O	S	12	0	0
			890	563	151	173	3			
5	J	111	Total	C	N	O	S	12	0	0
			890	563	151	173	3			

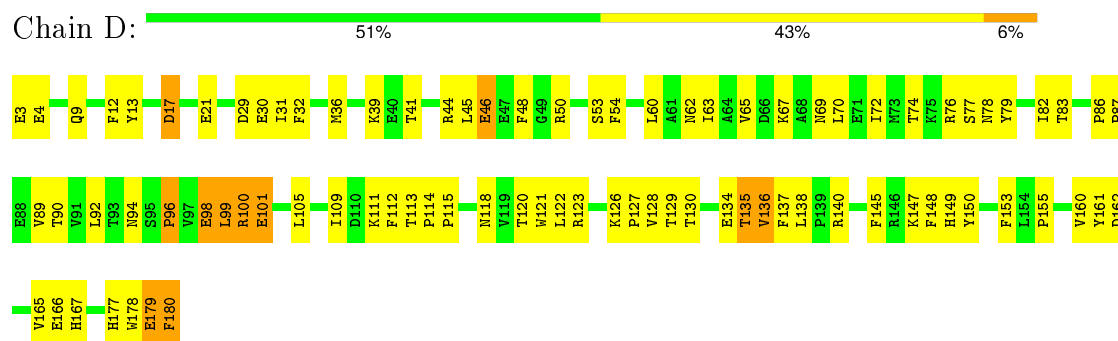
3 Residue-property plots

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.

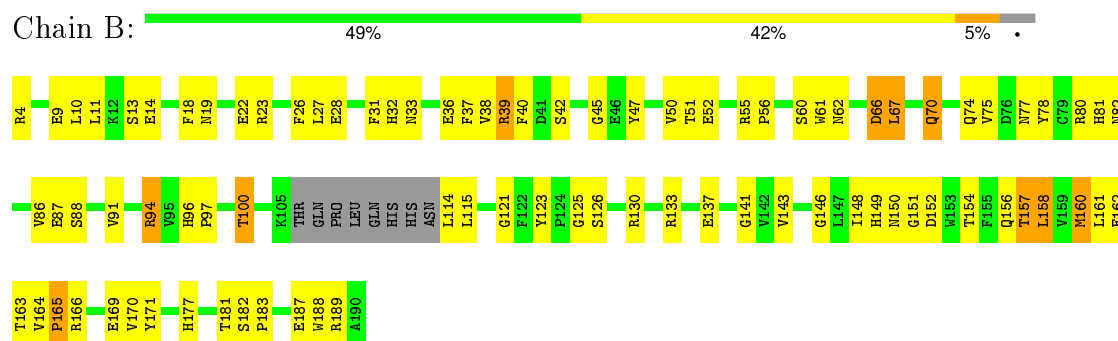
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



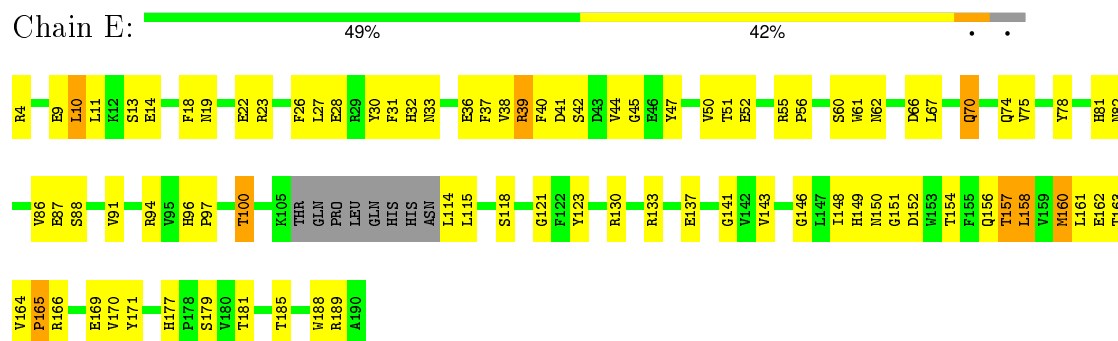
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



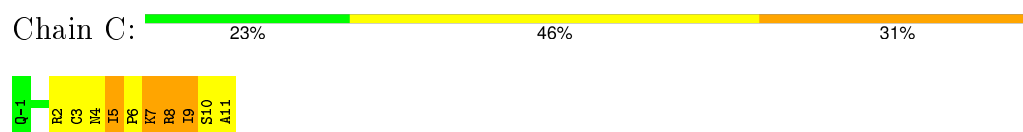
- Molecule 2: MHC class II antigen



- Molecule 2: MHC class II antigen



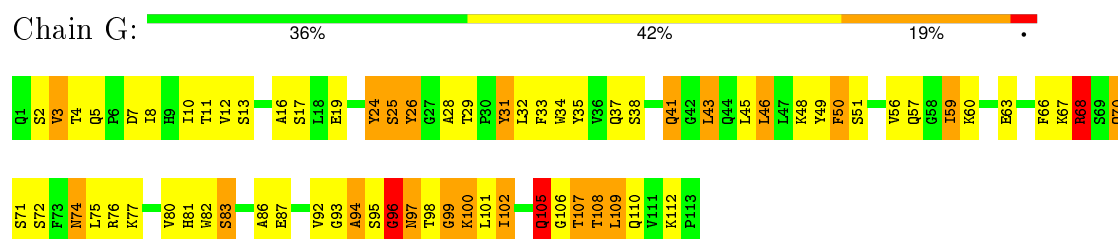
- Molecule 3: mimotope peptide



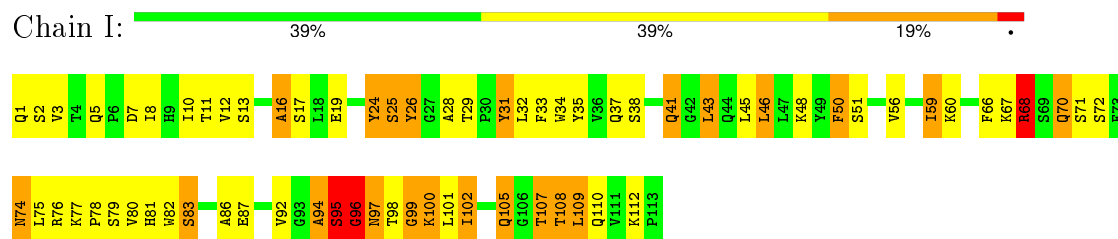
- Molecule 3: mimotope peptide



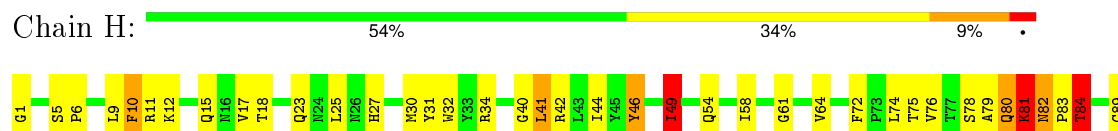
- Molecule 4: Ani2.3 TCR A chain

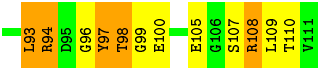


- Molecule 4: Ani2.3 TCR A chain

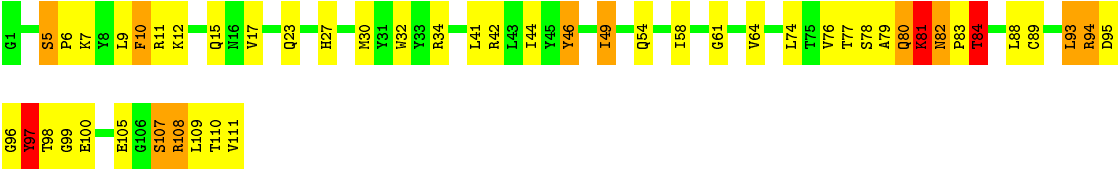


- Molecule 5: Ani2.3 TCR B chain





● Molecule 5: Ani2.3 TCR B chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	186.72Å 186.72Å 166.70Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.83 – 3.30 19.83 – 3.28	Depositor EDS
% Data completeness (in resolution range)	87.9 (19.83-3.30) 91.6 (19.83-3.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 3.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_629)	Depositor
R, R_{free}	0.263 , 0.285 0.218 , 0.224	Depositor DCC
R_{free} test set	2323 reflections (5.09%)	DCC
Wilson B-factor (Å ²)	81.9	Xtriage
Anisotropy	0.405	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 18.1	EDS
Estimated twinning fraction	0.189 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	0 of 46107 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	9630	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.55	0/1510	0.76	3/2059 (0.1%)
1	D	0.54	0/1510	0.75	3/2059 (0.1%)
2	B	0.50	0/1513	0.64	0/2050
2	E	0.47	0/1513	0.63	0/2050
3	C	0.68	0/108	0.98	0/142
3	F	0.63	0/108	0.94	0/142
4	G	0.81	5/901 (0.6%)	1.03	5/1221 (0.4%)
4	I	0.90	8/901 (0.9%)	0.94	4/1221 (0.3%)
5	H	0.64	0/910	0.87	3/1228 (0.2%)
5	J	0.66	0/910	0.89	3/1228 (0.2%)
All	All	0.62	13/9884 (0.1%)	0.80	21/13400 (0.2%)

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
4	G	0	2
4	I	0	2
5	H	0	2
5	J	0	2
All	All	0	8

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	I	68	ARG	CZ-NH2	9.87	1.45	1.33
4	I	68	ARG	CZ-NH1	7.33	1.42	1.33
4	G	68	ARG	CZ-NH1	6.62	1.41	1.33
4	I	105	GLN	CD-OE1	6.33	1.37	1.24
4	I	105	GLN	CD-NE2	6.27	1.48	1.32
4	G	105	GLN	CD-OE1	6.16	1.37	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	68	ARG	CZ-NH2	5.98	1.40	1.33
4	G	100	LYS	CE-NZ	5.94	1.64	1.49
4	I	100	LYS	CE-NZ	5.93	1.63	1.49
4	G	100	LYS	CD-CE	5.33	1.64	1.51
4	I	100	LYS	CD-CE	5.18	1.64	1.51
4	I	105	GLN	CG-CD	5.07	1.62	1.51
4	I	68	ARG	NE-CZ	5.06	1.39	1.33

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	68	ARG	NE-CZ-NH1	-16.61	112.00	120.30
4	I	68	ARG	NE-CZ-NH2	-11.34	114.63	120.30
1	A	50	ARG	NE-CZ-NH1	11.03	125.82	120.30
1	A	50	ARG	NE-CZ-NH2	-10.69	114.95	120.30
1	D	50	ARG	NE-CZ-NH2	10.61	125.61	120.30
1	D	50	ARG	NE-CZ-NH1	-9.89	115.36	120.30
4	G	68	ARG	NE-CZ-NH2	9.83	125.22	120.30
5	J	42	ARG	NE-CZ-NH2	-9.75	115.42	120.30
5	H	42	ARG	NE-CZ-NH2	9.59	125.10	120.30
5	J	42	ARG	NE-CZ-NH1	9.35	124.97	120.30
5	H	42	ARG	NE-CZ-NH1	-8.98	115.81	120.30
4	I	68	ARG	CD-NE-CZ	8.35	135.29	123.60
4	G	68	ARG	CD-NE-CZ	7.30	133.82	123.60
4	I	95	SER	N-CA-C	-7.23	91.47	111.00
5	J	49	ILE	CB-CA-C	-6.48	98.64	111.60
4	I	99	GLY	N-CA-C	-6.07	97.94	113.10
1	D	50	ARG	CA-CB-CG	6.05	126.70	113.40
5	H	49	ILE	CB-CA-C	-5.98	99.63	111.60
1	A	50	ARG	CD-NE-CZ	5.35	131.09	123.60
4	G	99	GLY	N-CA-C	-5.31	99.81	113.10
4	G	68	ARG	CG-CD-NE	-5.25	100.78	111.80

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	G	94	ALA	Peptide
4	G	96	GLY	Peptide
5	H	81	LYS	Peptide
5	H	82	ASN	Peptide
4	I	94	ALA	Peptide

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Mol	Chain	Res	Type	Group
4	I	96	GLY	Peptide
5	J	81	LYS	Peptide
5	J	82	ASN	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	1465	0	1403	85	0
1	D	1465	0	1403	92	0
2	B	1475	0	1410	82	0
2	E	1475	0	1410	80	0
3	C	107	0	117	20	0
3	F	107	0	117	19	0
4	G	878	0	853	84	0
4	I	878	0	853	80	0
5	H	890	0	855	61	0
5	J	890	0	855	66	0
All	All	9630	0	9276	592	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 32.

All (592) 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)
4:I:98:THR:HG22	4:I:99:GLY:HA3	1.25	1.13
4:I:24:TYR:CE2	4:I:71:SER:HA	1.84	1.11
4:G:98:THR:HG22	4:G:99:GLY:HA3	1.26	1.10
4:I:24:TYR:HE2	4:I:71:SER:HA	1.11	1.10
5:J:108:ARG:HH11	5:J:108:ARG:HB3	1.15	1.10
5:J:11:ARG:HD2	5:J:15:GLN:HE21	1.12	1.10
4:G:24:TYR:HE2	4:G:71:SER:HA	1.07	1.08
4:G:24:TYR:CE2	4:G:71:SER:HA	1.89	1.06
2:E:70:GLN:NE2	5:H:97:TYR:CD1	2.23	1.06
5:H:11:ARG:HD2	5:H:15:GLN:HE21	1.15	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:70:GLN:HE21	4:G:70:GLN:HA	1.20	1.05
5:H:108:ARG:HH11	5:H:108:ARG:HB3	1.16	1.04
4:G:66:PHE:CE2	4:G:68:ARG:HG2	1.97	1.00
4:I:70:GLN:HE21	4:I:70:GLN:HA	1.26	0.99
5:H:61:GLY:HA3	5:H:79:ALA:CB	1.93	0.97
2:B:70:GLN:NE2	5:J:97:TYR:CD1	2.34	0.96
4:G:24:TYR:HE2	4:G:71:SER:CA	1.78	0.95
1:A:135:THR:HG23	1:A:148:PHE:H	1.31	0.95
5:J:61:GLY:HA3	5:J:79:ALA:CB	1.95	0.95
2:E:70:GLN:HE21	5:H:97:TYR:HD1	1.06	0.94
4:I:28:ALA:O	4:I:29:THR:HG22	1.66	0.94
1:A:135:THR:CG2	1:A:148:PHE:H	1.80	0.94
4:G:98:THR:CG2	4:G:99:GLY:HA3	2.00	0.92
1:D:135:THR:HG23	1:D:148:PHE:H	1.33	0.92
4:I:24:TYR:HE2	4:I:71:SER:CA	1.81	0.92
2:B:70:GLN:HE21	5:J:97:TYR:HD1	0.96	0.92
4:I:7:ASP:O	4:I:107:THR:HB	1.69	0.91
4:I:98:THR:CG2	4:I:99:GLY:HA3	2.01	0.90
5:J:81:LYS:CA	5:J:83:PRO:HD3	2.02	0.89
5:J:108:ARG:HB3	5:J:108:ARG:NH1	1.87	0.89
5:H:81:LYS:CA	5:H:83:PRO:HD3	2.01	0.89
1:D:135:THR:CG2	1:D:148:PHE:H	1.85	0.89
5:J:11:ARG:HD2	5:J:15:GLN:NE2	1.88	0.88
5:H:81:LYS:HA	5:H:83:PRO:HD3	1.56	0.87
1:A:82:ILE:HB	2:B:33:ASN:OD1	1.75	0.87
2:E:70:GLN:NE2	5:H:97:TYR:HD1	1.66	0.86
4:G:28:ALA:O	4:G:29:THR:HG22	1.74	0.86
3:F:5:ILE:HD13	5:H:96:GLY:O	1.76	0.85
1:D:162:ASP:OD1	1:D:177:HIS:HB2	1.77	0.85
4:I:24:TYR:CE2	4:I:71:SER:CA	2.59	0.85
4:G:70:GLN:CA	4:G:70:GLN:HE21	1.90	0.85
5:H:11:ARG:HD2	5:H:15:GLN:NE2	1.92	0.84
5:H:108:ARG:HB3	5:H:108:ARG:NH1	1.92	0.84
1:D:82:ILE:HB	2:E:33:ASN:OD1	1.77	0.84
4:G:7:ASP:O	4:G:107:THR:HB	1.77	0.84
5:J:5:SER:HB2	5:J:6:PRO:HA	1.59	0.84
5:J:81:LYS:C	5:J:83:PRO:HD3	1.98	0.83
5:H:81:LYS:C	5:H:83:PRO:HD3	1.98	0.83
5:J:81:LYS:HA	5:J:83:PRO:HD3	1.59	0.83
5:H:5:SER:HB2	5:H:6:PRO:HA	1.61	0.82
4:I:70:GLN:HE21	4:I:70:GLN:CA	1.94	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:39:LYS:HG2	1:D:60:LEU:HD11	1.62	0.81
4:G:95:SER:O	4:G:96:GLY:C	2.17	0.81
1:A:160:VAL:HG12	1:A:179:GLU:HB2	1.64	0.80
3:F:5:ILE:H	3:F:5:ILE:HD12	1.48	0.78
1:D:13:TYR:CE2	1:D:67:LYS:HG3	2.19	0.78
1:D:13:TYR:HE2	1:D:67:LYS:HG3	1.48	0.77
2:E:31:PHE:CE2	2:E:36:GLU:HB2	2.20	0.77
1:A:180:PHE:HD2	1:A:180:PHE:O	1.68	0.76
1:D:180:PHE:O	1:D:180:PHE:HD2	1.68	0.76
1:A:39:LYS:HG2	1:A:60:LEU:HD11	1.68	0.76
2:E:157:THR:C	2:E:158:LEU:HD23	2.07	0.76
2:B:31:PHE:CE2	2:B:36:GLU:HB2	2.22	0.75
4:G:45:LEU:O	4:G:59:ILE:HD11	1.85	0.75
2:B:77:ASN:OD1	4:I:29:THR:OG1	2.05	0.74
5:J:80:GLN:HB2	5:J:82:ASN:ND2	2.01	0.74
1:A:147:LYS:NZ	1:A:149:HIS:HE1	1.85	0.74
5:H:80:GLN:HB2	5:H:82:ASN:ND2	2.02	0.74
2:B:114:LEU:HD23	2:B:163:THR:O	1.86	0.74
2:B:115:LEU:HD11	2:B:188:TRP:CD1	2.23	0.74
4:I:45:LEU:O	4:I:59:ILE:HD11	1.86	0.74
4:G:95:SER:O	4:G:96:GLY:O	2.06	0.73
4:G:37:GLN:HB2	4:G:43:LEU:HD22	1.71	0.73
2:B:77:ASN:HA	4:I:29:THR:HG21	1.69	0.72
5:J:97:TYR:CD1	5:J:97:TYR:N	2.58	0.72
2:B:157:THR:C	2:B:158:LEU:HD23	2.08	0.72
4:G:24:TYR:CE2	4:G:71:SER:CA	2.60	0.72
1:A:13:TYR:HE2	1:A:67:LYS:HG3	1.54	0.72
1:A:13:TYR:CE2	1:A:67:LYS:HG3	2.25	0.72
1:D:99:LEU:O	1:D:155:PRO:O	2.08	0.72
4:I:66:PHE:CE2	4:I:68:ARG:HG2	2.23	0.72
1:D:137:PHE:CE2	1:D:147:LYS:HD2	2.25	0.71
5:H:61:GLY:HA3	5:H:79:ALA:HB2	1.73	0.71
2:B:70:GLN:NE2	5:J:97:TYR:HD1	1.75	0.71
2:E:82:ASN:O	2:E:86:VAL:HG22	1.90	0.71
2:E:115:LEU:HD11	2:E:188:TRP:CD1	2.24	0.71
3:F:2:ARG:HH12	4:G:29:THR:CG2	2.03	0.70
1:A:36:MET:CE	1:A:63:ILE:HG13	2.21	0.70
4:G:70:GLN:NE2	4:G:70:GLN:HA	2.02	0.70
5:J:93:LEU:H	5:J:93:LEU:HD12	1.57	0.70
5:J:5:SER:CB	5:J:6:PRO:HA	2.17	0.70
1:D:160:VAL:HG12	1:D:179:GLU:HB2	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:5:SER:CB	5:H:6:PRO:HA	2.20	0.69
1:A:162:ASP:OD1	1:A:177:HIS:HB2	1.91	0.69
4:G:50:PHE:HD1	4:G:51:SER:H	1.39	0.69
1:D:98:GLU:OE1	1:D:101:GLU:HG2	1.92	0.69
1:A:99:LEU:O	1:A:155:PRO:O	2.09	0.69
2:B:11:LEU:HD13	3:C:6:PRO:HB3	1.73	0.69
5:H:97:TYR:CD1	5:H:97:TYR:N	2.61	0.69
2:E:18:PHE:HB2	2:E:23:ARG:HB3	1.75	0.69
2:B:96:HIS:HB2	2:B:97:PRO:HD2	1.75	0.69
2:E:31:PHE:HE2	2:E:36:GLU:HB2	1.58	0.68
2:B:10:LEU:HG	2:B:31:PHE:HD1	1.58	0.68
4:G:81:HIS:HD2	4:G:83:SER:H	1.40	0.68
4:G:5:GLN:HE21	4:G:107:THR:CG2	2.06	0.68
1:D:36:MET:CE	1:D:63:ILE:HG13	2.23	0.68
4:I:37:GLN:HB2	4:I:43:LEU:HD22	1.74	0.68
1:D:45:LEU:HD12	1:D:48:PHE:CZ	2.28	0.68
5:H:61:GLY:CA	5:H:79:ALA:HB2	2.23	0.68
1:D:135:THR:CG2	1:D:148:PHE:HB2	2.24	0.68
5:H:6:PRO:HD2	5:H:9:LEU:HD11	1.77	0.67
1:D:72:ILE:O	1:D:76:ARG:HG3	1.94	0.67
5:H:93:LEU:H	5:H:93:LEU:HD12	1.58	0.67
5:H:97:TYR:HB2	5:H:98:THR:C	2.15	0.67
1:A:121:TRP:O	1:A:122:LEU:HD23	1.94	0.67
2:E:114:LEU:HD23	2:E:163:THR:O	1.95	0.66
5:H:41:LEU:HD23	5:H:41:LEU:N	2.10	0.66
4:G:5:GLN:HE21	4:G:107:THR:HG23	1.60	0.66
5:J:61:GLY:HA3	5:J:79:ALA:HB2	1.77	0.66
2:B:31:PHE:HE2	2:B:36:GLU:HB2	1.60	0.66
2:E:96:HIS:HB2	2:E:97:PRO:HD2	1.78	0.66
4:I:67:LYS:CB	4:I:70:GLN:HB2	2.26	0.66
1:D:41:THR:HG21	1:D:54:PHE:HB3	1.78	0.66
3:F:5:ILE:N	3:F:5:ILE:HD12	2.11	0.65
1:A:72:ILE:O	1:A:76:ARG:HG3	1.95	0.65
4:I:67:LYS:HB2	4:I:70:GLN:HB2	1.78	0.65
4:I:5:GLN:HE21	4:I:107:THR:HG23	1.62	0.65
4:I:41:GLN:HB3	5:J:105:GLU:OE1	1.96	0.65
4:G:45:LEU:HD23	5:H:100:GLU:OE1	1.96	0.65
4:I:37:GLN:O	4:I:86:ALA:HB1	1.96	0.65
2:B:18:PHE:HB2	2:B:23:ARG:HB3	1.79	0.65
4:I:81:HIS:HD2	4:I:83:SER:H	1.43	0.64
4:G:67:LYS:HB2	4:G:70:GLN:HB2	1.77	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:61:GLY:CA	5:J:79:ALA:CB	2.73	0.64
2:E:10:LEU:HG	2:E:31:PHE:HD1	1.62	0.64
1:A:137:PHE:CE2	1:A:147:LYS:HD2	2.32	0.64
5:J:41:LEU:N	5:J:41:LEU:HD23	2.11	0.64
2:B:47:TYR:HB2	2:B:62:ASN:OD1	1.97	0.64
5:H:64:VAL:HG12	5:H:74:LEU:HA	1.79	0.64
2:E:55:ARG:N	2:E:56:PRO:HD2	2.13	0.64
4:I:5:GLN:HE21	4:I:107:THR:CG2	2.11	0.64
2:B:82:ASN:O	2:B:86:VAL:HG22	1.96	0.64
5:H:9:LEU:O	5:H:109:LEU:HD12	1.97	0.64
4:G:101:LEU:C	4:G:102:ILE:HD13	2.19	0.63
5:J:61:GLY:CA	5:J:79:ALA:HB2	2.28	0.63
3:F:7:LYS:HD2	3:F:8:ARG:N	2.13	0.63
4:G:37:GLN:O	4:G:86:ALA:HB1	1.97	0.63
4:I:50:PHE:HD1	4:I:51:SER:H	1.46	0.63
1:D:147:LYS:NZ	1:D:149:HIS:HE1	1.95	0.63
5:J:80:GLN:HB2	5:J:82:ASN:HD22	1.62	0.63
2:B:55:ARG:N	2:B:56:PRO:HD2	2.14	0.63
4:I:101:LEU:C	4:I:102:ILE:HD13	2.19	0.63
4:G:41:GLN:HB3	5:H:105:GLU:OE1	1.98	0.63
5:H:17:VAL:HG11	5:H:109:LEU:HD21	1.81	0.63
1:A:147:LYS:HZ2	1:A:149:HIS:HE1	1.46	0.63
4:I:95:SER:O	4:I:96:GLY:O	2.17	0.62
2:B:70:GLN:HE22	5:J:97:TYR:CA	2.12	0.62
2:E:81:HIS:CD2	3:F:2:ARG:HD2	2.33	0.62
4:G:98:THR:HB	4:G:100:LYS:H	1.63	0.62
3:C:7:LYS:HD3	5:J:95:ASP:HB3	1.81	0.62
4:G:70:GLN:CA	4:G:70:GLN:NE2	2.62	0.62
1:A:89:VAL:HG21	1:A:165:VAL:HG21	1.81	0.62
4:I:70:GLN:HA	4:I:70:GLN:NE2	2.07	0.62
1:A:135:THR:CG2	1:A:148:PHE:N	2.58	0.62
4:G:5:GLN:NE2	4:G:106:GLY:HA2	2.14	0.62
5:J:9:LEU:O	5:J:109:LEU:HD12	2.00	0.62
5:J:58:ILE:O	5:J:58:ILE:HG13	1.99	0.62
4:G:11:THR:HG23	4:G:110:GLN:HG3	1.82	0.62
5:J:97:TYR:HB2	5:J:98:THR:C	2.21	0.62
3:C:5:ILE:H	3:C:5:ILE:HD12	1.64	0.62
4:G:66:PHE:HE2	4:G:68:ARG:HG2	1.60	0.61
1:A:147:LYS:NZ	1:A:149:HIS:CE1	2.68	0.61
2:B:81:HIS:CD2	3:C:2:ARG:HD2	2.35	0.61
4:G:32:LEU:CD2	4:G:92:VAL:HG23	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:121:TRP:O	1:D:122:LEU:HD23	1.99	0.61
5:J:17:VAL:HG11	5:J:109:LEU:HD21	1.82	0.61
1:A:98:GLU:OE1	1:A:101:GLU:HG2	2.01	0.61
4:I:98:THR:HB	4:I:100:LYS:H	1.65	0.61
3:C:5:ILE:HD12	3:C:5:ILE:N	2.16	0.61
1:D:3:GLU:HA	2:E:18:PHE:CD2	2.35	0.61
3:C:7:LYS:HD2	3:C:8:ARG:N	2.16	0.61
1:D:89:VAL:HG21	1:D:165:VAL:HG21	1.83	0.61
5:H:61:GLY:CA	5:H:79:ALA:CB	2.71	0.61
4:I:95:SER:O	4:I:96:GLY:C	2.39	0.61
2:E:150:ASN:HB2	2:E:154:THR:O	2.01	0.61
2:E:26:PHE:HB3	2:E:42:SER:HB3	1.82	0.60
2:B:123:TYR:O	2:B:177:HIS:HE1	1.84	0.60
2:E:47:TYR:HB2	2:E:62:ASN:OD1	2.01	0.60
1:D:31:ILE:HG22	1:D:32:PHE:HD2	1.66	0.60
4:I:28:ALA:O	4:I:29:THR:CG2	2.47	0.60
5:H:27:HIS:HD2	5:H:93:LEU:HG	1.66	0.60
1:A:137:PHE:CD2	1:A:147:LYS:HD2	2.36	0.60
2:B:170:VAL:HG22	2:B:189:ARG:HG3	1.84	0.60
4:G:67:LYS:CB	4:G:70:GLN:HB2	2.31	0.60
2:E:156:GLN:HE21	2:E:158:LEU:HD21	1.66	0.60
1:A:135:THR:CG2	1:A:148:PHE:HB2	2.31	0.60
1:D:136:VAL:HG22	1:D:137:PHE:N	2.17	0.60
2:B:70:GLN:NE2	5:J:97:TYR:CB	2.65	0.60
1:D:137:PHE:CD2	1:D:147:LYS:HD2	2.36	0.59
4:I:70:GLN:CA	4:I:70:GLN:NE2	2.64	0.59
1:D:136:VAL:CG2	1:D:137:PHE:N	2.65	0.59
4:G:94:ALA:O	4:G:97:ASN:HA	2.03	0.59
5:J:64:VAL:HG12	5:J:74:LEU:HA	1.84	0.59
2:B:156:GLN:HE21	2:B:158:LEU:HD21	1.65	0.59
2:E:133:ARG:HG3	2:E:171:TYR:CE1	2.38	0.59
2:E:160:MET:HG3	2:E:161:LEU:N	2.18	0.59
2:B:133:ARG:HG3	2:B:171:TYR:CE1	2.37	0.59
1:A:12:PHE:C	1:A:12:PHE:CD1	2.75	0.59
5:J:61:GLY:HA3	5:J:79:ALA:HB3	1.82	0.59
4:I:45:LEU:HD23	5:J:100:GLU:OE1	2.03	0.59
1:D:92:LEU:N	1:D:92:LEU:HD23	2.18	0.59
1:A:31:ILE:HG22	1:A:32:PHE:HD2	1.68	0.58
2:B:66:ASP:HB2	5:J:97:TYR:OH	2.03	0.58
1:D:72:ILE:HD12	3:F:9:ILE:HG22	1.85	0.58
4:I:1:GLN:HG3	4:I:95:SER:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:98:THR:CB	4:G:99:GLY:HA3	2.33	0.58
2:E:123:TYR:O	2:E:177:HIS:HE1	1.85	0.58
2:E:14:GLU:HB2	2:E:27:LEU:HB2	1.85	0.58
1:D:101:GLU:O	1:D:155:PRO:HD2	2.03	0.58
1:A:69:ASN:OD1	3:C:9:ILE:HB	2.04	0.58
5:J:97:TYR:HB2	5:J:99:GLY:N	2.19	0.58
2:E:143:VAL:O	2:E:143:VAL:HG13	2.04	0.58
2:B:66:ASP:OD2	5:J:97:TYR:OH	2.22	0.57
1:A:101:GLU:OE2	1:A:101:GLU:HA	2.04	0.57
5:H:61:GLY:HA3	5:H:79:ALA:HB3	1.83	0.57
5:H:80:GLN:HB2	5:H:82:ASN:HD22	1.68	0.57
1:A:36:MET:HE3	1:A:63:ILE:HG13	1.86	0.57
4:I:43:LEU:HD23	4:I:43:LEU:N	2.19	0.57
1:A:92:LEU:HD23	1:A:92:LEU:N	2.19	0.57
4:I:32:LEU:CD2	4:I:92:VAL:HG23	2.35	0.57
2:B:26:PHE:HB3	2:B:42:SER:HB3	1.85	0.57
1:D:135:THR:HG22	1:D:148:PHE:HB2	1.86	0.57
1:A:136:VAL:HG22	1:A:137:PHE:N	2.21	0.56
1:D:101:GLU:OE2	1:D:101:GLU:HA	2.03	0.56
2:B:160:MET:HG3	2:B:161:LEU:N	2.20	0.56
2:B:51:THR:HA	2:E:51:THR:HA	1.88	0.56
1:A:36:MET:HE1	1:A:63:ILE:HG13	1.87	0.56
2:B:55:ARG:N	2:B:56:PRO:CD	2.68	0.56
2:B:61:TRP:CE2	3:C:7:LYS:HG3	2.40	0.56
1:A:136:VAL:CG2	1:A:137:PHE:N	2.68	0.56
1:D:147:LYS:HZ2	1:D:149:HIS:HE1	1.54	0.56
4:G:43:LEU:HD23	4:G:43:LEU:N	2.20	0.56
5:H:32:TRP:CZ3	5:H:89:CYS:HB2	2.40	0.56
1:A:135:THR:HG23	1:A:148:PHE:N	2.12	0.56
3:C:2:ARG:HG3	4:I:96:GLY:CA	2.36	0.56
3:C:2:ARG:HG3	4:I:96:GLY:HA2	1.87	0.56
2:B:70:GLN:HG2	4:I:50:PHE:CD2	2.41	0.56
2:E:55:ARG:N	2:E:56:PRO:CD	2.68	0.56
1:A:41:THR:HG21	1:A:54:PHE:HB3	1.88	0.56
4:G:7:ASP:OD2	4:G:10:ILE:HD11	2.06	0.55
1:D:36:MET:HE1	1:D:63:ILE:HG13	1.88	0.55
3:F:0:HIS:HB2	4:G:96:GLY:HA3	1.89	0.55
2:E:114:LEU:HD21	2:E:164:VAL:HG23	1.88	0.55
2:E:61:TRP:CE2	3:F:7:LYS:HG3	2.41	0.55
4:I:5:GLN:HB3	4:I:107:THR:HG22	1.87	0.55
1:D:17:ASP:N	1:D:17:ASP:OD1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:46:LEU:HD12	4:I:59:ILE:HG13	1.89	0.55
2:E:170:VAL:HG22	2:E:189:ARG:HG3	1.88	0.55
1:D:113:THR:OG1	1:D:114:PRO:HA	2.07	0.55
1:D:70:LEU:HA	2:E:9:GLU:OE1	2.06	0.55
1:D:180:PHE:O	1:D:180:PHE:CD2	2.57	0.55
2:E:81:HIS:ND1	3:F:2:ARG:NH1	2.55	0.55
4:G:34:TRP:O	4:G:46:LEU:HB2	2.07	0.55
4:I:34:TRP:O	4:I:46:LEU:HB2	2.07	0.55
1:A:101:GLU:O	1:A:155:PRO:HD2	2.06	0.55
5:J:82:ASN:N	5:J:83:PRO:HD3	2.21	0.54
2:E:81:HIS:CG	3:F:2:ARG:HH11	2.26	0.54
1:D:96:PRO:HG3	2:E:118:SER:OG	2.07	0.54
1:A:123:ARG:HG3	1:A:161:TYR:CE2	2.42	0.54
2:B:143:VAL:HG13	2:B:143:VAL:O	2.07	0.54
4:G:98:THR:HG22	4:G:99:GLY:CA	2.18	0.54
4:I:7:ASP:OD2	4:I:10:ILE:HD11	2.07	0.54
4:G:19:GLU:HA	4:G:75:LEU:O	2.07	0.54
1:D:135:THR:CG2	1:D:148:PHE:N	2.63	0.54
4:I:19:GLU:HA	4:I:75:LEU:O	2.07	0.54
1:A:3:GLU:HA	2:B:18:PHE:CD2	2.42	0.54
5:H:58:ILE:O	5:H:58:ILE:HG13	2.07	0.54
5:H:27:HIS:CD2	5:H:93:LEU:HG	2.43	0.54
4:G:32:LEU:HD23	4:G:92:VAL:HG23	1.88	0.54
2:B:70:GLN:HE22	5:J:97:TYR:HA	1.72	0.54
4:I:11:THR:HG23	4:I:110:GLN:HG3	1.89	0.54
4:I:98:THR:CB	4:I:99:GLY:HA3	2.37	0.54
2:B:114:LEU:HD21	2:B:164:VAL:HG23	1.90	0.53
2:E:11:LEU:HD13	3:F:6:PRO:HB3	1.88	0.53
1:D:123:ARG:HG3	1:D:161:TYR:CE2	2.43	0.53
4:I:98:THR:HG22	4:I:99:GLY:CA	2.18	0.53
2:B:67:LEU:HA	5:J:97:TYR:HE1	1.74	0.53
4:I:66:PHE:CZ	4:I:68:ARG:HG2	2.43	0.53
2:B:26:PHE:HZ	3:C:4:ASN:ND2	2.06	0.53
1:D:135:THR:HG21	1:D:148:PHE:HB2	1.89	0.53
5:J:27:HIS:HD2	5:J:93:LEU:HG	1.73	0.53
1:A:45:LEU:HD12	1:A:48:PHE:CZ	2.42	0.53
2:B:70:GLN:NE2	5:J:97:TYR:CG	2.75	0.53
2:B:150:ASN:HB2	2:B:154:THR:O	2.08	0.53
1:D:147:LYS:NZ	1:D:149:HIS:CE1	2.76	0.53
1:D:109:ILE:HG22	1:D:112:PHE:CE1	2.44	0.53
2:B:36:GLU:HG2	2:B:50:VAL:HG21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:14:GLU:HB2	2:B:27:LEU:HB2	1.91	0.53
4:G:28:ALA:O	4:G:29:THR:CG2	2.52	0.52
1:D:36:MET:HE3	1:D:63:ILE:HG13	1.90	0.52
4:G:2:SER:HB3	4:G:25:SER:HB2	1.91	0.52
4:G:29:THR:HG23	4:G:29:THR:O	2.09	0.52
3:C:9:ILE:HG23	3:C:10:SER:O	2.09	0.52
1:D:118:ASN:HB2	1:D:166:GLU:HB2	1.92	0.52
2:B:37:PHE:CD1	2:B:38:VAL:HG12	2.45	0.52
1:D:12:PHE:C	1:D:12:PHE:CD1	2.83	0.52
4:I:67:LYS:HB3	4:I:70:GLN:HB2	1.92	0.52
1:A:135:THR:HG21	1:A:148:PHE:H	1.71	0.52
2:B:158:LEU:HD23	2:B:158:LEU:N	2.25	0.52
4:G:49:TYR:CD2	4:G:49:TYR:O	2.63	0.52
1:A:70:LEU:HA	2:B:9:GLU:OE1	2.08	0.52
4:G:5:GLN:HB3	4:G:107:THR:HG22	1.91	0.52
2:B:74:GLN:NE2	2:B:78:TYR:HB2	2.25	0.52
2:B:149:HIS:HD2	2:B:151:GLY:H	1.58	0.52
2:E:158:LEU:HD23	2:E:158:LEU:N	2.25	0.52
2:E:31:PHE:CD2	2:E:36:GLU:HB2	2.45	0.51
2:B:28:GLU:O	2:B:39:ARG:HA	2.10	0.51
1:D:60:LEU:HD12	5:H:49:ILE:HD11	1.92	0.51
4:G:2:SER:HB3	4:G:25:SER:CB	2.41	0.51
5:H:94:ARG:HA	5:H:97:TYR:O	2.10	0.51
1:A:109:ILE:HG22	1:A:112:PHE:CE1	2.46	0.51
5:J:80:GLN:O	5:J:83:PRO:HG3	2.11	0.51
2:B:31:PHE:CD2	2:B:36:GLU:HB2	2.45	0.51
2:E:149:HIS:HD2	2:E:151:GLY:H	1.57	0.51
4:I:24:TYR:HE2	4:I:71:SER:C	2.13	0.51
5:H:82:ASN:N	5:H:83:PRO:HD3	2.26	0.51
4:I:16:ALA:O	4:I:80:VAL:HG23	2.09	0.51
4:G:46:LEU:HD12	4:G:59:ILE:HG13	1.94	0.50
1:A:113:THR:OG1	1:A:114:PRO:HA	2.11	0.50
4:G:16:ALA:O	4:G:80:VAL:HG23	2.10	0.50
4:G:5:GLN:HE22	4:G:106:GLY:HA2	1.76	0.50
1:D:3:GLU:HG2	1:D:4:GLU:N	2.26	0.50
5:H:81:LYS:HA	5:H:83:PRO:CD	2.36	0.50
1:A:72:ILE:HD13	3:C:11:ALA:HA	1.94	0.50
1:A:17:ASP:OD1	1:A:17:ASP:N	2.44	0.50
2:E:70:GLN:HG2	4:G:50:PHE:CD2	2.47	0.50
5:J:81:LYS:HA	5:J:83:PRO:CD	2.37	0.50
5:H:81:LYS:C	5:H:83:PRO:CD	2.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:81:HIS:NE2	3:C:2:ARG:HD2	2.27	0.50
5:H:34:ARG:HB3	5:H:44:ILE:HD11	1.92	0.50
5:H:18:THR:OG1	5:H:75:THR:HG23	2.11	0.50
4:I:33:PHE:HD2	4:I:48:LYS:HB3	1.77	0.50
2:E:87:GLU:HA	2:E:91:VAL:HG23	1.94	0.50
2:E:36:GLU:HG2	2:E:50:VAL:HG21	1.93	0.50
2:B:10:LEU:HD12	2:B:11:LEU:N	2.27	0.50
2:B:166:ARG:HB2	2:B:169:GLU:OE2	2.11	0.50
1:A:135:THR:HG22	1:A:148:PHE:HB2	1.93	0.49
1:D:21:GLU:CD	1:D:136:VAL:HG23	2.33	0.49
2:B:70:GLN:HE22	5:J:97:TYR:CB	2.25	0.49
5:J:81:LYS:C	5:J:83:PRO:CD	2.76	0.49
5:J:32:TRP:CZ3	5:J:89:CYS:HB2	2.47	0.49
4:I:32:LEU:HD23	4:I:92:VAL:HG23	1.94	0.49
4:I:60:LYS:O	4:I:77:LYS:HE3	2.12	0.49
5:H:80:GLN:O	5:H:83:PRO:HG3	2.13	0.49
1:D:62:ASN:ND2	3:F:6:PRO:HD3	2.28	0.49
5:J:10:PHE:N	5:J:10:PHE:CD2	2.62	0.49
5:J:80:GLN:CB	5:J:82:ASN:ND2	2.75	0.49
4:I:70:GLN:HB3	4:I:72:SER:OG	2.12	0.49
1:A:45:LEU:O	1:A:46:GLU:C	2.50	0.49
2:E:74:GLN:NE2	2:E:78:TYR:HB2	2.28	0.49
4:I:94:ALA:HB2	4:I:102:ILE:HG12	1.94	0.49
4:G:25:SER:O	4:G:26:TYR:C	2.52	0.49
2:E:87:GLU:HG3	2:E:88:SER:N	2.27	0.49
4:G:24:TYR:HE2	4:G:71:SER:C	2.16	0.49
4:G:32:LEU:HD21	4:G:92:VAL:HG23	1.95	0.49
1:A:118:ASN:HB2	1:A:166:GLU:HB2	1.95	0.49
5:H:97:TYR:HB2	5:H:99:GLY:N	2.27	0.48
4:I:29:THR:HG23	4:I:29:THR:O	2.12	0.48
4:I:102:ILE:N	4:I:102:ILE:HD13	2.28	0.48
2:E:166:ARG:HB2	2:E:169:GLU:OE2	2.13	0.48
3:C:7:LYS:HD2	3:C:8:ARG:H	1.78	0.48
1:A:96:PRO:HG2	2:B:100:THR:HG21	1.96	0.48
1:A:123:ARG:HG3	1:A:161:TYR:CD2	2.48	0.48
5:J:6:PRO:HD2	5:J:9:LEU:HD11	1.96	0.48
1:D:115:PRO:HB3	1:D:145:PHE:CD1	2.49	0.48
1:A:147:LYS:HZ3	1:A:149:HIS:CE1	2.29	0.48
5:J:27:HIS:CD2	5:J:93:LEU:HG	2.48	0.48
1:A:105:LEU:O	1:A:150:TYR:HA	2.12	0.48
1:A:135:THR:HG21	1:A:148:PHE:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:45:LEU:O	1:D:46:GLU:C	2.52	0.48
2:E:52:GLU:OE2	2:E:55:ARG:NH2	2.47	0.48
1:D:29:ASP:CG	2:E:149:HIS:HE2	2.16	0.48
5:H:10:PHE:CD2	5:H:10:PHE:N	2.66	0.48
4:G:67:LYS:HD3	4:G:70:GLN:HG2	1.95	0.48
3:C:4:ASN:OD1	3:C:5:ILE:N	2.46	0.47
2:E:37:PHE:CD1	2:E:38:VAL:HG12	2.49	0.47
5:J:46:TYR:CE2	5:J:54:GLN:HG3	2.50	0.47
5:J:109:LEU:HD12	5:J:109:LEU:HA	1.62	0.47
1:D:115:PRO:HB2	1:D:137:PHE:CD1	2.48	0.47
4:I:94:ALA:O	4:I:97:ASN:HA	2.14	0.47
2:E:28:GLU:O	2:E:39:ARG:HA	2.13	0.47
1:D:96:PRO:HG2	2:E:100:THR:HG21	1.96	0.47
3:F:2:ARG:HH12	4:G:29:THR:HG23	1.78	0.47
1:A:177:HIS:NE2	1:A:179:GLU:HB3	2.29	0.47
4:G:66:PHE:CZ	4:G:68:ARG:HG2	2.46	0.47
4:G:97:ASN:OD1	4:G:98:THR:O	2.32	0.47
2:E:10:LEU:HB3	2:E:31:PHE:HB2	1.95	0.47
3:C:2:ARG:CG	4:I:96:GLY:HA2	2.44	0.47
4:I:87:GLU:HA	4:I:108:THR:HA	1.96	0.47
4:G:102:ILE:N	4:G:102:ILE:HD13	2.27	0.47
4:G:10:ILE:O	4:G:109:LEU:HD23	2.15	0.47
3:F:9:ILE:HG23	3:F:10:SER:O	2.14	0.47
1:A:62:ASN:ND2	3:C:6:PRO:HD3	2.30	0.47
1:D:69:ASN:OD1	3:F:9:ILE:HB	2.14	0.47
2:B:70:GLN:NE2	5:J:97:TYR:HB3	2.30	0.46
2:E:31:PHE:HD2	2:E:36:GLU:CA	2.28	0.46
4:G:33:PHE:HD2	4:G:48:LYS:HB3	1.79	0.46
1:A:111:LYS:HG2	1:A:140:ARG:CZ	2.45	0.46
1:A:98:GLU:HB3	1:A:101:GLU:HB2	1.96	0.46
5:J:32:TRP:NE1	5:J:74:LEU:HB2	2.29	0.46
4:G:72:SER:HB2	4:G:74:ASN:HD21	1.80	0.46
1:D:148:PHE:O	1:D:149:HIS:ND1	2.49	0.46
1:A:3:GLU:HG2	1:A:4:GLU:N	2.29	0.46
2:E:130:ARG:HD3	2:E:137:GLU:OE2	2.15	0.46
1:D:135:THR:HG21	1:D:148:PHE:H	1.77	0.46
2:B:31:PHE:HD2	2:B:36:GLU:CA	2.29	0.46
1:D:96:PRO:HG2	2:E:100:THR:CG2	2.46	0.46
1:D:123:ARG:HG3	1:D:161:TYR:CD2	2.51	0.46
2:B:164:VAL:HA	2:B:165:PRO:HD3	1.76	0.46
2:E:114:LEU:HD21	2:E:164:VAL:CG2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:105:LEU:O	1:D:150:TYR:HA	2.16	0.46
5:H:46:TYR:CE2	5:H:54:GLN:HG3	2.50	0.46
4:G:31:TYR:O	4:G:93:GLY:N	2.38	0.46
5:J:88:LEU:HD23	5:J:88:LEU:HA	1.71	0.46
1:D:160:VAL:O	1:D:160:VAL:HG23	2.16	0.45
4:G:35:TYR:HB3	4:G:43:LEU:HB3	1.97	0.45
1:D:134:GLU:O	1:D:134:GLU:HG3	2.17	0.45
4:I:10:ILE:O	4:I:109:LEU:HD23	2.16	0.45
4:I:1:GLN:HG3	4:I:95:SER:CB	2.45	0.45
4:I:2:SER:HB3	4:I:25:SER:HB2	1.98	0.45
5:H:76:VAL:O	5:H:76:VAL:HG12	2.15	0.45
1:A:180:PHE:O	1:A:180:PHE:CD2	2.57	0.45
2:E:32:HIS:CD2	2:E:33:ASN:HD22	2.34	0.45
2:B:10:LEU:HB3	2:B:31:PHE:HB2	1.99	0.45
1:D:70:LEU:HB2	2:E:9:GLU:HB2	1.99	0.45
1:D:30:GLU:HB2	1:D:138:LEU:HD21	1.98	0.45
4:G:46:LEU:HA	4:G:46:LEU:HD12	1.49	0.45
1:A:98:GLU:OE1	1:A:101:GLU:OE1	2.35	0.45
1:D:122:LEU:HD23	1:D:127:PRO:HA	1.98	0.45
2:B:87:GLU:HG3	2:B:88:SER:N	2.31	0.45
1:A:74:THR:HG22	1:A:79:TYR:HA	1.99	0.45
1:A:166:GLU:O	1:A:167:HIS:HB2	2.17	0.45
1:D:9:GLN:HB3	2:E:13:SER:HB2	1.98	0.45
4:I:24:TYR:CE2	4:I:71:SER:C	2.90	0.45
2:E:10:LEU:HD12	2:E:11:LEU:N	2.32	0.45
4:I:81:HIS:CD2	4:I:82:TRP:N	2.84	0.45
1:D:123:ARG:HB2	1:D:128:VAL:CG2	2.47	0.45
4:I:25:SER:O	4:I:26:TYR:C	2.53	0.45
1:A:89:VAL:CG2	1:A:165:VAL:HG21	2.46	0.45
1:D:86:PRO:HA	1:D:87:PRO:HD3	1.67	0.45
1:D:178:TRP:C	1:D:178:TRP:CE3	2.89	0.45
2:E:40:PHE:HE1	2:E:45:GLY:O	2.00	0.45
2:E:70:GLN:NE2	5:H:97:TYR:CG	2.80	0.44
2:E:121:GLY:HA2	2:E:154:THR:HB	1.99	0.44
4:I:12:VAL:HG22	4:I:13:SER:N	2.32	0.44
2:B:94:ARG:HD2	2:B:94:ARG:N	2.32	0.44
5:H:61:GLY:HA2	5:H:79:ALA:HB2	1.98	0.44
4:G:5:GLN:NE2	4:G:107:THR:HG23	2.31	0.44
2:E:152:ASP:OD1	2:E:154:THR:OG1	2.28	0.44
1:D:44:ARG:NH2	2:E:152:ASP:HB3	2.32	0.44
5:J:34:ARG:HB3	5:J:44:ILE:HD11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:81:HIS:CD2	4:G:82:TRP:N	2.85	0.44
5:J:76:VAL:HG12	5:J:76:VAL:O	2.16	0.44
2:B:130:ARG:HD3	2:B:137:GLU:OE2	2.17	0.44
5:J:80:GLN:C	5:J:82:ASN:H	2.21	0.44
4:G:60:LYS:O	4:G:77:LYS:HE3	2.17	0.44
4:G:12:VAL:HG22	4:G:13:SER:N	2.32	0.44
2:B:70:GLN:NE2	5:J:97:TYR:CA	2.81	0.44
1:D:177:HIS:CD2	1:D:177:HIS:C	2.90	0.44
1:A:178:TRP:C	1:A:178:TRP:CE3	2.90	0.44
2:E:146:GLY:O	2:E:157:THR:OG1	2.35	0.44
2:B:19:ASN:ND2	2:B:22:GLU:OE1	2.51	0.44
1:D:44:ARG:HH22	2:E:152:ASP:HB3	1.83	0.44
1:D:126:LYS:HA	1:D:127:PRO:HD3	1.84	0.43
1:D:178:TRP:O	1:D:178:TRP:HE3	2.01	0.43
2:B:146:GLY:O	2:B:157:THR:OG1	2.29	0.43
1:A:123:ARG:HB2	1:A:128:VAL:CG2	2.48	0.43
1:A:29:ASP:CG	2:B:149:HIS:HE2	2.20	0.43
5:H:11:ARG:HG3	5:H:17:VAL:HB	1.99	0.43
5:H:82:ASN:OD1	5:H:83:PRO:N	2.51	0.43
3:F:7:LYS:HD2	3:F:8:ARG:H	1.80	0.43
2:B:87:GLU:HA	2:B:91:VAL:HG23	2.00	0.43
4:G:12:VAL:HG22	4:G:13:SER:H	1.84	0.43
4:G:5:GLN:HE21	4:G:107:THR:HG22	1.83	0.43
1:D:65:VAL:HG11	3:F:6:PRO:HG2	2.01	0.43
2:B:52:GLU:OE2	2:B:55:ARG:NH2	2.52	0.43
2:B:26:PHE:CZ	3:C:4:ASN:ND2	2.86	0.43
4:G:24:TYR:HD2	4:G:24:TYR:H	1.66	0.43
1:D:147:LYS:HZ3	1:D:149:HIS:CE1	2.36	0.43
1:A:9:GLN:HB3	2:B:13:SER:HB2	2.00	0.43
5:J:77:THR:OG1	5:J:79:ALA:HB2	2.18	0.43
2:E:11:LEU:HD12	2:E:30:TYR:CE2	2.54	0.43
1:D:98:GLU:HB3	1:D:101:GLU:HB2	2.00	0.43
3:F:8:ARG:HE	3:F:8:ARG:HB2	1.64	0.43
1:D:166:GLU:O	1:D:167:HIS:HB2	2.19	0.43
1:D:111:LYS:HG2	1:D:140:ARG:CZ	2.48	0.43
4:G:70:GLN:HB3	4:G:72:SER:OG	2.19	0.43
2:E:70:GLN:HG2	4:G:50:PHE:CE2	2.54	0.43
1:A:115:PRO:HB3	1:A:145:PHE:CD1	2.53	0.43
2:B:80:ARG:HG3	2:B:80:ARG:HH11	1.84	0.43
2:E:19:ASN:ND2	2:E:22:GLU:OE1	2.52	0.43
1:D:3:GLU:HA	2:E:18:PHE:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:2:SER:HB3	4:I:25:SER:CB	2.48	0.43
5:H:1:GLY:HA3	5:H:25:LEU:HD21	2.01	0.43
2:E:41:ASP:HB3	2:E:44:VAL:HG23	2.00	0.43
1:A:115:PRO:HB2	1:A:137:PHE:CD1	2.54	0.43
2:E:157:THR:O	2:E:158:LEU:HD23	2.18	0.43
1:D:126:LYS:HB3	1:D:126:LYS:HE3	1.65	0.43
4:I:33:PHE:CD2	4:I:48:LYS:HB3	2.54	0.43
5:J:11:ARG:HG3	5:J:17:VAL:HB	2.01	0.42
2:E:148:ILE:HB	2:E:156:GLN:O	2.19	0.42
2:B:125:GLY:O	2:B:126:SER:C	2.58	0.42
1:A:98:GLU:CB	1:A:101:GLU:HB2	2.49	0.42
5:H:108:ARG:CB	5:H:108:ARG:NH1	2.75	0.42
5:J:94:ARG:HA	5:J:97:TYR:O	2.19	0.42
4:G:24:TYR:CE2	4:G:71:SER:C	2.93	0.42
2:B:114:LEU:HD21	2:B:164:VAL:CG2	2.49	0.42
2:B:121:GLY:HA2	2:B:154:THR:HB	2.01	0.42
2:E:41:ASP:HB3	2:E:44:VAL:CG2	2.49	0.42
2:E:96:HIS:HB3	2:E:179:SER:OG	2.19	0.42
4:G:11:THR:HG23	4:G:110:GLN:CG	2.49	0.42
1:D:135:THR:HG23	1:D:148:PHE:N	2.16	0.42
1:A:160:VAL:O	1:A:160:VAL:HG23	2.20	0.42
2:B:148:ILE:HB	2:B:156:GLN:O	2.19	0.42
1:D:89:VAL:CG2	1:D:165:VAL:HG21	2.49	0.42
1:D:36:MET:SD	1:D:60:LEU:HD23	2.60	0.42
4:I:46:LEU:HD12	4:I:46:LEU:HA	1.55	0.42
4:I:32:LEU:HD21	4:I:92:VAL:HG23	2.01	0.42
4:I:78:PRO:HD2	4:I:79:SER:H	1.85	0.42
1:A:30:GLU:HB2	1:A:138:LEU:HD21	2.01	0.42
4:G:94:ALA:HB2	4:G:102:ILE:HG12	2.01	0.42
5:H:80:GLN:C	5:H:82:ASN:H	2.22	0.42
1:A:11:GLU:OE2	2:B:11:LEU:HD22	2.20	0.42
5:H:84:THR:HG22	5:H:110:THR:HA	2.02	0.42
2:E:96:HIS:CB	2:E:97:PRO:HD2	2.47	0.42
2:B:182:SER:HA	2:B:183:PRO:HD3	1.88	0.42
1:D:77:SER:C	1:D:79:TYR:H	2.24	0.42
1:A:133:SER:OG	1:A:150:TYR:HB2	2.20	0.41
4:G:87:GLU:HA	4:G:108:THR:HA	2.01	0.41
1:D:82:ILE:HG23	1:D:82:ILE:O	2.20	0.41
5:H:64:VAL:HG21	5:H:72:PHE:CZ	2.55	0.41
1:A:134:GLU:HG3	1:A:134:GLU:O	2.20	0.41
4:I:24:TYR:HD2	4:I:24:TYR:H	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:HIS:CD2	1:A:177:HIS:C	2.94	0.41
1:A:12:PHE:HD1	1:A:12:PHE:C	2.22	0.41
1:A:86:PRO:HA	1:A:87:PRO:HD3	1.68	0.41
5:J:84:THR:HG22	5:J:110:THR:HA	2.02	0.41
4:I:12:VAL:HG22	4:I:13:SER:H	1.85	0.41
1:A:23:MET:HE2	1:A:30:GLU:HG3	2.02	0.41
4:G:3:VAL:HG13	4:G:4:THR:N	2.36	0.41
4:G:57:GLN:NE2	4:G:63:GLU:HG3	2.36	0.41
5:J:7:LYS:O	5:J:107:SER:HA	2.21	0.41
2:B:32:HIS:O	2:B:33:ASN:HB2	2.20	0.41
4:I:35:TYR:HB3	4:I:43:LEU:HB3	2.01	0.41
5:H:31:TYR:N	5:H:31:TYR:CD1	2.89	0.41
4:G:45:LEU:HD22	5:H:100:GLU:HB2	2.01	0.41
1:A:122:LEU:HD23	1:A:127:PRO:HA	2.02	0.41
2:E:164:VAL:HA	2:E:165:PRO:HD3	1.75	0.41
2:E:74:GLN:O	2:E:78:TYR:HB3	2.20	0.41
4:G:105:GLN:HA	5:H:40:GLY:N	2.35	0.41
4:I:67:LYS:HB2	4:I:70:GLN:CB	2.49	0.41
1:A:148:PHE:O	1:A:149:HIS:ND1	2.54	0.41
5:H:1:GLY:CA	5:H:25:LEU:HD21	2.50	0.41
2:E:141:GLY:HA3	2:E:162:GLU:HB2	2.03	0.41
1:D:137:PHE:HB3	1:D:145:PHE:HD1	1.85	0.41
2:E:32:HIS:CD2	2:E:33:ASN:ND2	2.89	0.41
4:G:12:VAL:HG12	4:G:109:LEU:HD21	2.03	0.41
1:A:180:PHE:C	1:A:180:PHE:CD2	2.92	0.41
3:C:5:ILE:HD13	5:J:96:GLY:O	2.21	0.41
5:J:110:THR:HG22	5:J:111:VAL:H	1.85	0.41
4:I:31:TYR:CD1	4:I:31:TYR:N	2.88	0.41
4:I:72:SER:HB2	4:I:74:ASN:HD21	1.86	0.41
1:A:82:ILE:O	1:A:82:ILE:HG23	2.20	0.41
1:A:50:ARG:HD3	1:A:51:PHE:CZ	2.56	0.41
4:I:5:GLN:NE2	4:I:107:THR:HG23	2.31	0.40
1:D:177:HIS:NE2	1:D:179:GLU:HB3	2.35	0.40
1:D:99:LEU:C	1:D:100:ARG:HG3	2.42	0.40
2:B:141:GLY:HA3	2:B:162:GLU:HB2	2.03	0.40
4:I:24:TYR:CD2	4:I:24:TYR:N	2.90	0.40
5:J:82:ASN:OD1	5:J:83:PRO:N	2.54	0.40
1:D:180:PHE:C	1:D:180:PHE:CD2	2.94	0.40
1:D:105:LEU:HG	1:D:153:PHE:CE1	2.56	0.40
1:A:13:TYR:HD2	1:A:67:LYS:HA	1.86	0.40
1:A:126:LYS:HA	1:A:127:PRO:HD3	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:74:THR:HG22	1:D:79:TYR:HA	2.04	0.40
4:I:98:THR:HB	4:I:100:LYS:N	2.35	0.40
2:B:96:HIS:CB	2:B:97:PRO:HD2	2.44	0.40
2:B:152:ASP:OD1	2:B:154:THR:OG1	2.35	0.40
2:B:40:PHE:HE1	2:B:45:GLY:O	2.04	0.40
2:E:70:GLN:HE22	5:H:97:TYR:CB	2.35	0.40
5:H:109:LEU:HA	5:H:109:LEU:HD12	1.62	0.40
1:A:135:THR:OG1	1:A:136:VAL:O	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	176/178 (99%)	155 (88%)	21 (12%)	0	100	100
1	D	176/178 (99%)	154 (88%)	20 (11%)	2 (1%)	17	57
2	B	175/187 (94%)	155 (89%)	19 (11%)	1 (1%)	30	68
2	E	175/187 (94%)	153 (87%)	21 (12%)	1 (1%)	30	68
3	C	11/13 (85%)	11 (100%)	0	0	100	100
3	F	11/13 (85%)	11 (100%)	0	0	100	100
4	G	111/113 (98%)	94 (85%)	16 (14%)	1 (1%)	21	60
4	I	111/113 (98%)	96 (86%)	13 (12%)	2 (2%)	11	46
5	H	109/111 (98%)	94 (86%)	14 (13%)	1 (1%)	21	60
5	J	109/111 (98%)	94 (86%)	13 (12%)	2 (2%)	11	46
All	All	1164/1204 (97%)	1017 (87%)	137 (12%)	10 (1%)	21	60

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	I	96	GLY
4	G	96	GLY
1	D	78	ASN
5	J	84	THR
5	H	84	THR
4	I	16	ALA
5	J	97	TYR
1	D	96	PRO
2	B	165	PRO
2	E	165	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	163/163 (100%)	144 (88%)	19 (12%)	7	28
1	D	163/163 (100%)	146 (90%)	17 (10%)	9	34
2	B	163/171 (95%)	149 (91%)	14 (9%)	13	45
2	E	163/171 (95%)	148 (91%)	15 (9%)	11	40
3	C	12/12 (100%)	7 (58%)	5 (42%)	0	0
3	F	12/12 (100%)	8 (67%)	4 (33%)	0	1
4	G	94/94 (100%)	68 (72%)	26 (28%)	0	2
4	I	94/94 (100%)	67 (71%)	27 (29%)	0	1
5	H	96/96 (100%)	79 (82%)	17 (18%)	2	10
5	J	96/96 (100%)	80 (83%)	16 (17%)	3	13
All	All	1056/1072 (98%)	896 (85%)	160 (15%)	3	16

All (160) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	PHE
1	A	17	ASP
1	A	46	GLU
1	A	53	SER

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Mol	Chain	Res	Type
1	A	83	THR
1	A	90	THR
1	A	94	ASN
1	A	98	GLU
1	A	99	LEU
1	A	100	ARG
1	A	101	GLU
1	A	120	THR
1	A	126	LYS
1	A	129	THR
1	A	130	THR
1	A	135	THR
1	A	136	VAL
1	A	179	GLU
1	A	180	PHE
2	B	4	ARG
2	B	39	ARG
2	B	60	SER
2	B	66	ASP
2	B	67	LEU
2	B	70	GLN
2	B	75	VAL
2	B	94	ARG
2	B	100	THR
2	B	157	THR
2	B	158	LEU
2	B	160	MET
2	B	181	THR
2	B	187	GLU
3	C	3	CYS
3	C	5	ILE
3	C	7	LYS
3	C	8	ARG
3	C	9	ILE
1	D	17	ASP
1	D	46	GLU
1	D	53	SER
1	D	83	THR
1	D	90	THR
1	D	94	ASN
1	D	98	GLU
1	D	99	LEU

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Mol	Chain	Res	Type
1	D	100	ARG
1	D	101	GLU
1	D	120	THR
1	D	129	THR
1	D	130	THR
1	D	135	THR
1	D	136	VAL
1	D	179	GLU
1	D	180	PHE
2	E	4	ARG
2	E	10	LEU
2	E	39	ARG
2	E	60	SER
2	E	66	ASP
2	E	67	LEU
2	E	70	GLN
2	E	75	VAL
2	E	94	ARG
2	E	100	THR
2	E	157	THR
2	E	158	LEU
2	E	160	MET
2	E	181	THR
2	E	185	THR
3	F	3	CYS
3	F	5	ILE
3	F	7	LYS
3	F	9	ILE
4	G	3	VAL
4	G	8	ILE
4	G	17	SER
4	G	24	TYR
4	G	25	SER
4	G	26	TYR
4	G	31	TYR
4	G	38	SER
4	G	41	GLN
4	G	43	LEU
4	G	46	LEU
4	G	50	PHE
4	G	56	VAL
4	G	59	ILE

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Mol	Chain	Res	Type
4	G	68	ARG
4	G	70	GLN
4	G	74	ASN
4	G	76	ARG
4	G	83	SER
4	G	97	ASN
4	G	102	ILE
4	G	105	GLN
4	G	107	THR
4	G	108	THR
4	G	109	LEU
4	G	112	LYS
5	H	10	PHE
5	H	12	LYS
5	H	23	GLN
5	H	30	MET
5	H	41	LEU
5	H	46	TYR
5	H	49	ILE
5	H	78	SER
5	H	80	GLN
5	H	81	LYS
5	H	84	THR
5	H	93	LEU
5	H	94	ARG
5	H	97	TYR
5	H	98	THR
5	H	107	SER
5	H	108	ARG
4	I	3	VAL
4	I	8	ILE
4	I	17	SER
4	I	24	TYR
4	I	25	SER
4	I	26	TYR
4	I	31	TYR
4	I	38	SER
4	I	41	GLN
4	I	43	LEU
4	I	46	LEU
4	I	50	PHE
4	I	56	VAL

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Mol	Chain	Res	Type
4	I	59	ILE
4	I	68	ARG
4	I	70	GLN
4	I	74	ASN
4	I	76	ARG
4	I	83	SER
4	I	95	SER
4	I	97	ASN
4	I	102	ILE
4	I	105	GLN
4	I	107	THR
4	I	108	THR
4	I	109	LEU
4	I	112	LYS
5	J	5	SER
5	J	10	PHE
5	J	12	LYS
5	J	23	GLN
5	J	30	MET
5	J	46	TYR
5	J	49	ILE
5	J	78	SER
5	J	80	GLN
5	J	81	LYS
5	J	84	THR
5	J	93	LEU
5	J	94	ARG
5	J	97	TYR
5	J	107	SER
5	J	108	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	HIS
2	B	64	GLN
2	B	70	GLN
2	B	74	GLN
2	B	156	GLN
3	C	-1	GLN
1	D	149	HIS
2	E	32	HIS

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Mol	Chain	Res	Type
2	E	64	GLN
2	E	70	GLN
2	E	156	GLN
4	G	5	GLN
4	G	44	GLN
4	G	57	GLN
4	G	70	GLN
4	G	81	HIS
4	G	105	GLN
4	G	110	GLN
5	H	15	GLN
5	H	23	GLN
4	I	44	GLN
4	I	57	GLN
4	I	70	GLN
4	I	81	HIS
4	I	110	GLN
5	J	15	GLN
5	J	23	GLN
5	J	39	GLN

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å²)	Q<0.9
1	A	178/178 (100%)	-0.05	0	100	100	58, 84, 126, 148	0
1	D	178/178 (100%)	-0.23	0	100	100	62, 86, 126, 149	0
2	B	179/187 (95%)	-0.10	0	100	100	60, 93, 143, 163	0
2	E	179/187 (95%)	-0.21	0	100	100	62, 94, 143, 163	0
3	C	13/13 (100%)	-0.12	0	100	100	66, 76, 137, 145	0
3	F	13/13 (100%)	0.08	1 (7%)	16	13	66, 77, 139, 143	0
4	G	113/113 (100%)	-0.09	0	100	100	69, 91, 118, 133	3 (2%)
4	I	113/113 (100%)	-0.23	0	100	100	70, 92, 120, 137	3 (2%)
5	H	111/111 (100%)	-0.23	0	100	100	64, 86, 121, 155	3 (2%)
5	J	111/111 (100%)	-0.09	0	100	100	63, 85, 119, 154	3 (2%)
All	All	1188/1204 (98%)	-0.15	1 (0%)	95	96	58, 89, 133, 163	12 (1%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	11	ALA	3.3

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.