



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:44 PM GMT

PDB ID : 4MJI
Title : T cell response to a HIV reverse transcriptase epitope presented by the protective allele HLA-B*51:01
Authors : Rizkallah, P.J.; Cole, D.K.; Sewell, A.K.; Motozono, C.; Takiguchi, M.
Deposited on : 2013-09-03
Resolution : 2.99 Å(reported)

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

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

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

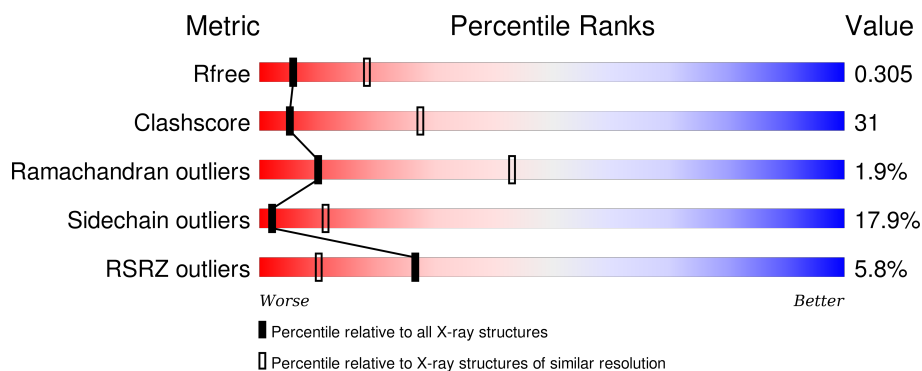
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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>5%</div> <div> <div></div> <div>52%</div> <div>39%</div> <div>9%</div> </div> </div>
1	F	276	<div> <div>3%</div> <div> <div></div> <div>46%</div> <div>44%</div> <div>9%</div> </div> </div>
2	B	99	<div> <div></div> <div> <div></div> <div>63%</div> <div>32%</div> <div>5%</div> </div> </div>
2	G	99	<div> <div>3%</div> <div> <div></div> <div>59%</div> <div>30%</div> <div>11%</div> </div> </div>
3	C	8	<div> <div></div> <div> <div></div> <div>38%</div> <div>63%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	H	8	<div><div></div><div>38%</div><div>63%</div></div>
4	D	195	<div><div>10%</div><div>40%</div><div>42%</div><div>14%</div><div></div><div></div></div>
4	I	195	<div><div>14%</div><div>44%</div><div>39%</div><div>15%</div><div></div><div></div></div>
5	E	242	<div><div>5%</div><div>46%</div><div>45%</div><div>7%</div><div></div><div></div></div>
5	J	242	<div><div>4%</div><div>52%</div><div>40%</div><div>8%</div><div></div><div></div></div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 13067 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, B-51 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2263	1412	412	432	7			
1	F	275	Total	C	N	O	S	0	0	0
			2255	1407	411	430	7			

- 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
			829	528	140	158	3			
2	G	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			

- Molecule 3 is a protein called HIV Reverse Transcriptase peptide Marker.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	8	Total	C	N	O	0	0	0
			60	40	8	12			
3	H	8	Total	C	N	O	0	0	0
			60	40	8	12			

- Molecule 4 is a protein called T-Cell Receptor Chain alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	192	Total	C	N	O	S	0	0	0
			1492	912	261	311	8			
4	I	194	Total	C	N	O	S	0	0	0
			1502	915	263	316	8			

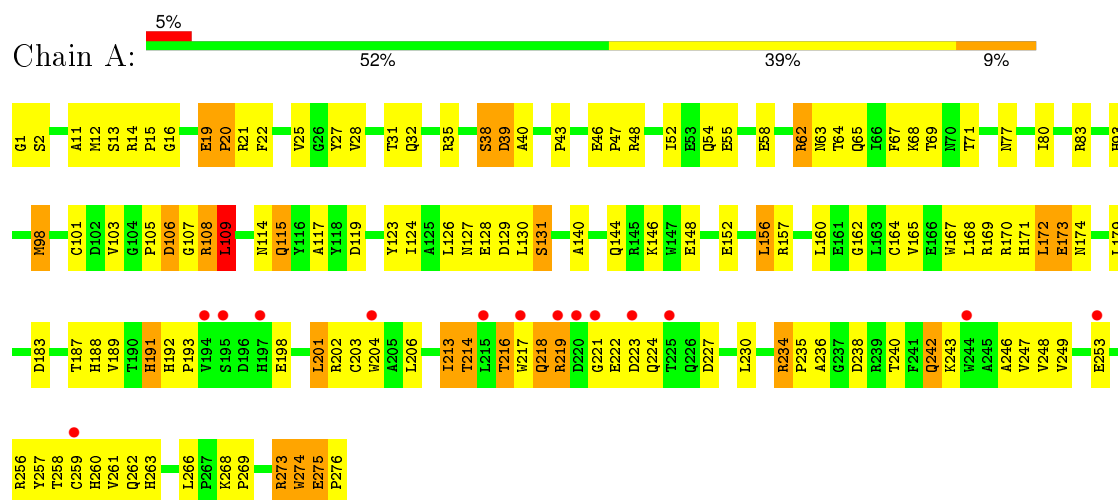
- Molecule 5 is a protein called T-cell Receptor Beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	240	Total	C	N	O	S	0	0	0
			1884	1189	327	363	5			
5	J	241	Total	C	N	O	S	0	0	0
			1893	1193	328	367	5			

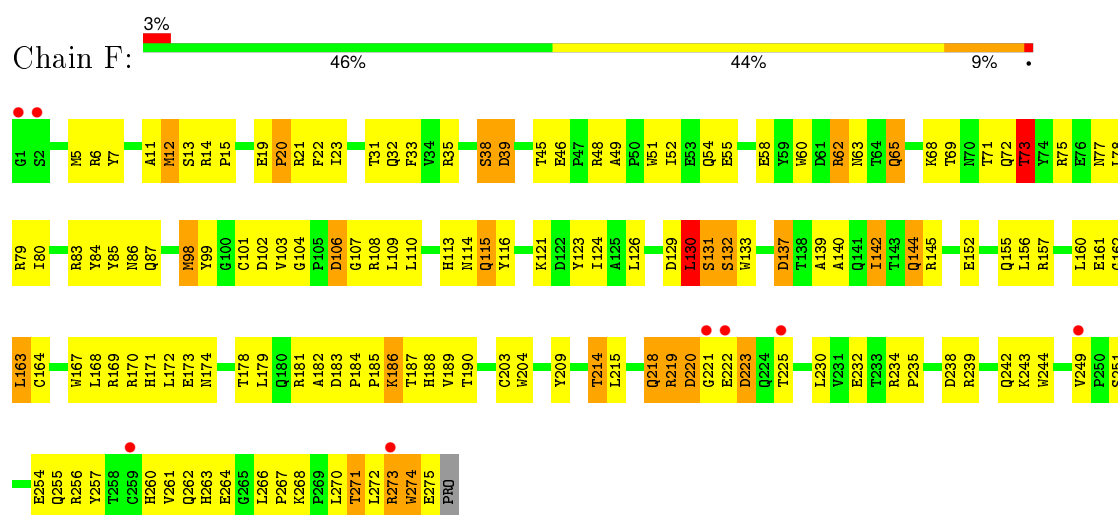
3 Residue-property plots

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, B-51 alpha chain



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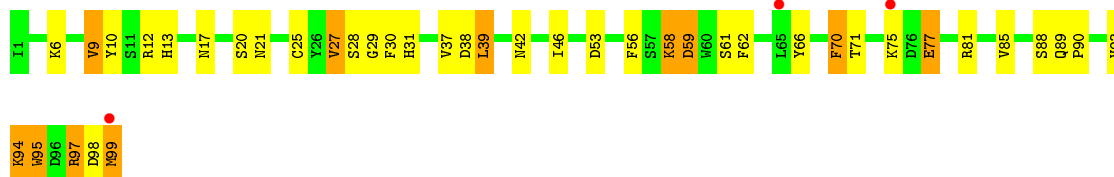


- Molecule 2: Beta-2-microglobulin





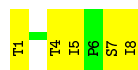
- Molecule 2: Beta-2-microglobulin



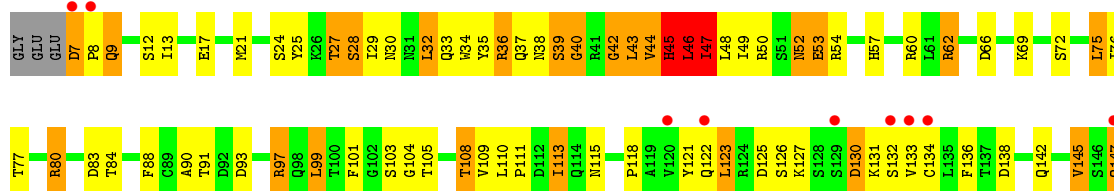
- Molecule 3: HIV Reverse Transcriptase peptide Marker



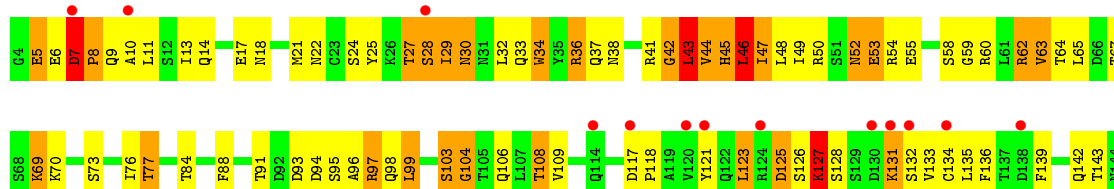
- Molecule 3: HIV Reverse Transcriptase peptide Marker



- Molecule 4: T-Cell Receptor Chain alpha



- Molecule 4: T-Cell Receptor Chain alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	45.51Å 88.87Å 129.27Å 102.91° 95.92° 90.09°	Depositor
Resolution (Å)	64.75 – 2.99 64.75 – 2.99	Depositor EDS
% Data completeness (in resolution range)	98.7 (64.75-2.99) 91.3 (64.75-2.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.242 , 0.304 0.242 , 0.305	Depositor DCC
R_{free} test set	1965 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	47.3	Xtriage
Anisotropy	0.885	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 43.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 39174 reflections	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	13067	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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	0.57	0/2329	0.83	1/3170 (0.0%)
1	F	0.58	0/2320	0.84	3/3158 (0.1%)
2	B	0.62	0/852	0.76	0/1152
2	G	0.56	0/852	0.81	1/1152 (0.1%)
3	C	0.60	0/61	0.87	0/82
3	H	0.73	0/61	0.96	0/82
4	D	0.66	1/1515 (0.1%)	0.93	2/2049 (0.1%)
4	I	0.64	0/1524	0.93	4/2062 (0.2%)
5	E	0.55	0/1934	0.78	2/2631 (0.1%)
5	J	0.55	0/1943	0.77	2/2643 (0.1%)
All	All	0.59	1/13391 (0.0%)	0.84	15/18181 (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	F	0	1
4	D	0	2
4	I	0	8
5	E	0	1
All	All	0	12

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	47	ILE	N-CA	6.01	1.58	1.46

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	43	LEU	CA-CB-CG	7.77	133.17	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	42	GLY	N-CA-C	6.58	129.55	113.10
4	I	123	LEU	CA-CB-CG	6.52	130.31	115.30
5	J	63	LEU	CA-CB-CG	6.37	129.94	115.30
4	D	46	LEU	N-CA-C	6.30	128.02	111.00
1	A	109	LEU	CA-CB-CG	6.20	129.56	115.30
4	I	53	GLU	N-CA-C	5.83	126.75	111.00
2	G	59	ASP	C-N-CA	-5.58	107.75	121.70
5	E	97	SER	CB-CA-C	-5.55	99.56	110.10
5	E	219	LEU	CA-CB-CG	5.54	128.04	115.30
1	F	73	THR	CB-CA-C	5.32	125.95	111.60
1	F	273	ARG	NE-CZ-NH1	5.29	122.94	120.30
5	J	159	LEU	CB-CG-CD1	-5.23	102.11	111.00
4	I	46	LEU	CA-CB-CG	5.19	127.23	115.30
1	F	98	MET	CG-SD-CE	5.04	108.26	100.20

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	45	HIS	Peptide
4	D	46	LEU	Peptide
5	E	208	ASN	Peptide
1	F	221	GLY	Peptide
4	I	104	GLY	Peptide
4	I	127	LYS	Peptide
4	I	131	LYS	Peptide
4	I	43	LEU	Peptide
4	I	45	HIS	Peptide
4	I	46	LEU	Peptide
4	I	7	ASP	Peptide
4	I	8	PRO	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	2263	0	2113	137	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2255	0	2106	135	0
2	B	829	0	794	30	0
2	G	829	0	794	38	0
3	C	60	0	64	17	0
3	H	60	0	64	11	0
4	D	1492	0	1429	121	0
4	I	1502	0	1433	151	0
5	E	1884	0	1794	120	0
5	J	1893	0	1798	109	0
All	All	13067	0	12389	777	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 31.

All (777) 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:D:36:ARG:HA	4:D:45:HIS:O	1.31	1.27
1:F:249:VAL:HG11	1:F:257:TYR:CE1	1.76	1.19
1:F:189:VAL:O	1:F:274:TRP:HE3	1.24	1.17
4:I:29:ILE:N	4:I:29:ILE:HD12	1.57	1.16
4:I:36:ARG:HA	4:I:45:HIS:O	1.44	1.14
1:A:129:ASP:O	1:A:129:ASP:OD1	1.67	1.13
4:I:29:ILE:H	4:I:29:ILE:CD1	1.63	1.09
1:A:32:GLN:HE21	1:A:48:ARG:HG3	1.08	1.09
4:D:62:ARG:HG2	4:D:62:ARG:HH11	1.18	1.09
4:D:125:ASP:OD2	4:D:130:ASP:HB3	1.51	1.08
1:A:275:GLU:HG3	1:A:276:PRO:HD3	1.31	1.07
1:F:114:ASN:HD22	1:F:156:LEU:CD2	1.69	1.06
1:F:6:ARG:HD3	1:F:113:HIS:HE2	1.17	1.05
1:F:215:LEU:HG	1:F:261:VAL:HG12	1.37	1.03
4:I:34:TRP:HH2	5:J:103:GLY:O	1.39	1.01
1:F:249:VAL:HG11	1:F:257:TYR:HE1	1.18	1.01
4:I:47:ILE:HD11	4:I:63:VAL:HG21	1.40	1.00
4:D:36:ARG:CA	4:D:45:HIS:O	2.09	1.00
4:D:138:ASP:OD1	5:E:197:ARG:NH2	1.96	0.99
1:A:275:GLU:CG	1:A:276:PRO:HD3	1.92	0.99
4:I:34:TRP:CZ3	4:I:48:LEU:HD12	1.97	0.99
1:A:77:ASN:ND2	3:C:8:ILE:H	1.60	0.99
4:I:46:LEU:HD13	4:I:47:ILE:HA	1.45	0.99
4:I:34:TRP:HH2	5:J:103:GLY:C	1.64	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:129:ASP:O	1:F:129:ASP:OD1	1.82	0.98
1:F:189:VAL:O	1:F:274:TRP:CE3	2.16	0.97
4:I:34:TRP:CH2	5:J:103:GLY:O	2.18	0.97
1:A:77:ASN:HD21	3:C:8:ILE:H	1.12	0.97
4:D:123:LEU:HD12	5:E:131:GLU:O	1.64	0.96
4:I:62:ARG:HG2	4:I:62:ARG:HH21	1.30	0.96
4:I:30:ASN:ND2	4:I:91:THR:HB	1.80	0.96
4:D:52:ASN:HD22	4:D:52:ASN:N	1.63	0.96
4:D:52:ASN:HD22	4:D:52:ASN:H	1.06	0.95
4:I:29:ILE:H	4:I:29:ILE:HD12	0.80	0.94
1:A:146:LYS:HD2	3:C:8:ILE:CD1	1.97	0.94
4:I:146:SER:O	4:I:155:ILE:HD11	1.68	0.93
4:I:7:ASP:HB3	4:I:103:SER:HB3	1.48	0.93
1:F:77:ASN:HD21	3:H:8:ILE:H	1.01	0.93
4:I:47:ILE:HD11	4:I:63:VAL:CG2	1.98	0.92
1:F:114:ASN:HD22	1:F:156:LEU:HD22	1.31	0.91
1:A:114:ASN:ND2	1:A:156:LEU:HD21	1.84	0.91
4:I:30:ASN:HD22	4:I:91:THR:HB	1.34	0.91
1:F:77:ASN:ND2	3:H:8:ILE:H	1.67	0.91
2:G:9:VAL:HG22	2:G:95:TRP:HB3	1.50	0.90
4:D:27:THR:HG21	4:D:93:ASP:OD1	1.71	0.90
4:I:34:TRP:CH2	5:J:103:GLY:C	2.46	0.90
1:A:106:ASP:OD1	1:A:108:ARG:HG2	1.71	0.89
4:I:41:ARG:HH12	5:J:12:SER:HB2	1.35	0.89
4:I:125:ASP:HA	5:J:130:PHE:HA	1.54	0.89
1:A:109:LEU:O	1:A:109:LEU:HD12	1.73	0.88
2:G:21:ASN:HB3	2:G:70:PHE:CE2	2.09	0.87
1:F:130:LEU:HD12	1:F:130:LEU:H	1.39	0.87
4:I:36:ARG:HH12	5:J:105:LEU:H	1.23	0.86
5:J:174:THR:HG23	5:J:194:SER:HB2	1.54	0.86
1:A:14:ARG:NH1	1:A:21:ARG:HB2	1.91	0.86
2:B:17:ASN:ND2	2:B:97:ARG:HH12	1.74	0.86
1:F:219:ARG:HG3	1:F:219:ARG:HH11	1.42	0.85
4:D:52:ASN:H	4:D:52:ASN:ND2	1.73	0.85
1:F:163:LEU:HD23	4:I:29:ILE:HD11	1.58	0.84
1:F:155:GLN:NE2	4:I:50:ARG:HH12	1.75	0.84
4:I:8:PRO:HB2	4:I:9:GLN:C	1.97	0.84
4:I:34:TRP:HZ3	4:I:48:LEU:HD12	1.40	0.83
5:E:227:GLN:NE2	5:E:227:GLN:HA	1.93	0.83
4:I:27:THR:O	4:I:28:SER:O	1.96	0.83
1:A:146:LYS:HD2	3:C:8:ILE:CG1	2.08	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:GLN:NE2	1:A:48:ARG:HG3	1.91	0.82
1:F:249:VAL:CG1	1:F:257:TYR:HE1	1.93	0.82
1:A:146:LYS:HD2	3:C:8:ILE:HD13	1.59	0.82
5:E:227:GLN:HB2	5:E:231:LYS:HD3	1.61	0.82
1:F:32:GLN:HE21	1:F:48:ARG:HG3	1.44	0.81
1:F:80:ILE:HD12	3:H:8:ILE:HA	1.61	0.81
5:J:225:TRP:CB	5:J:231:LYS:HG3	2.10	0.81
5:E:87:ARG:HD2	5:E:117:GLU:HG2	1.62	0.81
1:F:189:VAL:HB	1:F:274:TRP:HB2	1.62	0.81
5:E:174:THR:HG23	5:E:194:SER:HB2	1.63	0.81
1:F:114:ASN:HD22	1:F:156:LEU:HD21	1.45	0.81
4:D:159:CYS:HB3	5:E:195:ARG:HH21	1.45	0.80
1:A:216:THR:HG23	1:A:260:HIS:HB3	1.61	0.80
1:A:146:LYS:HD2	3:C:8:ILE:HG12	1.63	0.80
4:D:99:LEU:CD2	5:E:105:LEU:HD13	2.11	0.80
4:D:60:ARG:NH2	4:D:83:ASP:OD2	2.14	0.79
4:D:32:LEU:HG	4:D:48:LEU:HD11	1.64	0.79
1:F:215:LEU:HG	1:F:261:VAL:CG1	2.13	0.79
1:A:130:LEU:HB2	1:A:157:ARG:HD2	1.65	0.79
4:D:34:TRP:CZ3	4:D:46:LEU:HB2	2.18	0.79
4:D:62:ARG:NH1	4:D:62:ARG:HG2	1.91	0.79
1:A:13:SER:HB3	1:A:15:PRO:HD3	1.64	0.78
4:I:46:LEU:HD22	4:I:47:ILE:N	1.98	0.78
4:I:27:THR:HG21	4:I:93:ASP:OD1	1.84	0.78
4:I:14:GLN:O	4:I:17:GLU:HG2	1.82	0.78
4:I:34:TRP:CE3	4:I:48:LEU:HD12	2.18	0.78
2:G:21:ASN:HB3	2:G:70:PHE:HE2	1.46	0.78
1:A:274:TRP:HE3	1:A:275:GLU:H	1.29	0.77
1:A:146:LYS:CD	3:C:8:ILE:CD1	2.61	0.77
5:J:225:TRP:HB3	5:J:231:LYS:HG3	1.66	0.77
4:D:84:THR:CG2	4:D:109:VAL:H	1.97	0.77
5:E:112:ARG:HG3	5:E:156:HIS:CE1	2.20	0.77
1:A:146:LYS:CD	3:C:8:ILE:HD13	2.15	0.76
4:D:84:THR:HG22	4:D:109:VAL:H	1.49	0.76
2:B:34:ASP:O	2:B:84:HIS:HD2	1.69	0.76
4:D:33:GLN:HE22	4:D:72:SER:HB3	1.49	0.76
1:F:6:ARG:HD3	1:F:113:HIS:NE2	1.98	0.76
4:I:96:ALA:O	4:I:98:GLN:N	2.18	0.75
4:I:34:TRP:HB2	4:I:47:ILE:O	1.86	0.75
1:F:114:ASN:ND2	1:F:156:LEU:HD22	2.01	0.75
4:D:156:THR:HB	4:D:174:VAL:H	1.49	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:129:ASP:O	1:F:131:SER:N	2.19	0.75
5:E:207:ARG:HG2	5:E:207:ARG:O	1.86	0.75
1:F:63:ASN:HD21	3:H:1:THR:HG22	1.52	0.74
4:D:145:VAL:HA	4:D:191:SER:HB2	1.70	0.74
5:E:164:ASN:HB2	5:E:209:HIS:ND1	2.03	0.74
1:F:214:THR:O	1:F:261:VAL:HA	1.88	0.74
5:E:84:ARG:O	5:E:84:ARG:HG2	1.87	0.74
5:E:164:ASN:HB2	5:E:209:HIS:CE1	2.23	0.74
4:D:43:LEU:CD1	4:D:45:HIS:HD2	2.00	0.73
5:E:33:THR:HB	5:E:53:GLN:HE21	1.54	0.73
1:F:55:GLU:O	1:F:60:TRP:HZ3	1.70	0.73
4:I:133:VAL:HG21	5:J:130:PHE:CE2	2.23	0.73
1:F:218:GLN:OE1	1:F:260:HIS:CE1	2.41	0.73
4:I:139:PHE:HD1	4:I:143:THR:HB	1.54	0.73
5:E:33:THR:HB	5:E:53:GLN:NE2	2.02	0.73
1:A:273:ARG:HG2	1:A:273:ARG:HH21	1.52	0.73
4:I:46:LEU:O	4:I:47:ILE:HG23	1.88	0.73
5:E:219:LEU:HD22	5:E:232:PRO:O	1.89	0.73
4:I:46:LEU:CD1	4:I:47:ILE:HA	2.18	0.73
5:E:71:VAL:CG1	5:E:73:PRO:HD3	2.18	0.73
4:D:152:ASP:CG	4:D:179:LYS:HG3	2.09	0.72
1:A:16:GLY:O	4:I:60:ARG:HA	1.89	0.72
1:A:129:ASP:O	1:A:131:SER:N	2.22	0.72
4:I:34:TRP:CZ2	4:I:99:LEU:HD21	2.24	0.72
1:F:62:ARG:O	1:F:65:GLN:HG3	1.90	0.72
1:A:77:ASN:ND2	3:C:8:ILE:N	2.38	0.71
4:I:36:ARG:CA	4:I:45:HIS:O	2.34	0.71
1:A:14:ARG:NH1	1:A:21:ARG:HD2	2.06	0.70
4:I:5:GLU:HG3	4:I:6:GLU:H	1.56	0.70
5:J:189:ARG:HH11	5:J:189:ARG:HG2	1.55	0.70
4:I:195:GLU:CD	4:I:195:GLU:H	1.95	0.70
4:D:195:GLU:CD	4:D:195:GLU:H	1.95	0.70
1:F:152:GLU:HG3	1:F:152:GLU:O	1.92	0.70
4:I:41:ARG:HG3	4:I:42:GLY:N	2.06	0.70
1:F:249:VAL:CG1	1:F:257:TYR:CE1	2.66	0.69
4:I:84:THR:HG22	4:I:109:VAL:H	1.56	0.69
1:A:106:ASP:CG	1:A:108:ARG:HG2	2.12	0.69
1:A:214:THR:O	1:A:261:VAL:HA	1.92	0.69
4:D:43:LEU:CD1	4:D:45:HIS:CD2	2.76	0.69
5:E:225:TRP:CG	5:E:225:TRP:O	2.45	0.69
4:I:146:SER:O	4:I:155:ILE:CD1	2.39	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:188:HIS:HB2	1:F:274:TRP:CZ3	2.28	0.69
1:A:275:GLU:OE1	1:A:275:GLU:HA	1.91	0.69
1:A:77:ASN:HD21	3:C:8:ILE:N	1.88	0.69
5:J:28:PRO:HG3	5:J:35:LEU:HD12	1.75	0.69
4:I:46:LEU:HD13	4:I:47:ILE:CA	2.23	0.68
2:G:9:VAL:CG2	2:G:95:TRP:HB3	2.21	0.68
4:D:33:GLN:HE22	4:D:72:SER:CB	2.06	0.68
5:J:141:GLN:O	5:J:200:ALA:HB2	1.93	0.68
5:E:9:GLN:NE2	5:E:93:TYR:O	2.26	0.68
4:I:34:TRP:HZ2	4:I:99:LEU:HD21	1.58	0.68
4:I:99:LEU:HD22	5:J:105:LEU:HD13	1.74	0.68
2:B:11:SER:HB2	2:B:21:ASN:ND2	2.07	0.68
4:D:118:PRO:O	4:D:196:ASP:HB3	1.94	0.68
4:D:25:TYR:CB	4:D:91:THR:HG21	2.24	0.68
4:D:57:HIS:NE2	4:D:62:ARG:HD3	2.09	0.68
5:J:124:PRO:HD3	5:J:232:PRO:HB3	1.76	0.68
2:B:17:ASN:HD21	2:B:97:ARG:HH12	1.40	0.67
1:F:219:ARG:HG3	1:F:219:ARG:NH1	2.08	0.67
4:I:159:CYS:HB3	5:J:195:ARG:HH22	1.59	0.67
1:A:129:ASP:O	1:A:129:ASP:CG	2.32	0.67
1:A:202:ARG:HG3	1:A:246:ALA:HB2	1.75	0.67
1:F:22:PHE:H	1:F:38:SER:HB3	1.58	0.67
1:F:114:ASN:ND2	1:F:156:LEU:CD2	2.51	0.67
1:F:6:ARG:CD	1:F:113:HIS:HE2	2.01	0.67
1:F:130:LEU:HB2	1:F:157:ARG:HD2	1.76	0.67
1:F:255:GLN:HG3	1:F:273:ARG:HD2	1.76	0.67
5:E:163:VAL:O	5:E:164:ASN:HB3	1.94	0.67
4:I:62:ARG:HG2	4:I:62:ARG:NH2	2.01	0.67
4:I:123:LEU:HD21	4:I:135:LEU:HB2	1.76	0.67
4:D:62:ARG:CG	4:D:62:ARG:HH11	2.02	0.67
2:G:29:GLY:HA2	2:G:61:SER:HB2	1.76	0.67
4:I:29:ILE:N	4:I:29:ILE:CD1	2.35	0.67
1:F:163:LEU:CD2	4:I:29:ILE:HD11	2.25	0.66
4:I:52:ASN:C	4:I:52:ASN:HD22	1.97	0.66
1:A:103:VAL:CG1	1:A:168:LEU:HD23	2.24	0.66
5:E:227:GLN:HE21	5:E:228:ASP:H	1.44	0.66
5:E:28:PRO:HG3	5:E:35:LEU:HD12	1.76	0.66
2:G:20:SER:HA	2:G:71:THR:HG22	1.78	0.66
1:F:21:ARG:HG3	1:F:39:ASP:OD1	1.94	0.65
2:B:2:GLN:HG2	2:B:32:PRO:HD2	1.77	0.65
5:E:71:VAL:HG12	5:E:73:PRO:HD3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:ILE:O	1:A:83:ARG:HB2	1.97	0.65
1:A:167:TRP:CD1	3:C:1:THR:N	2.65	0.65
5:J:156:HIS:HB3	5:J:217:TYR:HB2	1.78	0.65
4:I:34:TRP:HE1	4:I:36:ARG:HE	1.44	0.65
4:I:41:ARG:NH1	5:J:12:SER:HB2	2.09	0.65
5:J:40:GLN:O	5:J:91:ALA:HB1	1.97	0.65
1:A:218:GLN:HG3	1:A:258:THR:O	1.96	0.64
1:F:62:ARG:HE	1:F:65:GLN:NE2	1.95	0.64
5:J:85:THR:CG2	5:J:115:VAL:HG21	2.28	0.64
5:J:51:TYR:OH	5:J:53:GLN:NE2	2.31	0.64
4:D:156:THR:HG22	4:D:157:ASP:O	1.97	0.64
4:D:148:SER:HB2	4:D:153:VAL:HG13	1.80	0.64
1:A:201:LEU:HD13	1:A:217:TRP:CZ2	2.32	0.64
5:J:198:VAL:HG22	5:J:199:SER:H	1.63	0.64
5:J:224:GLU:HA	5:J:224:GLU:OE1	1.97	0.63
4:D:125:ASP:HA	5:E:130:PHE:HA	1.80	0.63
4:D:84:THR:HG22	4:D:108:THR:HA	1.81	0.63
5:E:227:GLN:HE21	5:E:227:GLN:HA	1.63	0.63
4:I:152:ASP:OD1	4:I:177:SER:HB3	1.99	0.63
4:I:9:GLN:OE1	4:I:9:GLN:HA	1.99	0.63
4:I:93:ASP:O	4:I:94:ASP:HB2	1.99	0.63
1:A:234:ARG:HD3	2:B:10:TYR:CZ	2.34	0.63
5:E:134:GLU:HA	5:E:137:ILE:HG13	1.81	0.63
5:J:85:THR:HG22	5:J:115:VAL:HG21	1.81	0.63
1:F:129:ASP:CG	1:F:129:ASP:O	2.37	0.62
4:D:34:TRP:CZ3	4:D:46:LEU:CB	2.81	0.62
5:E:32:HIS:HE1	5:E:106:PHE:HD2	1.47	0.62
5:E:118:ASP:HB2	5:E:120:LYS:HG3	1.78	0.62
2:G:39:LEU:HB3	2:G:46:ILE:HD12	1.81	0.62
4:I:139:PHE:CD1	4:I:143:THR:HB	2.32	0.62
5:E:134:GLU:HA	5:E:137:ILE:CG1	2.29	0.62
4:I:25:TYR:HB3	4:I:91:THR:HG21	1.82	0.62
1:A:69:THR:HA	5:E:58:ALA:HB1	1.82	0.62
4:D:36:ARG:CB	4:D:45:HIS:O	2.48	0.62
4:I:99:LEU:CD2	5:J:105:LEU:HD13	2.30	0.62
4:D:43:LEU:HD23	5:E:109:GLU:OE2	2.00	0.61
4:I:159:CYS:HB3	5:J:195:ARG:NH2	2.15	0.61
1:A:13:SER:HB3	1:A:15:PRO:CD	2.29	0.61
1:F:204:TRP:HH2	2:G:99:MET:HA	1.64	0.61
4:I:34:TRP:HE3	4:I:48:LEU:HB2	1.64	0.61
5:J:159:LEU:HD11	5:J:194:SER:HB3	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:52:ILE:C	1:F:54:GLN:H	2.03	0.61
4:I:133:VAL:CG2	5:J:130:PHE:CE2	2.83	0.61
5:J:50:ILE:HD13	5:J:70:ALA:HB3	1.83	0.61
4:D:25:TYR:HB3	4:D:91:THR:HG21	1.82	0.61
4:I:34:TRP:HB3	4:I:48:LEU:HA	1.83	0.61
1:F:139:ALA:O	1:F:142:ILE:HG23	2.01	0.60
2:B:34:ASP:O	2:B:84:HIS:CD2	2.54	0.60
5:E:121:ASN:O	5:E:123:PHE:HD1	1.84	0.60
3:C:5:ILE:HB	3:C:6:PRO:HD2	1.82	0.60
5:E:209:HIS:ND1	5:E:209:HIS:N	2.50	0.60
5:E:227:GLN:HE21	5:E:227:GLN:CA	2.15	0.60
4:D:99:LEU:HD22	5:E:105:LEU:HD13	1.82	0.60
1:A:22:PHE:H	1:A:38:SER:HB3	1.66	0.60
4:D:113:ILE:HD12	4:D:115:ASN:H	1.66	0.60
1:F:98:MET:HG2	2:G:56:PHE:HE1	1.67	0.60
1:A:103:VAL:HG13	1:A:168:LEU:HD23	1.84	0.59
5:J:189:ARG:HG2	5:J:189:ARG:NH1	2.13	0.59
5:E:72:ARG:N	5:E:73:PRO:HD3	2.17	0.59
4:D:125:ASP:OD2	4:D:130:ASP:CB	2.38	0.59
1:A:171:HIS:O	1:A:174:ASN:N	2.35	0.59
5:E:67:ARG:HD3	5:E:84:ARG:HE	1.68	0.59
1:A:234:ARG:HD3	2:B:10:TYR:CE2	2.37	0.59
1:A:273:ARG:HG2	1:A:273:ARG:NH2	2.14	0.59
5:E:152:PHE:HE1	5:E:155:ASP:HA	1.66	0.59
4:I:84:THR:CG2	4:I:109:VAL:H	2.14	0.59
1:A:219:ARG:HG2	1:A:224:GLN:HB2	1.82	0.59
2:G:89:GLN:HG3	2:G:90:PRO:HD2	1.85	0.59
5:J:16:THR:CG2	5:J:17:GLU:N	2.65	0.59
4:D:37:GLN:O	4:D:45:HIS:HB2	2.02	0.59
1:F:84:TYR:OH	3:H:8:ILE:HG23	2.03	0.59
4:D:122:GLN:HG2	4:D:184:CYS:SG	2.43	0.59
2:B:21:ASN:HB3	2:B:70:PHE:CE2	2.38	0.58
4:D:32:LEU:HG	4:D:48:LEU:CD1	2.33	0.58
4:I:125:ASP:OD1	4:I:125:ASP:N	2.21	0.58
1:F:48:ARG:O	1:F:239:ARG:NH2	2.35	0.58
5:J:225:TRP:HB2	5:J:231:LYS:HG3	1.82	0.58
5:E:219:LEU:HB3	5:E:223:ASP:OD1	2.04	0.58
2:G:27:VAL:HG13	2:G:30:PHE:CE2	2.39	0.58
1:F:218:GLN:HA	1:F:222:GLU:O	2.03	0.58
1:A:216:THR:CG2	1:A:260:HIS:HB3	2.31	0.58
1:F:137:ASP:OD1	1:F:137:ASP:C	2.41	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:234:ARG:NH1	1:F:242:GLN:OE1	2.37	0.58
4:D:130:ASP:OD2	4:D:131:LYS:N	2.36	0.58
4:D:34:TRP:CZ3	4:D:47:ILE:HA	2.39	0.58
1:F:223:ASP:HB3	1:F:225:THR:HG23	1.84	0.58
4:D:52:ASN:N	4:D:52:ASN:ND2	2.34	0.58
1:F:189:VAL:HB	1:F:274:TRP:CB	2.31	0.58
4:D:38:ASN:HD22	4:D:88:PHE:HE2	1.50	0.58
5:J:124:PRO:HB3	5:J:235:GLN:NE2	2.19	0.58
2:B:19:LYS:HD3	2:B:20:SER:O	2.04	0.58
4:I:176:TRP:CD2	5:J:148:LEU:HD21	2.38	0.58
4:I:50:ARG:O	4:I:53:GLU:HB2	2.02	0.57
1:A:65:GLN:NE2	5:E:59:ASP:OD2	2.37	0.57
4:I:34:TRP:CE3	4:I:48:LEU:HB2	2.38	0.57
5:J:225:TRP:HB2	5:J:231:LYS:CG	2.34	0.57
1:F:133:TRP:HB2	1:F:144:GLN:NE2	2.18	0.57
2:G:9:VAL:CG1	2:G:93:VAL:HG12	2.35	0.57
1:A:93:HIS:HD2	1:A:119:ASP:OD2	1.87	0.57
4:I:118:PRO:O	4:I:196:ASP:CB	2.52	0.57
5:E:71:VAL:HG13	5:E:73:PRO:HD3	1.86	0.57
5:J:211:ARG:NH1	5:J:213:GLN:OE1	2.38	0.57
4:D:62:ARG:HB3	4:D:75:LEU:HD23	1.86	0.57
4:D:181:ASP:N	4:D:181:ASP:OD2	2.33	0.57
5:J:18:LYS:HD3	5:J:117:GLU:OE1	2.03	0.57
2:G:9:VAL:HG22	2:G:95:TRP:CB	2.30	0.57
5:E:32:HIS:HE1	5:E:106:PHE:CD2	2.23	0.57
4:I:62:ARG:HH21	4:I:62:ARG:CG	2.13	0.57
1:A:106:ASP:OD2	1:A:108:ARG:HG2	2.04	0.57
1:A:123:TYR:CZ	1:A:140:ALA:HA	2.40	0.57
4:D:126:SER:O	4:D:127:LYS:HB2	2.05	0.57
1:A:114:ASN:HD22	1:A:156:LEU:HD21	1.69	0.57
5:J:49:LEU:HA	5:J:62:GLY:HA3	1.86	0.56
1:F:49:ALA:O	1:F:52:ILE:HG22	2.05	0.56
1:A:64:THR:O	1:A:68:LYS:HG3	2.05	0.56
4:D:121:TYR:O	4:D:134:CYS:HA	2.04	0.56
2:G:27:VAL:HG13	2:G:30:PHE:HE2	1.70	0.56
4:D:164:ARG:HH22	5:E:169:HIS:CD2	2.23	0.56
3:H:4:THR:OG1	4:I:96:ALA:HA	2.05	0.56
1:A:14:ARG:HH11	1:A:21:ARG:HB2	1.71	0.56
5:E:37:TRP:HB2	5:E:50:ILE:HG22	1.88	0.56
5:E:130:PHE:HE1	5:E:148:LEU:HB2	1.70	0.56
1:A:189:VAL:HB	1:A:274:TRP:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:GLU:HG3	1:A:276:PRO:CD	2.21	0.56
1:F:14:ARG:NH1	1:F:21:ARG:HB2	2.20	0.56
5:E:121:ASN:O	5:E:123:PHE:CD1	2.59	0.56
5:J:142:LYS:HD3	5:J:197:ARG:HE	1.71	0.56
4:I:47:ILE:HD12	4:I:48:LEU:N	2.21	0.56
4:D:125:ASP:N	4:D:125:ASP:OD1	2.38	0.56
4:D:8:PRO:O	4:D:9:GLN:O	2.24	0.56
4:I:46:LEU:O	4:I:47:ILE:CG2	2.54	0.55
1:F:123:TYR:CZ	1:F:140:ALA:HA	2.41	0.55
4:D:46:LEU:O	4:D:47:ILE:HG23	2.06	0.55
1:F:35:ARG:HD3	2:G:53:ASP:OD2	2.06	0.55
5:J:163:VAL:O	5:J:163:VAL:HG13	2.05	0.55
4:D:123:LEU:HB2	4:D:133:VAL:HG23	1.88	0.55
4:I:133:VAL:HG21	5:J:130:PHE:CD2	2.41	0.55
5:E:20:LYS:O	5:E:85:THR:HB	2.06	0.55
5:E:127:VAL:HG12	5:E:239:ALA:HB2	1.88	0.55
4:I:8:PRO:HB3	4:I:106:GLN:H	1.72	0.55
5:J:179:LEU:HG	5:J:180:LYS:H	1.72	0.55
5:J:205:ASP:HB3	5:J:207:ARG:HH11	1.71	0.54
4:I:36:ARG:NH1	5:J:105:LEU:HB2	2.21	0.54
1:F:214:THR:C	1:F:215:LEU:HD12	2.27	0.54
4:D:152:ASP:OD1	4:D:177:SER:HB3	2.07	0.54
4:I:46:LEU:HG	5:J:104:GLU:HB2	1.89	0.54
4:D:34:TRP:HZ3	4:D:46:LEU:HB2	1.72	0.54
4:D:159:CYS:CB	5:E:195:ARG:HH21	2.19	0.54
4:I:34:TRP:HZ2	4:I:99:LEU:CD2	2.21	0.54
5:J:189:ARG:HH11	5:J:189:ARG:CG	2.20	0.54
2:B:20:SER:HA	2:B:71:THR:HG22	1.90	0.54
5:E:168:VAL:HG22	5:E:170:SER:H	1.72	0.54
4:I:32:LEU:HD13	4:I:34:TRP:CE3	2.42	0.54
2:B:21:ASN:HB3	2:B:70:PHE:HE2	1.73	0.54
4:I:126:SER:C	4:I:127:LYS:HG2	2.28	0.54
4:I:36:ARG:NH2	4:I:46:LEU:HB2	2.23	0.54
5:E:34:ALA:HB3	5:E:98:SER:HB3	1.90	0.54
1:A:187:THR:HA	1:A:204:TRP:O	2.08	0.54
1:A:160:LEU:O	1:A:165:VAL:HG13	2.07	0.54
1:F:234:ARG:HD2	2:G:10:TYR:CZ	2.43	0.53
4:D:156:THR:O	4:D:173:ALA:HB1	2.08	0.53
1:F:103:VAL:HG13	1:F:168:LEU:HD23	1.90	0.53
4:I:47:ILE:HD12	4:I:47:ILE:C	2.29	0.53
1:A:103:VAL:HG11	1:A:168:LEU:HD23	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:VAL:HG13	1:A:168:LEU:CD2	2.39	0.53
4:I:8:PRO:HA	4:I:104:GLY:O	2.08	0.53
5:E:32:HIS:ND1	5:E:97:SER:HB3	2.24	0.53
4:I:11:LEU:HD11	4:I:13:ILE:HG23	1.89	0.53
1:A:191:HIS:CG	1:A:191:HIS:O	2.61	0.53
5:E:224:GLU:HA	5:E:224:GLU:OE1	2.09	0.53
2:G:98:ASP:C	2:G:99:MET:HG2	2.29	0.53
4:I:46:LEU:HD22	4:I:47:ILE:H	1.70	0.53
4:I:118:PRO:O	4:I:196:ASP:HB3	2.09	0.53
1:F:220:ASP:HB2	1:F:256:ARG:NH1	2.23	0.53
5:J:72:ARG:NE	5:J:75:GLY:O	2.42	0.53
4:I:126:SER:O	4:I:127:LYS:HG2	2.08	0.53
2:G:17:ASN:HD21	2:G:97:ARG:HH22	1.55	0.53
1:F:69:THR:O	1:F:73:THR:CG2	2.57	0.53
4:I:43:LEU:O	4:I:44:VAL:HG22	2.09	0.53
5:E:18:LYS:HD2	5:E:117:GLU:OE1	2.09	0.53
5:E:156:HIS:HB3	5:E:217:TYR:HB2	1.91	0.52
1:A:219:ARG:O	1:A:219:ARG:HG3	2.08	0.52
5:E:114:THR:HG22	5:E:116:LEU:HD21	1.91	0.52
5:J:72:ARG:CZ	5:J:75:GLY:O	2.57	0.52
5:J:35:LEU:HD13	5:J:72:ARG:HD2	1.91	0.52
1:A:109:LEU:O	1:A:109:LEU:CD1	2.52	0.52
1:A:52:ILE:CD1	1:A:55:GLU:HG3	2.39	0.52
1:F:230:LEU:CD2	1:F:243:LYS:HE3	2.39	0.52
4:I:48:LEU:C	4:I:48:LEU:HD23	2.30	0.52
1:A:222:GLU:HG3	1:A:223:ASP:H	1.75	0.52
1:F:109:LEU:HD22	1:F:161:GLU:HG2	1.92	0.52
5:E:178:PRO:HB3	5:E:192:LEU:HB2	1.91	0.52
4:D:34:TRP:HZ3	4:D:47:ILE:HA	1.74	0.52
4:I:172:SER:O	5:J:195:ARG:NH2	2.42	0.52
5:J:71:VAL:O	5:J:78:SER:HA	2.10	0.52
1:A:263:HIS:O	1:A:266:LEU:HB2	2.10	0.52
5:J:164:ASN:HD22	5:J:209:HIS:H	1.58	0.52
1:F:171:HIS:O	1:F:174:ASN:N	2.42	0.52
1:A:152:GLU:OE2	4:D:97:ARG:NH2	2.30	0.52
5:J:178:PRO:HB3	5:J:192:LEU:HB2	1.92	0.52
5:E:163:VAL:O	5:E:163:VAL:HG23	2.10	0.51
1:F:188:HIS:HB2	1:F:274:TRP:CH2	2.45	0.51
1:F:189:VAL:CB	1:F:274:TRP:HB2	2.37	0.51
4:I:53:GLU:O	4:I:55:GLU:N	2.42	0.51
1:A:35:ARG:HD3	2:B:53:ASP:OD2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:45:ARG:HH22	4:I:164:ARG:HG3	1.76	0.51
5:J:118:ASP:HB2	5:J:120:LYS:HG2	1.90	0.51
1:A:14:ARG:NH1	1:A:21:ARG:CB	2.70	0.51
5:E:227:GLN:HE21	5:E:228:ASP:N	2.08	0.51
1:F:234:ARG:HD2	2:G:10:TYR:CE1	2.45	0.51
1:F:98:MET:O	1:F:114:ASN:HA	2.11	0.51
4:I:76:ILE:HD12	4:I:76:ILE:N	2.26	0.51
1:F:126:LEU:HD12	1:F:132:SER:O	2.10	0.51
1:A:144:GLN:NE2	1:A:148:GLU:OE2	2.43	0.51
4:D:57:HIS:CD2	4:D:62:ARG:HB2	2.46	0.51
1:A:213:ILE:HG13	1:A:263:HIS:HB2	1.92	0.51
5:J:215:GLN:NE2	5:J:216:PHE:O	2.43	0.51
1:F:182:ALA:O	1:F:184:PRO:HD3	2.10	0.51
4:I:33:GLN:HE21	4:I:34:TRP:N	2.09	0.51
5:E:200:ALA:O	5:E:204:GLN:HB2	2.11	0.51
1:F:69:THR:O	1:F:73:THR:HG22	2.11	0.51
4:D:43:LEU:CD2	5:E:109:GLU:OE2	2.59	0.50
4:I:38:ASN:CB	4:I:88:PHE:HE2	2.25	0.50
1:A:106:ASP:OD2	1:A:108:ARG:HD3	2.11	0.50
1:A:167:TRP:CZ3	1:A:170:ARG:HD3	2.45	0.50
4:I:178:ASN:N	4:I:178:ASN:OD1	2.45	0.50
5:J:65:ASN:HB3	5:J:67:ARG:H	1.76	0.50
5:J:132:PRO:HG3	5:J:143:ALA:HB1	1.93	0.50
5:J:233:VAL:HG12	5:J:234:THR:N	2.27	0.50
1:A:168:LEU:O	1:A:172:LEU:HD12	2.12	0.50
1:F:35:ARG:HD3	2:G:53:ASP:CG	2.32	0.50
5:J:134:GLU:HA	5:J:137:ILE:HG22	1.93	0.50
4:I:180:SER:C	4:I:182:PHE:H	2.14	0.50
5:J:14:LYS:HE3	5:J:16:THR:OG1	2.12	0.50
5:E:50:ILE:HG12	5:E:51:TYR:H	1.77	0.50
2:B:12:ARG:HD2	2:B:13:HIS:CE1	2.47	0.50
3:H:7:SER:O	3:H:8:ILE:HB	2.12	0.50
1:F:63:ASN:ND2	3:H:1:THR:HG22	2.23	0.50
5:J:65:ASN:HB2	5:J:68:PHE:HD2	1.77	0.50
1:A:198:GLU:HG2	1:A:248:VAL:HG22	1.94	0.50
4:D:33:GLN:NE2	4:D:72:SER:CB	2.74	0.50
1:F:62:ARG:HH21	1:F:65:GLN:NE2	2.10	0.50
1:A:40:ALA:HB3	1:A:43:PRO:HA	1.93	0.50
1:A:58:GLU:O	1:A:62:ARG:HB2	2.11	0.50
4:I:34:TRP:NE1	4:I:36:ARG:NE	2.59	0.50
4:I:37:GLN:O	4:I:44:VAL:HA	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:34:ALA:HA	5:J:52:PHE:O	2.12	0.50
1:F:186:LYS:HG3	1:F:186:LYS:O	2.11	0.50
5:E:40:GLN:O	5:E:91:ALA:HB1	2.12	0.50
4:I:33:GLN:O	4:I:34:TRP:HB3	2.12	0.49
1:A:146:LYS:HD3	3:C:8:ILE:CD1	2.42	0.49
4:I:118:PRO:O	4:I:196:ASP:HB2	2.11	0.49
4:D:12:SER:HB3	4:D:110:LEU:HD11	1.92	0.49
5:E:227:GLN:NE2	5:E:227:GLN:CA	2.64	0.49
4:I:176:TRP:CH2	5:J:150:THR:HG21	2.47	0.49
5:J:9:GLN:HG2	5:J:95:CYS:HB3	1.94	0.49
4:D:47:ILE:HD12	4:D:48:LEU:N	2.26	0.49
4:I:8:PRO:HB2	4:I:10:ALA:N	2.27	0.49
5:E:72:ARG:CZ	5:E:75:GLY:O	2.60	0.49
5:E:64:PRO:HG2	5:E:68:PHE:CD2	2.48	0.49
4:D:178:ASN:OD1	4:D:178:ASN:N	2.45	0.49
5:J:172:VAL:HG22	5:J:196:LEU:HD13	1.94	0.49
5:J:65:ASN:HB2	5:J:68:PHE:CD2	2.48	0.49
1:F:20:PRO:HG2	1:F:75:ARG:HG2	1.92	0.49
5:E:124:PRO:HB3	5:E:235:GLN:NE2	2.28	0.49
1:A:238:ASP:OD1	1:A:240:THR:OG1	2.30	0.49
1:F:77:ASN:HD21	3:H:8:ILE:N	1.87	0.49
1:F:55:GLU:O	1:F:60:TRP:CZ3	2.58	0.49
1:F:14:ARG:N	1:F:15:PRO:CD	2.76	0.49
2:G:17:ASN:HD21	2:G:97:ARG:NH2	2.11	0.49
5:E:114:THR:HG22	5:E:116:LEU:CD2	2.42	0.49
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.46	0.49
4:D:50:ARG:HB3	4:D:52:ASN:HD21	1.78	0.49
1:A:234:ARG:NH1	1:A:242:GLN:OE1	2.41	0.49
1:A:14:ARG:HH11	1:A:21:ARG:CB	2.25	0.49
1:A:52:ILE:HD12	1:A:55:GLU:CG	2.43	0.49
1:A:253:GLU:OE1	1:A:256:ARG:HD3	2.12	0.49
1:A:224:GLN:HG3	1:A:227:ASP:HB2	1.94	0.49
4:D:43:LEU:HD13	4:D:45:HIS:CD2	2.47	0.49
4:D:180:SER:C	4:D:182:PHE:H	2.16	0.49
1:A:249:VAL:HG11	1:A:257:TYR:CZ	2.48	0.49
1:A:52:ILE:O	1:A:52:ILE:HG13	2.12	0.49
5:E:14:LYS:NZ	5:E:22:VAL:HG13	2.28	0.49
4:I:34:TRP:HE3	4:I:48:LEU:CB	2.26	0.48
1:A:25:VAL:HG21	2:B:54:LEU:O	2.13	0.48
4:D:34:TRP:CZ2	5:E:104:GLU:HA	2.48	0.48
4:I:152:ASP:OD1	4:I:177:SER:CB	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:71:VAL:O	5:E:72:ARG:HB2	2.12	0.48
1:A:249:VAL:HG11	1:A:257:TYR:CE2	2.49	0.48
2:B:92:ILE:HG13	2:B:92:ILE:O	2.14	0.48
2:B:40:LEU:HD21	2:B:81:ARG:NH1	2.28	0.48
4:D:38:ASN:HB2	4:D:44:VAL:HG13	1.94	0.48
4:I:123:LEU:HD21	4:I:135:LEU:CB	2.42	0.48
5:J:70:ALA:HA	5:J:79:THR:O	2.14	0.48
1:F:104:GLY:HA2	1:F:110:LEU:HD22	1.95	0.48
4:I:46:LEU:HD22	4:I:47:ILE:CA	2.42	0.48
4:D:145:VAL:HA	4:D:191:SER:CB	2.40	0.48
1:F:234:ARG:HD3	2:G:10:TYR:CE2	2.49	0.48
1:A:227:ASP:O	1:A:247:VAL:HG23	2.14	0.48
1:A:52:ILE:HD12	1:A:55:GLU:HG3	1.94	0.48
4:D:27:THR:OG1	4:D:28:SER:N	2.46	0.48
4:I:5:GLU:CG	4:I:6:GLU:H	2.25	0.48
2:B:37:VAL:HG22	2:B:82:VAL:HG22	1.96	0.48
4:D:111:PRO:HG3	4:D:160:VAL:HG21	1.96	0.48
1:A:106:ASP:OD1	1:A:107:GLY:N	2.47	0.48
5:J:51:TYR:CD1	5:J:51:TYR:C	2.87	0.48
4:D:46:LEU:O	4:D:47:ILE:CG2	2.62	0.48
4:I:41:ARG:CG	4:I:42:GLY:N	2.76	0.48
4:D:34:TRP:CZ3	4:D:47:ILE:CA	2.97	0.48
1:A:126:LEU:HD11	1:A:130:LEU:HA	1.96	0.48
5:E:74:GLU:O	5:E:74:GLU:OE2	2.31	0.48
2:G:9:VAL:HG11	2:G:93:VAL:HG12	1.96	0.47
1:F:52:ILE:C	1:F:54:GLN:N	2.67	0.47
3:C:5:ILE:CB	3:C:6:PRO:HD2	2.44	0.47
1:F:80:ILE:CD1	3:H:8:ILE:HA	2.39	0.47
1:F:22:PHE:HB3	1:F:71:THR:HG23	1.96	0.47
1:F:85:TYR:O	1:F:87:GLN:N	2.47	0.47
4:D:36:ARG:HB3	4:D:44:VAL:HG12	1.97	0.47
1:F:106:ASP:OD1	1:F:108:ARG:N	2.35	0.47
4:D:43:LEU:HD13	4:D:45:HIS:HD2	1.77	0.47
5:J:39:ARG:HB3	5:J:49:LEU:HD11	1.96	0.47
4:D:8:PRO:HD2	4:D:104:GLY:O	2.14	0.47
1:F:106:ASP:OD1	1:F:107:GLY:N	2.47	0.47
4:D:47:ILE:C	4:D:47:ILE:HD12	2.35	0.47
1:F:219:ARG:O	1:F:222:GLU:N	2.46	0.47
4:I:5:GLU:CG	4:I:6:GLU:N	2.77	0.47
4:I:5:GLU:HG3	4:I:6:GLU:N	2.28	0.47
5:J:141:GLN:O	5:J:200:ALA:CB	2.60	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:TRP:CZ3	1:A:259:CYS:HB2	2.49	0.47
1:F:167:TRP:O	1:F:168:LEU:C	2.53	0.47
1:F:58:GLU:N	1:F:58:GLU:OE1	2.30	0.47
5:E:179:LEU:HG	5:E:180:LYS:H	1.80	0.47
4:I:7:ASP:HB3	4:I:103:SER:CB	2.34	0.47
1:F:130:LEU:HD12	1:F:130:LEU:N	2.19	0.47
5:E:28:PRO:HB2	5:E:97:SER:OG	2.14	0.47
1:F:230:LEU:HD21	1:F:243:LYS:HE3	1.97	0.47
4:D:97:ARG:HG2	5:E:101:GLY:C	2.35	0.47
4:I:64:THR:HB	4:I:73:SER:HB2	1.97	0.47
1:A:275:GLU:CB	1:A:276:PRO:HD3	2.45	0.47
4:D:133:VAL:HA	4:D:175:ALA:O	2.15	0.47
4:D:43:LEU:HD11	4:D:45:HIS:CD2	2.49	0.47
5:E:134:GLU:HA	5:E:137:ILE:HG12	1.95	0.46
1:F:129:ASP:OD1	1:F:132:SER:OG	2.33	0.46
1:A:103:VAL:HA	1:A:108:ARG:O	2.15	0.46
5:E:141:GLN:O	5:E:200:ALA:CB	2.63	0.46
1:A:146:LYS:HE3	1:A:146:LYS:HB2	1.74	0.46
4:I:47:ILE:CD1	4:I:63:VAL:HG21	2.29	0.46
5:J:72:ARG:N	5:J:73:PRO:HD3	2.30	0.46
4:I:123:LEU:CD2	4:I:135:LEU:HB2	2.45	0.46
1:A:38:SER:O	1:A:43:PRO:HG3	2.15	0.46
4:I:125:ASP:HB2	4:I:128:SER:HB3	1.97	0.46
4:I:32:LEU:C	4:I:32:LEU:HD12	2.36	0.46
1:F:114:ASN:ND2	1:F:156:LEU:HD21	2.20	0.46
5:J:141:GLN:CG	5:J:141:GLN:O	2.63	0.46
5:J:16:THR:HG22	5:J:17:GLU:N	2.30	0.46
5:E:50:ILE:HD13	5:E:52:PHE:CE2	2.50	0.46
1:F:169:ARG:HH11	1:F:169:ARG:HB3	1.80	0.46
1:F:80:ILE:O	1:F:83:ARG:HB2	2.16	0.46
5:E:225:TRP:CD2	5:E:225:TRP:O	2.69	0.46
5:E:164:ASN:CG	5:E:164:ASN:O	2.53	0.46
5:E:49:LEU:HA	5:E:62:GLY:HA3	1.98	0.46
5:J:85:THR:CG2	5:J:115:VAL:CG2	2.94	0.46
1:F:204:TRP:CH2	2:G:99:MET:HA	2.49	0.46
1:F:11:ALA:HA	1:F:21:ARG:O	2.16	0.46
4:D:9:GLN:HA	4:D:9:GLN:OE1	2.15	0.46
5:E:85:THR:HG23	5:E:115:VAL:HG11	1.97	0.46
5:E:163:VAL:O	5:E:163:VAL:CG2	2.64	0.46
1:F:84:TYR:OH	3:H:8:ILE:CG2	2.63	0.45
4:D:159:CYS:HB3	5:E:195:ARG:NH2	2.23	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:15:VAL:HB	5:J:218:GLY:O	2.16	0.45
4:I:34:TRP:HE3	4:I:48:LEU:CG	2.29	0.45
4:I:52:ASN:C	4:I:52:ASN:ND2	2.69	0.45
5:J:87:ARG:HA	5:J:115:VAL:HB	1.98	0.45
1:A:235:PRO:O	2:B:10:TYR:OH	2.27	0.45
4:D:90:ALA:HB2	4:D:101:PHE:CE1	2.51	0.45
4:I:121:TYR:O	4:I:134:CYS:HA	2.16	0.45
4:D:99:LEU:HA	4:D:99:LEU:HD12	1.85	0.45
5:E:209:HIS:C	5:E:210:PHE:CD1	2.90	0.45
4:D:182:PHE:HE1	4:D:187:ALA:HA	1.81	0.45
1:A:52:ILE:C	1:A:54:GLN:H	2.19	0.45
1:A:183:ASP:O	1:A:263:HIS:CE1	2.70	0.45
1:F:72:GLN:OE1	1:F:75:ARG:NH1	2.49	0.45
4:I:99:LEU:HD22	5:J:105:LEU:CD1	2.44	0.45
1:F:113:HIS:ND1	1:F:115:GLN:NE2	2.64	0.45
1:A:273:ARG:HD3	1:A:273:ARG:H	1.80	0.45
4:I:159:CYS:SG	4:I:160:VAL:N	2.89	0.45
2:G:20:SER:CA	2:G:71:THR:HG22	2.44	0.45
4:D:25:TYR:HB2	4:D:91:THR:HG21	1.99	0.45
4:I:76:ILE:N	4:I:76:ILE:CD1	2.80	0.45
1:A:1:GLY:HA2	1:A:105:PRO:HA	1.98	0.45
1:A:13:SER:HB2	1:A:93:HIS:H	1.81	0.45
5:J:124:PRO:CG	5:J:235:GLN:HE22	2.29	0.45
5:E:125:PRO:HB3	5:E:152:PHE:HB3	1.99	0.45
5:E:139:HIS:O	5:E:139:HIS:CD2	2.70	0.45
5:E:147:CYS:O	5:E:193:SER:HA	2.17	0.45
4:I:34:TRP:CB	4:I:48:LEU:HA	2.46	0.45
5:J:159:LEU:C	5:J:159:LEU:HD23	2.38	0.45
4:I:136:PHE:HB2	4:I:188:PHE:CZ	2.52	0.45
1:A:63:ASN:OD1	3:C:1:THR:HB	2.16	0.45
5:E:9:GLN:C	5:E:10:THR:HG22	2.37	0.45
1:F:14:ARG:NH1	1:F:21:ARG:HD2	2.32	0.45
5:J:209:HIS:CD2	5:J:242:TRP:CD1	3.05	0.45
5:J:119:LEU:HD12	5:J:119:LEU:HA	1.80	0.45
4:D:134:CYS:HB2	4:D:175:ALA:HB3	1.98	0.45
5:E:210:PHE:N	5:E:210:PHE:CD1	2.85	0.45
5:J:85:THR:HG22	5:J:86:GLU:N	2.31	0.45
5:E:127:VAL:HG12	5:E:239:ALA:CB	2.47	0.45
2:B:45:ARG:NH2	4:I:164:ARG:HG3	2.32	0.45
4:D:21:MET:HG2	4:D:105:THR:HG21	1.98	0.45
4:I:49:ILE:HD13	4:I:65:LEU:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:137:ILE:O	5:E:141:GLN:HA	2.17	0.44
1:F:13:SER:HB3	1:F:78:LEU:HD13	2.00	0.44
1:F:254:GLU:O	1:F:257:TYR:HB2	2.17	0.44
1:A:171:HIS:O	1:A:172:LEU:C	2.56	0.44
5:J:159:LEU:HD21	5:J:161:TRP:CD1	2.52	0.44
2:G:37:VAL:HG11	2:G:66:TYR:CD2	2.53	0.44
2:B:30:PHE:HD2	2:B:30:PHE:H	1.65	0.44
4:I:36:ARG:HG3	4:I:45:HIS:O	2.17	0.44
1:A:11:ALA:HA	1:A:21:ARG:O	2.17	0.44
5:E:225:TRP:H	5:E:225:TRP:HE3	1.66	0.44
4:I:18:ASN:CG	4:I:77:THR:HG22	2.38	0.44
4:D:35:TYR:O	4:D:46:LEU:HA	2.18	0.44
5:E:205:ASP:HA	5:E:206:PRO:HD3	1.74	0.44
4:D:197:THR:CG2	4:D:197:THR:O	2.65	0.44
4:D:43:LEU:HG	5:E:109:GLU:OE2	2.17	0.44
4:D:60:ARG:HH22	4:D:83:ASP:CG	2.21	0.44
5:E:139:HIS:HD2	5:E:139:HIS:O	2.01	0.44
5:J:133:SER:HB3	5:J:136:GLU:H	1.83	0.44
4:I:69:LYS:O	4:I:70:LYS:C	2.55	0.44
4:D:118:PRO:O	4:D:196:ASP:CB	2.65	0.44
5:J:87:ARG:HG2	5:J:115:VAL:O	2.17	0.44
5:E:50:ILE:HG12	5:E:51:TYR:N	2.32	0.44
1:A:19:GLU:O	1:A:20:PRO:O	2.36	0.44
5:E:225:TRP:HB2	5:E:231:LYS:HG3	2.00	0.44
5:J:37:TRP:HB2	5:J:50:ILE:HG22	1.99	0.44
1:F:130:LEU:CD1	1:F:130:LEU:H	2.11	0.44
1:F:33:PHE:C	1:F:48:ARG:HB2	2.38	0.44
5:E:72:ARG:NE	5:E:75:GLY:O	2.51	0.44
5:J:163:VAL:CG1	5:J:163:VAL:O	2.66	0.44
1:F:5:MET:HB2	1:F:168:LEU:HD13	1.99	0.44
1:A:1:GLY:HA2	1:A:105:PRO:CA	2.48	0.44
1:A:19:GLU:C	1:A:20:PRO:O	2.55	0.44
5:J:185:LEU:HD13	5:J:187:ASP:O	2.17	0.44
1:F:187:THR:HA	1:F:204:TRP:O	2.17	0.44
1:A:93:HIS:CD2	1:A:119:ASP:OD2	2.69	0.44
4:I:48:LEU:HD23	4:I:49:ILE:N	2.32	0.43
1:A:48:ARG:HD2	1:A:48:ARG:HA	1.80	0.43
1:A:218:GLN:HB2	1:A:221:GLY:HA2	2.00	0.43
2:G:38:ASP:HB2	2:G:81:ARG:HB3	1.98	0.43
5:E:24:LEU:HB2	5:E:80:LEU:HB3	2.00	0.43
1:F:263:HIS:HB3	1:F:266:LEU:HG	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:ARG:HH12	1:A:21:ARG:HD2	1.82	0.43
4:I:34:TRP:HH2	5:J:103:GLY:CA	2.29	0.43
5:E:64:PRO:HG2	5:E:68:PHE:CE2	2.53	0.43
5:E:124:PRO:HB3	5:E:235:GLN:HE21	1.83	0.43
4:D:90:ALA:HB2	4:D:101:PHE:CD1	2.53	0.43
1:A:67:PHE:O	1:A:71:THR:N	2.44	0.43
4:D:156:THR:HG21	5:E:195:ARG:NH2	2.33	0.43
5:E:83:GLN:O	5:E:84:ARG:C	2.57	0.43
2:G:25:CYS:HB2	2:G:39:LEU:HD11	2.01	0.43
5:E:129:VAL:HG11	5:E:240:GLU:O	2.19	0.43
4:I:181:ASP:N	4:I:181:ASP:OD2	2.31	0.43
1:F:45:THR:HG22	1:F:60:TRP:HD1	1.82	0.43
5:J:205:ASP:HA	5:J:206:PRO:HD3	1.93	0.43
1:A:236:ALA:HB1	2:B:12:ARG:HG3	2.00	0.43
5:E:132:PRO:HD2	5:E:203:TRP:CZ2	2.54	0.43
4:I:36:ARG:NH1	5:J:105:LEU:H	2.04	0.43
1:A:171:HIS:O	1:A:173:GLU:N	2.52	0.43
4:D:195:GLU:N	4:D:195:GLU:CD	2.68	0.43
4:I:84:THR:HG22	4:I:108:THR:HA	2.00	0.43
5:E:118:ASP:OD2	5:E:120:LYS:HE2	2.18	0.43
1:F:185:PRO:HD2	1:F:266:LEU:HD21	2.00	0.43
1:F:183:ASP:HB2	1:F:209:TYR:HB3	2.00	0.43
1:A:188:HIS:O	1:A:204:TRP:HB2	2.19	0.43
4:D:48:LEU:C	4:D:48:LEU:HD23	2.39	0.43
1:F:33:PHE:HD1	1:F:52:ILE:HD13	1.84	0.43
5:J:218:GLY:O	5:J:219:LEU:HD23	2.18	0.43
4:D:147:GLN:O	4:D:190:ASN:ND2	2.52	0.43
5:J:124:PRO:CB	5:J:235:GLN:NE2	2.81	0.43
5:E:87:ARG:HH11	5:E:117:GLU:HG2	1.84	0.43
4:D:118:PRO:CG	4:D:194:PRO:HB2	2.49	0.43
1:A:218:GLN:HA	1:A:222:GLU:O	2.19	0.43
5:J:152:PHE:HE1	5:J:155:ASP:HA	1.83	0.43
5:J:74:GLU:CA	5:J:74:GLU:OE2	2.67	0.43
4:D:66:ASP:OD2	4:D:69:LYS:HD2	2.18	0.43
5:E:87:ARG:HG2	5:E:115:VAL:O	2.19	0.43
5:E:134:GLU:O	5:E:137:ILE:HG13	2.19	0.43
1:A:192:HIS:HA	1:A:193:PRO:HD2	1.85	0.43
4:D:7:ASP:HA	4:D:103:SER:HB3	2.01	0.43
5:E:209:HIS:C	5:E:210:PHE:HD1	2.22	0.42
4:D:39:SER:O	4:D:40:GLY:O	2.37	0.42
4:D:32:LEU:HD12	4:D:50:ARG:NH1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:177:SER:HB2	4:D:182:PHE:CD2	2.54	0.42
1:A:222:GLU:HG3	1:A:223:ASP:N	2.33	0.42
1:F:235:PRO:O	2:G:10:TYR:OH	2.28	0.42
1:F:51:TRP:CE2	1:F:179:LEU:HD11	2.55	0.42
4:I:136:PHE:HB2	4:I:188:PHE:CE2	2.55	0.42
5:E:7:VAL:O	5:E:108:GLY:HA2	2.19	0.42
2:G:31:HIS:CD2	2:G:62:PHE:CE2	3.08	0.42
4:I:46:LEU:HD13	4:I:47:ILE:N	2.34	0.42
5:E:51:TYR:CD1	5:E:51:TYR:C	2.93	0.42
4:I:34:TRP:CZ2	4:I:99:LEU:CD2	2.99	0.42
4:I:8:PRO:HB2	4:I:9:GLN:O	2.16	0.42
5:E:67:ARG:CD	5:E:84:ARG:HE	2.31	0.42
5:J:175:ASP:OD1	5:J:195:ARG:NH1	2.53	0.42
1:F:12:MET:HE3	1:F:21:ARG:HD3	2.01	0.42
4:I:163:MET:HE1	5:J:142:LYS:HE2	2.01	0.42
5:E:221:GLU:HG3	5:E:221:GLU:H	1.53	0.42
1:F:51:TRP:CZ3	1:F:52:ILE:HB	2.54	0.42
1:F:45:THR:HG22	1:F:60:TRP:CD1	2.55	0.42
4:D:25:TYR:HB3	4:D:91:THR:CG2	2.47	0.42
1:A:248:VAL:O	1:A:249:VAL:HG13	2.20	0.42
1:A:19:GLU:O	1:A:20:PRO:C	2.58	0.42
5:E:41:SER:O	5:E:42:LEU:C	2.58	0.42
4:I:34:TRP:CE3	4:I:48:LEU:CD1	2.99	0.42
2:B:20:SER:CA	2:B:71:THR:HG22	2.49	0.42
1:F:126:LEU:HD22	1:F:156:LEU:HD23	2.02	0.42
1:A:27:TYR:HA	1:A:32:GLN:HA	2.02	0.42
1:A:217:TRP:CE3	1:A:217:TRP:HA	2.54	0.41
4:D:46:LEU:H	4:D:46:LEU:HG	1.39	0.41
1:F:219:ARG:CG	1:F:219:ARG:HH11	2.22	0.41
5:E:9:GLN:HG3	5:E:95:CYS:HB3	2.02	0.41
5:E:34:ALA:HA	5:E:52:PHE:O	2.20	0.41
5:J:9:GLN:HA	5:J:26:CYS:HA	2.02	0.41
1:F:187:THR:O	1:F:188:HIS:HB3	2.20	0.41
1:A:109:LEU:C	1:A:109:LEU:CD1	2.89	0.41
4:D:60:ARG:HD2	4:D:80:ARG:NH2	2.35	0.41
1:A:126:LEU:HD12	1:A:127:ASN:H	1.85	0.41
4:D:152:ASP:HB2	4:D:179:LYS:HE3	2.02	0.41
1:F:133:TRP:HB2	1:F:144:GLN:HE22	1.83	0.41
5:J:142:LYS:HD2	5:J:197:ARG:HH21	1.85	0.41
1:A:28:VAL:HG11	1:A:179:LEU:HD13	2.03	0.41
1:A:77:ASN:HD22	1:A:80:ILE:HD12	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:173:GLU:HG2	1:F:174:ASN:OD1	2.19	0.41
3:C:7:SER:O	3:C:8:ILE:HB	2.20	0.41
4:I:148:SER:OG	4:I:154:TYR:HA	2.20	0.41
5:J:159:LEU:O	5:J:159:LEU:HD23	2.20	0.41
1:F:260:HIS:CE1	1:F:271:THR:HB	2.56	0.41
5:E:32:HIS:CE1	5:E:106:PHE:HD2	2.32	0.41
1:F:114:ASN:CB	1:F:156:LEU:HD21	2.50	0.41
1:A:106:ASP:OD2	1:A:108:ARG:CG	2.68	0.41
1:F:14:ARG:N	1:F:15:PRO:HD3	2.36	0.41
2:G:97:ARG:H	2:G:97:ARG:HG3	1.62	0.41
2:G:17:ASN:ND2	2:G:97:ARG:HH12	2.18	0.41
2:B:42:ASN:OD1	2:B:77:GLU:HG3	2.21	0.41
4:I:36:ARG:HB3	4:I:44:VAL:HG12	2.02	0.41
1:A:25:VAL:CG1	1:A:32:GLN:OE1	2.69	0.41
2:G:58:LYS:C	2:G:59:ASP:O	2.58	0.41
4:D:34:TRP:CH2	4:D:46:LEU:HB2	2.54	0.41
1:A:167:TRP:NE1	3:C:1:THR:HG23	2.36	0.41
1:A:21:ARG:HG3	1:A:39:ASP:OD1	2.21	0.41
5:J:124:PRO:CB	5:J:235:GLN:HE22	2.33	0.41
5:J:85:THR:HG21	5:J:115:VAL:CG2	2.51	0.41
5:J:62:GLY:O	5:J:63:LEU:C	2.59	0.41
5:J:179:LEU:HG	5:J:180:LYS:N	2.35	0.41
5:E:14:LYS:O	5:E:113:LEU:HA	2.21	0.41
1:F:98:MET:HE1	2:G:58:LYS:HA	2.02	0.41
4:D:155:ILE:HG22	4:D:156:THR:O	2.21	0.41
4:D:154:TYR:CG	4:D:155:ILE:N	2.88	0.41
2:B:70:PHE:CD2	2:B:70:PHE:O	2.74	0.41
5:J:125:PRO:HB3	5:J:152:PHE:HB3	2.03	0.41
4:D:39:SER:O	4:D:40:GLY:C	2.59	0.41
4:D:136:PHE:HB2	4:D:188:PHE:CZ	2.56	0.41
4:I:33:GLN:HE21	4:I:34:TRP:H	1.67	0.41
4:I:52:ASN:ND2	4:I:53:GLU:HG3	2.35	0.41
1:F:7:TYR:HB2	1:F:99:TYR:CZ	2.55	0.41
2:G:12:ARG:HD2	2:G:13:HIS:NE2	2.36	0.41
2:B:11:SER:HB2	2:B:21:ASN:HD21	1.82	0.40
4:I:118:PRO:HG2	4:I:194:PRO:HB2	2.03	0.40
4:I:88:PHE:HD1	4:I:103:SER:O	2.04	0.40
5:J:231:LYS:HA	5:J:232:PRO:HD3	1.78	0.40
1:F:72:GLN:HA	1:F:75:ARG:NH1	2.36	0.40
1:A:98:MET:HG2	1:A:115:GLN:HB3	2.03	0.40
5:J:147:CYS:O	5:J:193:SER:HA	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:232:GLU:OE2	2:G:6:LYS:HD2	2.21	0.40
1:A:234:ARG:HE	2:B:8:GLN:NE2	2.20	0.40
4:I:156:THR:O	4:I:173:ALA:HB1	2.21	0.40
1:F:116:TYR:HB2	1:F:124:ILE:HG22	2.03	0.40
2:G:94:LYS:HG2	2:G:94:LYS:H	1.52	0.40
1:A:167:TRP:O	1:A:168:LEU:C	2.58	0.40
4:I:123:LEU:HD12	5:J:132:PRO:HA	2.03	0.40
1:F:266:LEU:HD13	1:F:270:LEU:HD23	2.04	0.40
4:D:166:MET:O	4:D:167:ASP:C	2.59	0.40
4:I:58:SER:O	4:I:59:GLY:C	2.58	0.40
4:D:49:ILE:HD11	4:D:53:GLU:O	2.21	0.40
1:A:13:SER:O	1:A:14:ARG:HG3	2.21	0.40
1:F:52:ILE:O	1:F:54:GLN:N	2.54	0.40
2:B:31:HIS:CD2	2:B:62:PHE:CE2	3.08	0.40
2:G:42:ASN:OD1	2:G:77:GLU:HG3	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	274/276 (99%)	245 (89%)	25 (9%)	4 (2%)	13	50
1	F	273/276 (99%)	239 (88%)	26 (10%)	8 (3%)	6	29
2	B	97/99 (98%)	91 (94%)	6 (6%)	0	100	100
2	G	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	19	61
3	C	6/8 (75%)	6 (100%)	0	0	100	100
3	H	6/8 (75%)	6 (100%)	0	0	100	100
4	D	190/195 (97%)	166 (87%)	17 (9%)	7 (4%)	4	23
4	I	192/195 (98%)	163 (85%)	23 (12%)	6 (3%)	5	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
5	E	238/242 (98%)	213 (90%)	22 (9%)	3 (1%)	15 53
5	J	239/242 (99%)	219 (92%)	19 (8%)	1 (0%)	39 80
All	All	1612/1640 (98%)	1436 (89%)	146 (9%)	30 (2%)	10 43

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	9	GLN
4	D	28	SER
4	D	42	GLY
4	D	197	THR
1	F	130	LEU
4	I	28	SER
4	I	97	ARG
4	D	40	GLY
4	D	130	ASP
5	E	221	GLU
1	F	220	ASP
1	F	264	GLU
4	I	54	ARG
4	I	131	LYS
5	E	42	LEU
1	F	172	LEU
4	I	42	GLY
1	F	86	ASN
1	F	267	PRO
4	I	103	SER
5	J	42	LEU
1	A	172	LEU
1	A	269	PRO
5	E	18	LYS
1	F	20	PRO
2	G	85	VAL
4	D	97	ARG
1	A	20	PRO
1	F	162	GLY
1	A	162	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	234/234 (100%)	194 (83%)	40 (17%)	2	12
1	F	233/234 (100%)	187 (80%)	46 (20%)	1	9
2	B	94/94 (100%)	82 (87%)	12 (13%)	5	23
2	G	94/94 (100%)	81 (86%)	13 (14%)	4	20
3	C	7/7 (100%)	7 (100%)	0	100	100
3	H	7/7 (100%)	6 (86%)	1 (14%)	4	19
4	D	172/174 (99%)	131 (76%)	41 (24%)	1	4
4	I	173/174 (99%)	138 (80%)	35 (20%)	1	8
5	E	203/204 (100%)	168 (83%)	35 (17%)	2	12
5	J	204/204 (100%)	173 (85%)	31 (15%)	3	16
All	All	1421/1426 (100%)	1167 (82%)	254 (18%)	2	11

All (254) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	12	MET
1	A	19	GLU
1	A	31	THR
1	A	38	SER
1	A	39	ASP
1	A	46	GLU
1	A	47	PRO
1	A	62	ARG
1	A	98	MET
1	A	101	CYS
1	A	106	ASP
1	A	108	ARG
1	A	109	LEU
1	A	115	GLN
1	A	124	ILE

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Mol	Chain	Res	Type
1	A	128	GLU
1	A	131	SER
1	A	156	LEU
1	A	164	CYS
1	A	169	ARG
1	A	173	GLU
1	A	191	HIS
1	A	201	LEU
1	A	203	CYS
1	A	206	LEU
1	A	213	ILE
1	A	214	THR
1	A	216	THR
1	A	218	GLN
1	A	219	ARG
1	A	230	LEU
1	A	234	ARG
1	A	242	GLN
1	A	243	LYS
1	A	262	GLN
1	A	268	LYS
1	A	273	ARG
1	A	274	TRP
1	A	275	GLU
2	B	3	ARG
2	B	9	VAL
2	B	17	ASN
2	B	19	LYS
2	B	28	SER
2	B	30	PHE
2	B	39	LEU
2	B	44	GLU
2	B	49	VAL
2	B	70	PHE
2	B	77	GLU
2	B	99	MET
4	D	7	ASP
4	D	13	ILE
4	D	17	GLU
4	D	24	SER
4	D	27	THR
4	D	29	ILE

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Mol	Chain	Res	Type
4	D	30	ASN
4	D	32	LEU
4	D	36	ARG
4	D	39	SER
4	D	43	LEU
4	D	44	VAL
4	D	45	HIS
4	D	46	LEU
4	D	47	ILE
4	D	52	ASN
4	D	53	GLU
4	D	54	ARG
4	D	62	ARG
4	D	75	LEU
4	D	76	ILE
4	D	77	THR
4	D	80	ARG
4	D	99	LEU
4	D	108	THR
4	D	113	ILE
4	D	123	LEU
4	D	132	SER
4	D	142	GLN
4	D	145	VAL
4	D	147	GLN
4	D	149	LYS
4	D	158	LYS
4	D	167	ASP
4	D	171	ASN
4	D	178	ASN
4	D	181	ASP
4	D	186	ASN
4	D	195	GLU
4	D	197	THR
4	D	198	PHE
5	E	8	SER
5	E	10	THR
5	E	14	LYS
5	E	16	THR
5	E	26	CYS
5	E	33	THR
5	E	42	LEU

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Mol	Chain	Res	Type
5	E	47	GLU
5	E	51	TYR
5	E	65	ASN
5	E	74	GLU
5	E	85	THR
5	E	99	LEU
5	E	113	LEU
5	E	126	GLU
5	E	133	SER
5	E	158	GLU
5	E	166	LYS
5	E	167	GLU
5	E	173	CYS
5	E	175	ASP
5	E	177	GLN
5	E	192	LEU
5	E	195	ARG
5	E	196	LEU
5	E	197	ARG
5	E	199	SER
5	E	207	ARG
5	E	209	HIS
5	E	219	LEU
5	E	221	GLU
5	E	225	TRP
5	E	227	GLN
5	E	229	ARG
5	E	244	ARG
1	F	12	MET
1	F	19	GLU
1	F	23	ILE
1	F	31	THR
1	F	38	SER
1	F	39	ASP
1	F	46	GLU
1	F	62	ARG
1	F	65	GLN
1	F	68	LYS
1	F	73	THR
1	F	79	ARG
1	F	101	CYS
1	F	102	ASP

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Mol	Chain	Res	Type
1	F	106	ASP
1	F	115	GLN
1	F	121	LYS
1	F	130	LEU
1	F	131	SER
1	F	132	SER
1	F	137	ASP
1	F	142	ILE
1	F	144	GLN
1	F	145	ARG
1	F	160	LEU
1	F	163	LEU
1	F	164	CYS
1	F	170	ARG
1	F	178	THR
1	F	181	ARG
1	F	186	LYS
1	F	190	THR
1	F	203	CYS
1	F	214	THR
1	F	218	GLN
1	F	219	ARG
1	F	223	ASP
1	F	238	ASP
1	F	244	TRP
1	F	251	SER
1	F	262	GLN
1	F	268	LYS
1	F	271	THR
1	F	272	LEU
1	F	274	TRP
1	F	275	GLU
2	G	9	VAL
2	G	27	VAL
2	G	28	SER
2	G	39	LEU
2	G	58	LYS
2	G	70	PHE
2	G	75	LYS
2	G	77	GLU
2	G	88	SER
2	G	94	LYS

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Mol	Chain	Res	Type
2	G	95	TRP
2	G	97	ARG
2	G	99	MET
3	H	5	ILE
4	I	5	GLU
4	I	7	ASP
4	I	21	MET
4	I	22	ASN
4	I	24	SER
4	I	27	THR
4	I	29	ILE
4	I	30	ASN
4	I	34	TRP
4	I	36	ARG
4	I	43	LEU
4	I	44	VAL
4	I	46	LEU
4	I	47	ILE
4	I	52	ASN
4	I	62	ARG
4	I	63	VAL
4	I	67	THR
4	I	69	LYS
4	I	77	THR
4	I	95	SER
4	I	97	ARG
4	I	99	LEU
4	I	108	THR
4	I	117	ASP
4	I	125	ASP
4	I	127	LYS
4	I	132	SER
4	I	142	GLN
4	I	158	LYS
4	I	178	ASN
4	I	179	LYS
4	I	181	ASP
4	I	186	ASN
4	I	195	GLU
5	J	8	SER
5	J	10	THR
5	J	26	CYS

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Mol	Chain	Res	Type
5	J	33	THR
5	J	51	TYR
5	J	55	THR
5	J	65	ASN
5	J	74	GLU
5	J	98	SER
5	J	104	GLU
5	J	121	ASN
5	J	126	GLU
5	J	133	SER
5	J	137	ILE
5	J	142	LYS
5	J	150	THR
5	J	155	ASP
5	J	157	VAL
5	J	158	GLU
5	J	159	LEU
5	J	166	LYS
5	J	167	GLU
5	J	173	CYS
5	J	175	ASP
5	J	185	LEU
5	J	187	ASP
5	J	189	ARG
5	J	195	ARG
5	J	207	ARG
5	J	225	TRP
5	J	235	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	77	ASN
1	A	93	HIS
1	A	114	ASN
1	A	262	GLN
2	B	8	GLN
2	B	13	HIS
2	B	17	ASN
2	B	31	HIS
4	D	14	GLN

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Mol	Chain	Res	Type
4	D	30	ASN
4	D	33	GLN
4	D	38	ASN
4	D	45	HIS
4	D	52	ASN
4	D	171	ASN
4	D	189	ASN
5	E	53	GLN
5	E	139	HIS
5	E	169	HIS
5	E	177	GLN
5	E	215	GLN
5	E	227	GLN
5	E	235	GLN
1	F	32	GLN
1	F	65	GLN
1	F	77	ASN
1	F	96	GLN
1	F	114	ASN
1	F	115	GLN
1	F	144	GLN
1	F	155	GLN
1	F	171	HIS
1	F	260	HIS
1	F	262	GLN
2	G	8	GLN
2	G	17	ASN
4	I	14	GLN
4	I	30	ASN
4	I	33	GLN
4	I	52	ASN
4	I	171	ASN
4	I	186	ASN
4	I	189	ASN
5	J	13	ASN
5	J	32	HIS
5	J	53	GLN
5	J	164	ASN
5	J	182	GLN
5	J	209	HIS
5	J	235	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	276/276 (100%)	0.42	14 (5%) 32 12	35, 59, 113, 130	0
1	F	275/276 (99%)	0.35	8 (2%) 55 26	37, 59, 103, 124	0
2	B	99/99 (100%)	0.04	0 100 100	45, 57, 76, 82	0
2	G	99/99 (100%)	0.22	3 (3%) 54 25	49, 59, 79, 82	0
3	C	8/8 (100%)	0.53	0 100 100	48, 50, 58, 58	0
3	H	8/8 (100%)	0.69	0 100 100	45, 46, 53, 53	0
4	D	192/195 (98%)	0.58	20 (10%) 8 3	39, 63, 112, 124	0
4	I	194/195 (99%)	0.70	28 (14%) 3 1	39, 65, 113, 122	0
5	E	240/242 (99%)	0.40	11 (4%) 36 14	37, 69, 100, 129	0
5	J	241/242 (99%)	0.35	10 (4%) 41 16	37, 65, 95, 122	0
All	All	1632/1640 (99%)	0.41	94 (5%) 26 10	35, 61, 107, 130	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	1	GLY	5.0
1	A	225	THR	4.6
4	D	154	TYR	4.5
4	I	117	ASP	4.4
4	I	130	ASP	4.3
4	I	191	SER	4.3
1	A	194	VAL	4.1
4	D	183	ALA	3.9
4	I	183	ALA	3.8
5	J	225	TRP	3.7
4	D	192	ILE	3.7
5	J	224	GLU	3.5
4	I	190	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
4	I	193	ILE	3.5
1	A	217	TRP	3.5
4	I	154	TYR	3.4
4	I	180	SER	3.3
1	A	204	TRP	3.2
4	I	192	ILE	3.2
5	E	184	ALA	3.2
5	E	133	SER	3.1
1	A	195	SER	3.1
4	I	185	ALA	3.1
5	E	168	VAL	3.1
4	I	121	TYR	3.0
5	E	225	TRP	3.0
4	D	129	SER	3.0
5	J	168	VAL	2.9
5	J	208	ASN	2.9
4	D	8	PRO	2.9
5	E	169	HIS	2.9
4	D	134	CYS	2.9
4	D	182	PHE	2.8
5	E	196	LEU	2.8
4	I	124	ARG	2.8
5	E	129	VAL	2.8
4	I	134	CYS	2.7
5	J	184	ALA	2.7
1	A	253	GLU	2.7
2	G	75	LYS	2.7
1	A	223	ASP	2.6
4	I	181	ASP	2.6
5	J	210	PHE	2.6
4	D	179	LYS	2.6
1	F	222	GLU	2.6
4	I	151	SER	2.6
4	D	152	ASP	2.5
1	A	197	HIS	2.5
4	I	120	VAL	2.5
1	A	221	GLY	2.5
4	I	147	GLN	2.5
1	F	249	VAL	2.5
4	I	132	SER	2.4
5	J	242	TRP	2.4
1	A	219	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
4	D	149	LYS	2.4
1	F	273	ARG	2.4
4	I	138	ASP	2.4
5	E	243	GLY	2.4
5	J	133	SER	2.4
4	I	114	GLN	2.3
4	D	147	GLN	2.3
4	I	182	PHE	2.3
5	E	206	PRO	2.3
4	I	7	ASP	2.3
1	F	225	THR	2.3
4	I	176	TRP	2.3
1	A	259	CYS	2.3
4	D	132	SER	2.3
4	D	191	SER	2.3
1	A	244	TRP	2.3
4	I	145	VAL	2.3
2	G	99	MET	2.3
1	F	2	SER	2.2
1	F	259	CYS	2.2
5	E	120	LYS	2.2
4	I	10	ALA	2.2
5	J	236	ILE	2.2
4	I	131	LYS	2.2
4	D	7	ASP	2.2
1	A	215	LEU	2.1
4	D	150	ASP	2.1
4	D	180	SER	2.1
2	G	65	LEU	2.1
4	I	152	ASP	2.1
5	E	136	GLU	2.1
4	D	122	GLN	2.1
4	D	151	SER	2.0
4	I	28	SER	2.0
1	A	220	ASP	2.0
4	D	120	VAL	2.0
1	F	221	GLY	2.0
5	J	162	TRP	2.0
4	D	133	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.