



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:33 PM GMT

PDB ID : 1KTK
Title : Complex of Streptococcal pyrogenic enterotoxin C (SpeC) with a human T cell receptor beta chain (Vbeta2.1)
Authors : Sundberg, E.J.; Li, H.; Llera, A.S.; McCormick, J.K.; Tormo, J.; Karjalainen, K.; Schlievert, P.M.; Mariuzza, R.A.
Deposited on : 2002-01-16
Resolution : 3.00 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

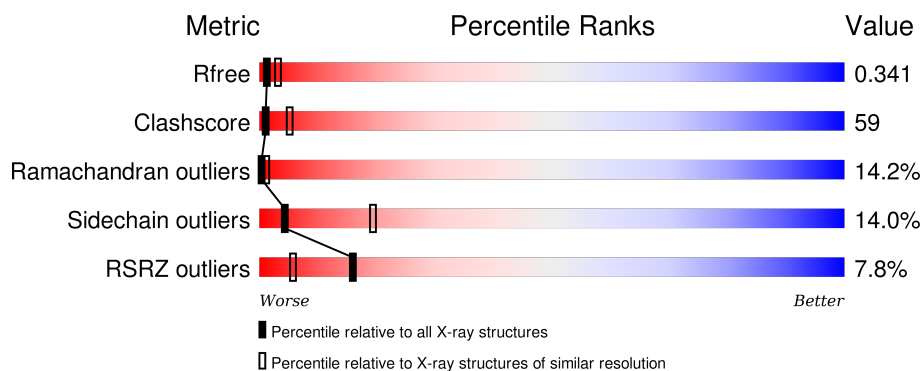
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	208	<div> <div>3%</div> <div>31% 50% 14% . .</div> </div>
1	B	208	<div> <div>6%</div> <div>24% 59% 12% . .</div> </div>
1	C	208	<div> <div>3%</div> <div>32% 57% 10% .</div> </div>
1	D	208	<div> <div>8%</div> <div>36% 50% 10% 5%</div> </div>
2	E	247	<div> <div>9%</div> <div>21% 46% 27% 7%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	247	<p>11% 15% 26% 16% 42%</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 9511 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 Exotoxin type C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	203	Total	C	N	O	S	0	0	0
			1664	1062	275	323	4			
1	B	200	Total	C	N	O	S	0	0	0
			1624	1042	267	311	4			
1	C	208	Total	C	N	O	S	0	0	0
			1699	1083	279	333	4			
1	D	198	Total	C	N	O	S	0	0	0
			1601	1028	267	303	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	ASP	ASN	CONFLICT	UNP P13380
B	26	ASP	ASN	CONFLICT	UNP P13380
C	26	ASP	ASN	CONFLICT	UNP P13380
D	26	ASP	ASN	CONFLICT	UNP P13380

- Molecule 2 is a protein called T-cell receptor beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	247	Total	C	N	O	S	0	0	0
			1879	1178	324	370	7			
2	F	144	Total	C	N	O	S	0	0	0
			1044	656	180	203	5			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	10	ARG	TRP	CONFLICT	UNP P01850
E	13	ALA	CYS	CONFLICT	UNP P01850
E	50	ALA	ASN	CONFLICT	UNP P01850
E	95	LEU	-	INSERTION	UNP P01850

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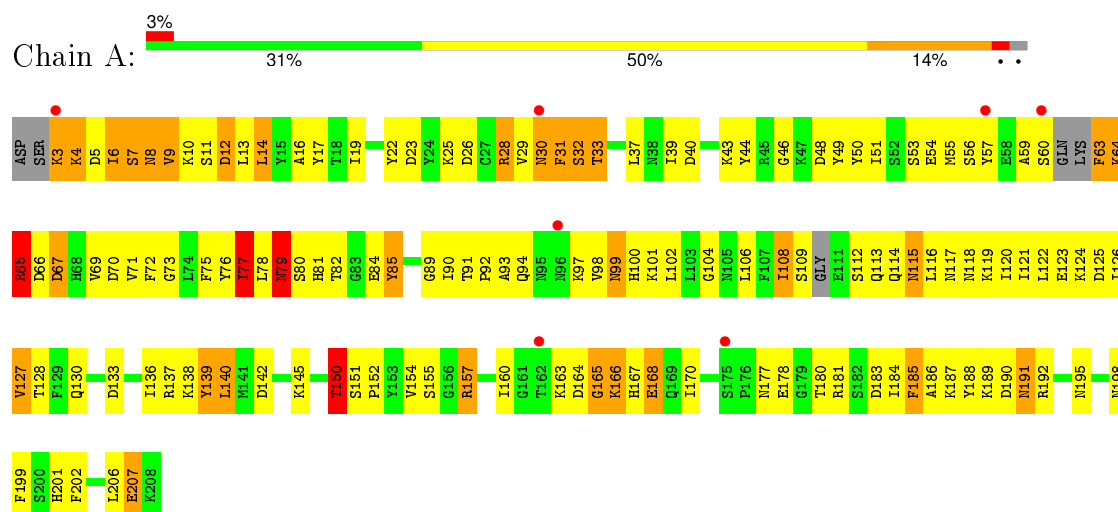
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Chain	Residue	Modelled	Actual	Comment	Reference
E	96	ALA	ARG	CONFLICT	UNP P01850
E	99	GLY	GLU	CONFLICT	UNP P01850
E	99	GLY	THR	CONFLICT	UNP P01850
E	101	SER	-	INSERTION	UNP P01850
E	102	THR	-	INSERTION	UNP P01850
E	?	-	PRO	DELETION	UNP P01850
E	?	-	LYS	DELETION	UNP P01850
E	?	-	ASN	DELETION	UNP P01850
E	105	THR	GLU	CONFLICT	UNP P01850
E	107	TYR	PHE	CONFLICT	UNP P01850
E	?	-	VAL	DELETION	UNP P01850
E	191	ALA	CYS	CONFLICT	UNP P01850
F	10	ARG	TRP	CONFLICT	UNP P01850
F	13	ALA	CYS	CONFLICT	UNP P01850
F	50	ALA	ASN	CONFLICT	UNP P01850
F	96	LEU	-	INSERTION	UNP P01850
F	97	ALA	ARG	CONFLICT	UNP P01850
F	98	GLY	GLU	CONFLICT	UNP P01850
F	100	GLY	THR	CONFLICT	UNP P01850
F	102	SER	-	INSERTION	UNP P01850
F	103	THR	-	INSERTION	UNP P01850
F	?	-	PRO	DELETION	UNP P01850
F	?	-	LYS	DELETION	UNP P01850
F	?	-	ASN	DELETION	UNP P01850
F	105	THR	GLU	CONFLICT	UNP P01850
F	107	TYR	PHE	CONFLICT	UNP P01850
F	?	-	VAL	DELETION	UNP P01850
F	191	ALA	CYS	CONFLICT	UNP P01850

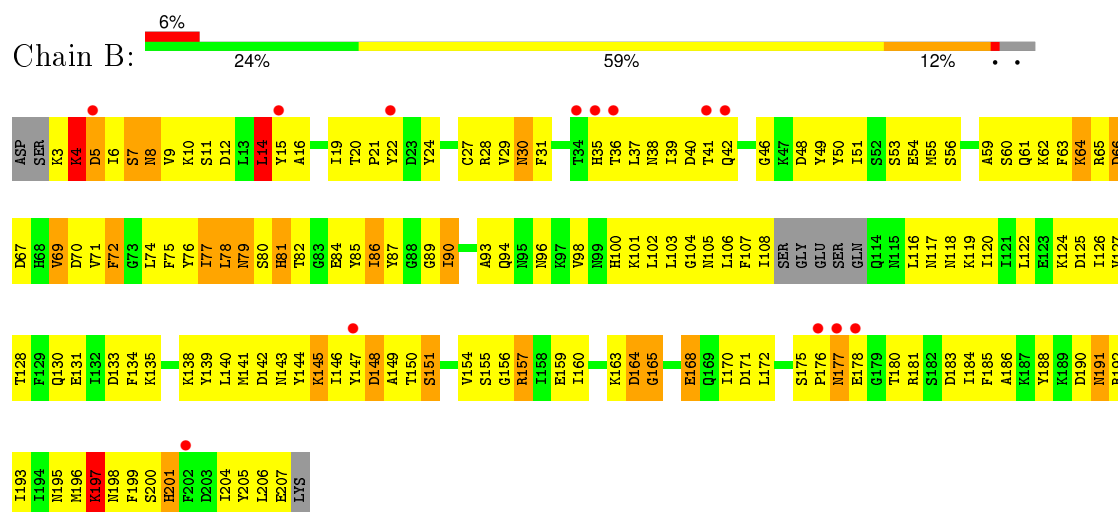
3 Residue-property plots [i](#)

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

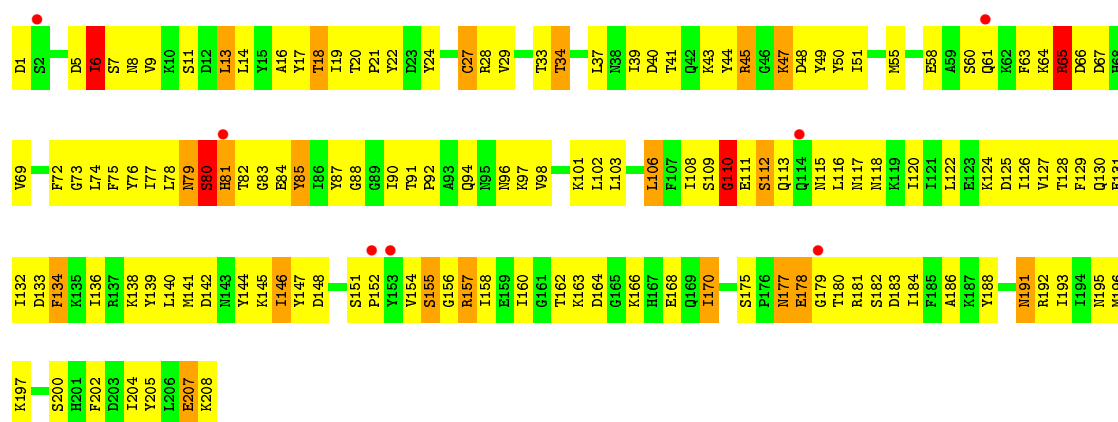


• Molecule 1: Exotoxin type C

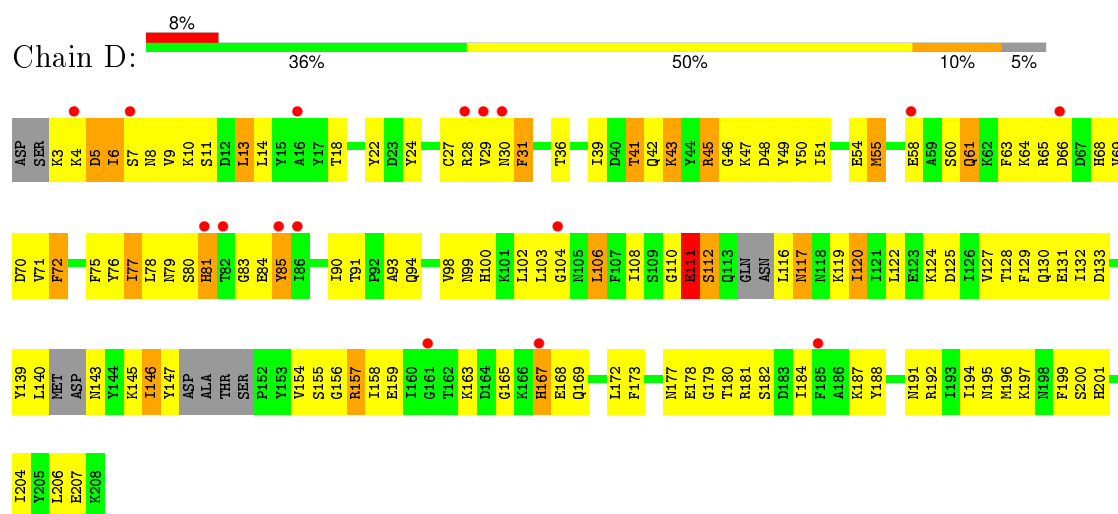


• Molecule 1: Exotoxin type C

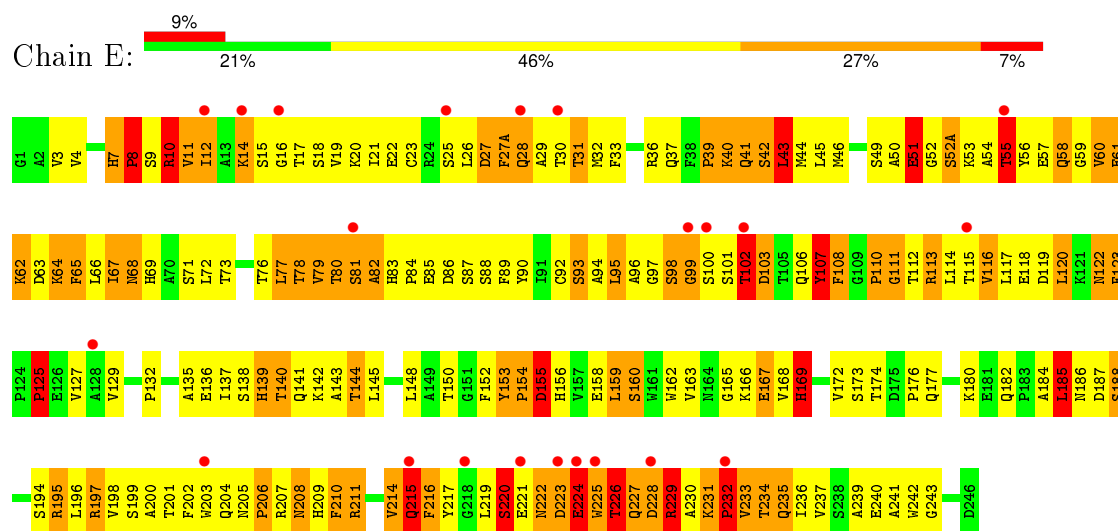




• Molecule 1: Exotoxin type C



• Molecule 2: T-cell receptor beta chain



• Molecule 2: T-cell receptor beta chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.38Å 146.76Å 135.69Å 90.00° 98.61° 90.00°	Depositor
Resolution (Å)	6.00 – 3.00 64.38 – 2.99	Depositor EDS
% Data completeness (in resolution range)	94.1 (6.00-3.00) 80.5 (64.38-2.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.09 (at 3.01Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.326 , 0.334 0.334 , 0.341	Depositor DCC
R_{free} test set	1913 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	78.6	Xtriage
Anisotropy	0.543	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 55.9	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 43707 reflections	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	9511	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% 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	0.65	0/1697	0.88	4/2282 (0.2%)
1	B	0.48	0/1659	0.80	3/2240 (0.1%)
1	C	0.64	1/1735 (0.1%)	0.85	3/2338 (0.1%)
1	D	0.49	0/1633	0.82	2/2197 (0.1%)
2	E	0.55	0/1924	1.02	11/2620 (0.4%)
2	F	0.48	0/1055	0.96	5/1421 (0.4%)
All	All	0.56	1/9703 (0.0%)	0.89	28/13098 (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
2	F	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	27	CYS	CB-SG	-5.29	1.73	1.81

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	7	HIS	C-N-CD	-15.24	87.06	120.60
2	F	85	GLU	N-CA-C	-9.54	85.23	111.00
1	B	4	LYS	N-CA-C	8.53	134.03	111.00
1	D	80	SER	N-CA-C	-8.38	88.37	111.00
1	A	79	ASN	N-CA-C	7.51	131.29	111.00
2	E	65	PHE	N-CA-C	-7.46	90.86	111.00
1	D	111	GLU	N-CA-C	-6.87	92.46	111.00
2	E	220	SER	N-CA-C	6.57	128.73	111.00
2	F	132	PRO	N-CA-CB	6.37	110.94	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	79	ASN	N-CA-C	6.30	128.01	111.00
2	E	225	TRP	N-CA-C	6.21	127.78	111.00
2	F	88	SER	N-CA-C	-6.16	94.37	111.00
2	E	214	VAL	N-CA-C	-5.83	95.27	111.00
2	E	8	PRO	N-CA-C	-5.81	96.98	112.10
2	E	7	HIS	C-N-CA	5.58	145.46	122.00
2	E	215	GLN	N-CA-C	5.55	125.98	111.00
1	A	67	ASP	N-CA-C	-5.51	96.12	111.00
1	C	80	SER	N-CA-C	-5.30	96.69	111.00
1	A	165	GLY	N-CA-C	5.24	126.20	113.10
1	C	110	GLY	N-CA-C	-5.18	100.14	113.10
2	F	84	PRO	N-CA-C	5.18	125.57	112.10
2	F	38	PHE	N-CA-C	-5.18	97.01	111.00
2	E	107	TYR	N-CA-C	5.15	124.91	111.00
1	B	5	ASP	N-CA-C	5.08	124.72	111.00
2	E	102	THR	N-CA-C	5.05	124.64	111.00
2	E	43	LEU	N-CA-C	5.04	124.60	111.00
1	A	139	TYR	N-CA-C	-5.03	97.43	111.00
1	B	79	ASN	N-CA-C	5.01	124.53	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	F	130	PHE	Sidechain

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	1664	0	1608	183	0
1	B	1624	0	1554	212	0
1	C	1699	0	1634	143	0
1	D	1601	0	1539	158	0
2	E	1879	0	1775	308	1
2	F	1044	0	965	144	0
All	All	9511	0	9075	1104	1

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 59.

All (1104) 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)
2:E:57:GLU:OE2	2:E:63:ASP:HB2	1.43	1.17
1:A:180:THR:HG22	2:E:54:ALA:HB2	1.30	1.10
2:E:15:SER:HA	2:E:82:ALA:O	1.52	1.09
2:E:79:VAL:HG13	2:E:80:THR:H	1.17	1.08
2:F:86:ASP:HB3	2:F:115:THR:HA	1.15	1.08
2:F:36:ARG:HG2	2:F:37:GLN:H	1.14	1.07
2:E:12:ILE:H	2:E:12:ILE:HD12	1.15	1.05
1:C:63:PHE:O	1:C:64:LYS:HG3	1.55	1.04
2:E:43:LEU:HD11	2:E:108:PHE:HZ	1.16	1.04
2:E:62:LYS:HA	2:E:62:LYS:HE2	1.40	1.01
1:D:69:VAL:HG21	1:D:90:ILE:HG23	1.38	1.01
1:B:124:LYS:HB2	1:B:127:VAL:HG22	1.40	1.01
2:F:19:VAL:HB	2:F:79:VAL:HG22	1.44	1.00
1:A:69:VAL:HG21	1:A:90:ILE:HG23	1.39	0.99
1:D:102:LEU:HD12	1:D:120:ILE:HG22	1.43	0.99
2:F:129:VAL:O	2:F:130:PHE:HA	1.64	0.97
1:B:51:ILE:HD13	1:B:84:GLU:HB2	1.45	0.97
1:B:8:ASN:O	1:B:12:ASP:HB2	1.64	0.96
1:C:69:VAL:HG21	1:C:90:ILE:HG23	1.45	0.96
2:F:30:THR:HG23	2:F:31:THR:H	1.31	0.96
1:A:28:ARG:HG2	1:A:40:ASP:HB3	1.46	0.96
1:B:76:TYR:HA	1:B:181:ARG:HB3	1.46	0.96
1:A:94:GLN:HE22	1:A:125:ASP:H	1.14	0.95
1:B:78:LEU:N	2:F:52:GLY:HA3	1.80	0.95
2:E:219:LEU:HD22	2:E:220:SER:H	1.30	0.94
2:E:18:SER:HA	2:E:80:THR:O	1.67	0.94
2:E:43:LEU:HD11	2:E:108:PHE:CZ	2.02	0.94
1:B:108:ILE:HG12	1:B:206:LEU:HB2	1.49	0.94
1:C:156:GLY:HA2	1:C:157:ARG:NH2	1.82	0.93
1:D:102:LEU:HD11	1:D:122:LEU:HG	1.50	0.93
1:C:6:ILE:HG23	1:C:7:SER:H	1.31	0.93
1:B:14:LEU:HD23	1:B:15:TYR:N	1.83	0.92
2:E:158:GLU:HB3	2:E:215:GLN:HB3	1.51	0.92
2:F:237:VAL:HG22	2:F:238:SER:H	1.35	0.92
1:D:119:LYS:O	1:D:120:ILE:HG13	1.70	0.91
1:A:94:GLN:NE2	1:A:125:ASP:H	1.68	0.91
1:B:48:ASP:O	1:B:82:THR:HB	1.68	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:113:ARG:HD3	2:E:156:HIS:CE1	2.07	0.89
2:E:113:ARG:HB3	2:E:156:HIS:HE1	1.37	0.89
1:A:30:ASN:O	1:A:65:ARG:HG3	1.72	0.89
2:E:159:LEU:HD12	2:E:160:SER:N	1.88	0.89
2:E:226:THR:HG23	2:E:227:GLN:N	1.88	0.89
1:A:94:GLN:HE21	1:A:124:LYS:HA	1.39	0.88
1:A:31:PHE:HE1	1:A:33:THR:HG23	1.38	0.88
2:E:144:THR:HA	2:E:197:ARG:HA	1.56	0.88
1:B:69:VAL:HG21	1:B:90:ILE:HD13	1.54	0.87
2:E:106:GLN:O	2:E:107:TYR:HB2	1.74	0.87
1:C:69:VAL:CG2	1:C:90:ILE:HG23	2.05	0.86
1:A:28:ARG:H	1:A:28:ARG:HD3	1.40	0.86
1:D:45:ARG:HH11	1:D:45:ARG:HG2	1.39	0.86
1:A:78:LEU:HD13	2:E:52:GLY:HA3	1.58	0.85
2:E:153:TYR:HB3	2:E:154:PRO:HD3	1.58	0.84
2:E:12:ILE:CD1	2:E:12:ILE:H	1.90	0.84
2:F:12:ILE:HA	2:F:115:THR:HG22	1.57	0.84
2:E:214:VAL:HB	2:E:237:VAL:HG23	1.60	0.84
2:E:186:ASN:C	2:E:188:SER:H	1.79	0.84
2:E:158:GLU:HB3	2:E:215:GLN:CB	2.08	0.83
2:E:64:LYS:HE3	2:E:64:LYS:HA	1.57	0.83
1:D:167:HIS:HE1	1:D:169:GLN:HG3	1.41	0.83
1:D:13:LEU:HD13	1:D:147:TYR:CD1	2.14	0.83
1:A:78:LEU:HD22	2:E:52:GLY:HA2	1.61	0.83
2:E:136:GLU:O	2:E:140:THR:HB	1.79	0.83
2:E:144:THR:HB	2:E:197:ARG:HB2	1.61	0.83
2:E:7:HIS:N	2:E:8:PRO:HD3	1.89	0.82
2:E:219:LEU:HG	2:E:233:VAL:HA	1.60	0.82
1:B:197:LYS:HG3	1:D:163:LYS:O	1.80	0.82
1:A:77:ILE:O	1:A:78:LEU:HD12	1.80	0.81
2:F:47:ALA:HB3	2:F:67:ILE:HG21	1.60	0.81
2:E:227:GLN:HG2	2:E:231:LYS:HD2	1.63	0.81
2:F:77:LEU:O	2:F:77:LEU:HD23	1.78	0.81
2:F:86:ASP:CB	2:F:115:THR:HA	2.06	0.81
1:D:29:VAL:O	1:D:65:ARG:HA	1.81	0.81
1:C:6:ILE:HG23	1:C:7:SER:N	1.96	0.80
2:E:64:LYS:O	2:E:80:THR:HG23	1.81	0.80
1:C:156:GLY:HA2	1:C:157:ARG:HH21	1.45	0.80
1:A:117:ASN:O	1:A:118:ASN:HB2	1.80	0.80
2:F:36:ARG:HG2	2:F:37:GLN:N	1.90	0.80
1:B:157:ARG:HG2	1:B:157:ARG:HH11	1.47	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:102:LEU:HD21	1:C:196:MET:HE1	1.64	0.79
1:B:64:LYS:NZ	1:B:65:ARG:HB3	1.97	0.79
1:B:190:ASP:OD1	1:B:192:ARG:HG2	1.83	0.79
1:D:178:GLU:O	1:D:180:THR:N	2.16	0.79
1:D:27:CYS:O	1:D:68:HIS:HA	1.81	0.79
2:E:120:LEU:HD22	2:E:221:GLU:O	1.83	0.78
2:E:219:LEU:HD22	2:E:220:SER:N	1.97	0.78
2:E:125:PRO:HB3	2:E:152:PHE:HB3	1.65	0.78
1:C:6:ILE:O	1:C:9:VAL:HB	1.84	0.77
1:B:9:VAL:HG22	1:B:175:SER:HB3	1.66	0.77
2:E:159:LEU:CD1	2:E:160:SER:H	1.96	0.77
1:B:69:VAL:HG21	1:B:90:ILE:CD1	2.14	0.77
1:B:78:LEU:HB2	2:F:52:GLY:HA2	1.67	0.77
1:C:126:ILE:HG23	1:C:193:ILE:HD12	1.65	0.77
2:E:79:VAL:HG13	2:E:80:THR:N	1.98	0.77
1:C:14:LEU:HD23	1:C:14:LEU:O	1.85	0.77
2:F:130:PHE:N	2:F:146:VAL:O	2.18	0.77
2:E:200:ALA:O	2:E:204:GLN:HG2	1.85	0.77
2:F:10:ARG:HH12	2:F:215:GLN:CB	1.98	0.77
1:A:77:ILE:C	1:A:78:LEU:HD12	2.05	0.76
2:E:208:ASN:HD22	2:E:208:ASN:C	1.87	0.76
2:F:206:PRO:O	2:F:208:ASN:N	2.18	0.76
1:D:5:ASP:O	1:D:7:SER:N	2.18	0.76
2:F:21:ILE:HD12	2:F:77:LEU:HD22	1.68	0.76
1:A:79:ASN:C	1:A:81:HIS:H	1.88	0.76
1:B:55:MET:HB3	1:B:59:ALA:CB	2.16	0.76
2:F:126:GLU:HA	2:F:126:GLU:OE1	1.83	0.76
1:D:129:PHE:CZ	1:D:194:ILE:HD11	2.21	0.76
1:A:102:LEU:HD12	1:A:120:ILE:HG22	1.67	0.76
2:E:231:LYS:O	2:E:231:LYS:HD3	1.86	0.75
2:E:122:ASN:O	2:E:123:PHE:HB2	1.86	0.75
2:E:201:THR:O	2:E:202:PHE:HB3	1.85	0.75
1:D:3:LYS:HD2	1:D:4:LYS:H	1.51	0.75
2:E:129:VAL:HG23	2:E:239:ALA:HB3	1.67	0.75
2:E:14:LYS:HB2	2:E:14:LYS:HZ2	1.52	0.75
1:C:88:GLY:O	1:C:90:ILE:HG12	1.87	0.75
2:E:166:LYS:HD2	2:E:166:LYS:N	2.02	0.74
1:A:69:VAL:CG2	1:A:90:ILE:HG23	2.14	0.74
1:C:43:LYS:HE3	1:C:44:TYR:CE2	2.22	0.74
1:B:28:ARG:HG3	1:B:66:ASP:OD1	1.88	0.74
1:A:79:ASN:HB2	2:E:30:THR:HG21	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:40:LYS:HG3	2:E:41:GLN:H	1.51	0.73
1:B:90:ILE:HG13	1:B:90:ILE:O	1.87	0.73
1:B:160:ILE:HG23	1:B:199:PHE:HE1	1.53	0.73
1:D:129:PHE:HA	1:D:132:ILE:HG22	1.71	0.73
1:C:65:ARG:HG3	1:C:66:ASP:OD2	1.88	0.73
1:D:69:VAL:HG21	1:D:90:ILE:CG2	2.17	0.73
2:E:144:THR:HA	2:E:197:ARG:CA	2.18	0.73
2:E:113:ARG:HD3	2:E:156:HIS:ND1	2.03	0.73
2:E:102:THR:O	2:E:103:ASP:HB3	1.88	0.73
1:C:157:ARG:HE	1:C:157:ARG:N	1.86	0.72
2:E:52:GLY:O	2:E:69:HIS:ND1	2.23	0.72
1:A:108:ILE:HG23	1:A:206:LEU:HB2	1.71	0.72
1:A:79:ASN:O	1:A:81:HIS:N	2.23	0.72
2:E:206:PRO:C	2:E:208:ASN:H	1.92	0.72
1:A:22:TYR:O	1:A:72:PHE:HA	1.89	0.72
2:F:19:VAL:HB	2:F:79:VAL:CG2	2.18	0.72
2:F:86:ASP:O	2:F:87:SER:HB3	1.88	0.72
2:F:6:GLN:OE1	2:F:91:ILE:HA	1.88	0.72
1:C:21:PRO:HB3	1:C:74:LEU:HD23	1.69	0.72
1:C:124:LYS:HB2	1:C:127:VAL:HG23	1.72	0.72
2:F:12:ILE:HA	2:F:115:THR:CG2	2.20	0.71
1:B:200:SER:O	1:B:201:HIS:HB3	1.90	0.71
2:E:66:LEU:HB3	2:E:78:THR:HG23	1.72	0.71
2:E:159:LEU:CD1	2:E:160:SER:N	2.54	0.71
1:D:6:ILE:HD11	1:D:173:PHE:CD2	2.25	0.71
1:A:99:ASN:OD1	1:A:121:ILE:HG21	1.90	0.71
1:C:45:ARG:HH11	1:C:45:ARG:HG3	1.54	0.71
2:E:226:THR:HG23	2:E:227:GLN:HG3	1.72	0.71
1:B:27:CYS:HB3	1:B:40:ASP:O	1.91	0.71
2:E:26:LEU:HD23	2:E:27:ASP:N	2.05	0.71
2:E:64:LYS:HB3	2:E:80:THR:HG21	1.73	0.71
1:A:28:ARG:HG2	1:A:40:ASP:CB	2.20	0.71
1:A:64:LYS:O	1:A:65:ARG:O	2.09	0.71
1:B:10:LYS:NZ	1:B:151:SER:HB3	2.05	0.71
2:E:226:THR:HG23	2:E:227:GLN:H	1.55	0.70
1:A:180:THR:HG22	2:E:54:ALA:CB	2.15	0.70
2:F:9:SER:O	2:F:112:THR:HG23	1.92	0.70
2:F:21:ILE:HD12	2:F:77:LEU:CD2	2.21	0.70
1:D:111:GLU:O	1:D:112:SER:CB	2.38	0.70
1:D:128:THR:HG23	1:D:131:GLU:H	1.56	0.70
1:D:159:GLU:HA	1:D:168:GLU:O	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:SER:H	1:A:189:LYS:HG2	1.57	0.70
2:F:12:ILE:HD12	2:F:233:VAL:HA	1.74	0.70
2:E:63:ASP:O	2:E:65:PHE:N	2.23	0.69
2:F:129:VAL:C	2:F:130:PHE:HA	2.12	0.69
1:B:11:SER:HA	1:B:14:LEU:HD22	1.74	0.69
2:E:173:SER:HB3	2:E:195:ARG:HD3	1.74	0.69
2:E:20:LYS:H	2:E:20:LYS:HD2	1.57	0.69
1:B:154:VAL:HG13	1:B:155:SER:H	1.56	0.69
1:A:69:VAL:HG21	1:A:90:ILE:CG2	2.20	0.69
1:A:180:THR:HB	2:E:53:LYS:O	1.93	0.69
2:F:115:THR:HG21	2:F:217:TYR:O	1.92	0.69
1:B:51:ILE:CD1	1:B:84:GLU:HB2	2.23	0.69
1:D:42:GLN:HG2	1:D:46:GLY:O	1.93	0.69
2:E:159:LEU:HD22	2:E:174:THR:HG21	1.75	0.69
1:C:17:TYR:O	1:C:19:ILE:N	2.26	0.69
2:E:52:GLY:O	2:E:52(A):SER:HB2	1.92	0.68
2:E:120:LEU:HD13	2:E:221:GLU:CB	2.24	0.68
2:E:219:LEU:HG	2:E:233:VAL:CA	2.23	0.68
1:B:102:LEU:HD21	1:B:122:LEU:HD23	1.75	0.68
2:E:64:LYS:HB3	2:E:80:THR:CG2	2.23	0.68
1:A:76:TYR:CD1	1:A:77:ILE:HG12	2.28	0.68
1:C:145:LYS:HB3	1:C:148:ASP:OD1	1.94	0.68
1:D:30:ASN:O	1:D:31:PHE:HB3	1.94	0.68
1:D:71:VAL:HG22	1:D:90:ILE:CD1	2.24	0.68
2:E:88:SER:OG	2:E:89:PHE:N	2.25	0.68
2:E:40:LYS:HG3	2:E:41:GLN:N	2.08	0.68
2:F:74:LEU:HG	2:F:75:SER:N	2.09	0.68
1:C:157:ARG:HE	1:C:157:ARG:H	1.42	0.67
1:D:36:THR:HG22	1:D:54:GLU:HA	1.76	0.67
1:D:71:VAL:HG22	1:D:90:ILE:HD13	1.75	0.67
1:B:154:VAL:HG13	1:B:155:SER:N	2.09	0.67
2:E:14:LYS:HB2	2:E:14:LYS:NZ	2.05	0.67
2:F:44:MET:C	2:F:45:LEU:HD22	2.15	0.67
2:E:219:LEU:HG	2:E:233:VAL:C	2.16	0.67
1:A:79:ASN:ND2	1:A:79:ASN:O	2.28	0.67
1:A:166:LYS:HD3	1:A:167:HIS:N	2.10	0.67
1:D:77:ILE:HG12	1:D:78:LEU:N	2.10	0.67
2:E:127:VAL:HG21	2:E:214:VAL:HG21	1.77	0.67
2:F:237:VAL:HG22	2:F:238:SER:N	2.10	0.66
1:C:69:VAL:HG21	1:C:90:ILE:CG2	2.22	0.66
2:E:186:ASN:C	2:E:188:SER:N	2.49	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:60:VAL:HG22	2:E:60:VAL:O	1.93	0.66
1:A:136:ILE:O	1:A:139:TYR:O	2.13	0.66
1:B:64:LYS:HZ3	1:B:65:ARG:HB3	1.60	0.66
2:F:207:ARG:HG2	2:F:207:ARG:O	1.95	0.66
1:A:56:SER:N	1:A:189:LYS:HG2	2.10	0.66
1:A:48:ASP:O	1:A:82:THR:CG2	2.44	0.66
1:C:21:PRO:HB3	1:C:74:LEU:CD2	2.25	0.66
1:C:96:ASN:O	1:C:98:VAL:HG13	1.96	0.66
1:C:7:SER:C	1:C:9:VAL:H	1.98	0.66
2:F:18:SER:HA	2:F:79:VAL:O	1.96	0.66
1:A:32:SER:HB2	1:A:37:LEU:HD12	1.78	0.66
2:E:142:LYS:HD2	2:E:197:ARG:HH11	1.60	0.66
1:D:111:GLU:O	1:D:112:SER:HB3	1.94	0.66
2:F:147:CYS:HG	2:F:194:SER:HG	1.34	0.66
2:F:86:ASP:OD1	2:F:116:VAL:HB	1.95	0.66
2:F:38:PHE:HA	2:F:88:SER:OG	1.96	0.65
2:E:15:SER:HB3	2:E:83:HIS:ND1	2.11	0.65
2:E:52(A):SER:O	2:E:53:LYS:C	2.33	0.65
1:C:122:LEU:HD12	1:C:196:MET:CE	2.26	0.65
1:C:41:THR:HG21	1:C:51:ILE:HG12	1.77	0.65
1:B:31:PHE:O	1:B:38:ASN:HB3	1.96	0.65
1:A:28:ARG:HH11	1:A:28:ARG:HG3	1.61	0.65
1:D:42:GLN:O	1:D:43:LYS:HG2	1.96	0.65
1:C:24:TYR:HE2	1:C:51:ILE:HD11	1.61	0.65
2:F:129:VAL:CG1	2:F:239:ALA:HB1	2.26	0.65
1:B:163:LYS:NZ	1:D:199:PHE:O	2.29	0.65
1:C:73:GLY:HA2	1:C:130:GLN:OE1	1.95	0.65
1:B:124:LYS:HB2	1:B:127:VAL:CG2	2.23	0.65
2:E:154:PRO:O	2:E:156:HIS:N	2.30	0.65
1:A:180:THR:CG2	2:E:54:ALA:HB2	2.17	0.65
1:D:6:ILE:HG13	1:D:10:LYS:HD2	1.78	0.65
1:B:201:HIS:HB3	1:D:103:LEU:CD1	2.26	0.65
1:B:78:LEU:H	2:F:52:GLY:HA3	1.59	0.65
2:E:158:GLU:CB	2:E:215:GLN:HB3	2.26	0.65
2:E:113:ARG:HB3	2:E:156:HIS:CE1	2.27	0.65
2:F:124:PRO:N	2:F:125:PRO:HD3	2.12	0.65
1:A:30:ASN:HD22	1:A:30:ASN:C	1.99	0.64
1:D:3:LYS:HD2	1:D:4:LYS:N	2.11	0.64
1:B:102:LEU:HD11	1:B:122:LEU:CD2	2.27	0.64
2:F:50:ALA:HB3	2:F:53:LYS:HB2	1.79	0.64
1:B:69:VAL:CG2	1:B:70:ASP:N	2.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:101:LYS:HB3	1:B:118:ASN:OD1	1.97	0.64
2:F:86:ASP:HB3	2:F:115:THR:CA	2.09	0.64
1:D:64:LYS:HG2	1:D:65:ARG:HG2	1.78	0.64
1:A:184:ILE:O	1:A:187:LYS:HG2	1.97	0.64
1:A:81:HIS:HA	2:E:28:GLN:HE21	1.61	0.64
1:D:116:LEU:O	1:D:119:LYS:HB2	1.98	0.64
2:F:129:VAL:HG13	2:F:239:ALA:HB1	1.79	0.64
2:F:30:THR:HG23	2:F:31:THR:N	2.09	0.64
2:E:22:GLU:HA	2:E:76:THR:HG22	1.79	0.64
1:C:126:ILE:CG2	1:C:193:ILE:HD12	2.27	0.64
1:C:122:LEU:HD12	1:C:196:MET:HE1	1.79	0.64
2:F:192:LEU:HD12	2:F:192:LEU:N	2.13	0.63
1:B:100:HIS:CD2	1:B:196:MET:HG3	2.33	0.63
2:E:57:GLU:OE2	2:E:63:ASP:CB	2.35	0.63
2:E:219:LEU:CG	2:E:233:VAL:HA	2.27	0.63
1:C:102:LEU:HD11	1:C:122:LEU:HG	1.79	0.63
2:F:194:SER:O	2:F:195:ARG:HB3	1.98	0.63
2:E:132:PRO:HD2	2:E:203:TRP:CZ2	2.33	0.63
1:D:69:VAL:HG23	1:D:91:THR:O	1.99	0.63
1:A:8:ASN:O	1:A:9:VAL:HG23	1.99	0.63
1:B:180:THR:HG21	2:F:53:LYS:CE	2.29	0.63
1:A:55:MET:SD	1:A:60:SER:HB3	2.39	0.63
2:E:216:PHE:CB	2:E:235:GLN:O	2.47	0.62
1:B:201:HIS:HB3	1:D:103:LEU:HD11	1.80	0.62
1:B:156:GLY:O	1:B:172:LEU:HB2	1.99	0.62
2:E:180:LYS:HE3	2:E:188:SER:OG	1.98	0.62
1:B:74:LEU:HB2	1:B:185:PHE:CE2	2.34	0.62
1:C:94:GLN:HE22	1:C:125:ASP:H	1.48	0.62
1:A:70:ASP:OD2	1:A:93:ALA:HA	1.99	0.62
1:D:167:HIS:CE1	1:D:169:GLN:HG3	2.30	0.62
1:A:130:GLN:HG3	1:A:188:TYR:CD2	2.34	0.62
1:A:55:MET:HG3	1:A:60:SER:HB3	1.81	0.62
1:A:114:GLN:NE2	1:A:115:ASN:H	1.98	0.62
1:B:63:PHE:CE2	1:B:90:ILE:HD11	2.34	0.62
1:A:139:TYR:O	1:A:140:LEU:CB	2.48	0.62
1:D:129:PHE:O	1:D:132:ILE:HG22	2.00	0.62
1:B:74:LEU:O	1:B:86:ILE:HG22	2.00	0.62
2:E:58:GLN:HG3	2:E:59:GLY:H	1.63	0.62
2:F:127:VAL:HB	2:F:149:ALA:HA	1.80	0.61
2:F:114:LEU:O	2:F:115:THR:HB	1.99	0.61
1:A:124:LYS:HB2	1:A:127:VAL:HG23	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:227:GLN:HE21	2:E:231:LYS:NZ	1.97	0.61
1:A:166:LYS:HD3	1:A:166:LYS:C	2.19	0.61
1:A:10:LYS:NZ	1:A:151:SER:HB3	2.14	0.61
2:E:140:THR:HG22	2:E:142:LYS:H	1.64	0.61
2:E:79:VAL:CG1	2:E:80:THR:H	1.99	0.61
1:A:78:LEU:HD13	2:E:52:GLY:CA	2.29	0.61
1:D:51:ILE:HD13	1:D:84:GLU:HB2	1.82	0.61
2:E:215:GLN:HG2	2:E:217:TYR:CE2	2.36	0.61
2:E:18:SER:CA	2:E:80:THR:O	2.46	0.61
1:B:106:LEU:HD23	1:B:107:PHE:N	2.15	0.61
1:A:157:ARG:HB2	1:A:170:ILE:O	2.01	0.61
1:D:45:ARG:HB3	1:D:49:TYR:CG	2.36	0.61
1:D:29:VAL:HB	1:D:64:LYS:O	2.00	0.61
1:D:45:ARG:CG	1:D:45:ARG:HH11	2.12	0.61
2:E:163:VAL:HG22	2:E:210:PHE:CE1	2.36	0.61
2:E:64:LYS:O	2:E:80:THR:CG2	2.49	0.61
1:B:78:LEU:HB2	2:F:52:GLY:CA	2.31	0.61
1:D:24:TYR:OH	1:D:45:ARG:NH1	2.30	0.61
1:A:184:ILE:C	1:A:186:ALA:H	2.04	0.61
2:F:41:GLN:O	2:F:42:SER:CB	2.49	0.61
1:C:128:THR:HG23	1:C:131:GLU:H	1.66	0.60
1:C:41:THR:HG21	1:C:51:ILE:CG1	2.31	0.60
1:C:49:TYR:CE1	1:C:82:THR:HG22	2.37	0.60
2:F:27(A):PHE:CG	2:F:28:GLN:N	2.68	0.60
2:E:79:VAL:O	2:E:80:THR:HG23	2.00	0.60
1:B:22:TYR:O	1:B:72:PHE:HA	2.01	0.60
2:F:187:ASP:O	2:F:188:SER:HB2	2.01	0.60
2:E:65:PHE:CE1	2:E:79:VAL:HG23	2.36	0.60
2:F:86:ASP:O	2:F:87:SER:CB	2.49	0.60
2:E:117:LEU:HD11	2:E:154:PRO:HG3	1.82	0.60
1:A:191:ASN:O	1:A:191:ASN:ND2	2.31	0.60
1:D:77:ILE:HG12	1:D:78:LEU:H	1.66	0.60
1:A:154:VAL:HG12	1:A:207:GLU:O	2.02	0.60
1:A:6:ILE:HG12	1:A:154:VAL:HG23	1.84	0.60
2:E:145:LEU:HD21	2:E:210:PHE:CD2	2.36	0.60
2:E:210:PHE:HB2	2:E:241:ALA:O	2.02	0.60
2:E:182:GLN:O	2:E:185:LEU:HD21	2.02	0.60
1:C:164:ASP:OD1	1:C:166:LYS:HE3	2.01	0.60
2:E:127:VAL:CG2	2:E:214:VAL:HG21	2.32	0.60
1:D:124:LYS:HB2	1:D:127:VAL:HG22	1.84	0.60
1:C:21:PRO:HG3	1:C:134:PHE:CE2	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:GLN:CD	1:A:115:ASN:H	2.06	0.59
2:E:215:GLN:O	2:E:215:GLN:HG3	2.00	0.59
1:D:140:LEU:HD21	1:D:204:ILE:HD13	1.85	0.59
2:E:15:SER:CA	2:E:82:ALA:O	2.42	0.59
1:B:105:ASN:O	1:B:204:ILE:HG12	2.03	0.59
1:C:157:ARG:NH2	1:C:207:GLU:OE2	2.36	0.59
1:B:55:MET:HB3	1:B:59:ALA:HB1	1.85	0.59
1:A:108:ILE:HG23	1:A:206:LEU:CB	2.32	0.59
1:C:6:ILE:HD13	1:C:6:ILE:C	2.22	0.59
1:D:158:ILE:HD11	1:D:172:LEU:HD21	1.83	0.59
1:C:129:PHE:HE2	1:C:160:ILE:HG13	1.67	0.59
1:B:180:THR:HG21	2:F:53:LYS:HE2	1.83	0.59
1:C:80:SER:O	1:C:81:HIS:HB2	2.01	0.59
2:E:219:LEU:CD1	2:E:233:VAL:HA	2.32	0.59
1:D:163:LYS:HD2	1:D:200:SER:HB2	1.84	0.59
1:B:184:ILE:HD12	1:B:184:ILE:N	2.17	0.59
2:E:45:LEU:HD23	2:E:58:GLN:HG2	1.84	0.59
1:B:103:LEU:CD1	1:D:201:HIS:HB3	2.32	0.59
2:F:61:GLU:O	2:F:62:LYS:HE2	2.03	0.59
2:E:22:GLU:HG2	2:E:76:THR:HG22	1.84	0.59
2:E:129:VAL:HG23	2:E:239:ALA:CB	2.33	0.59
1:B:201:HIS:CG	1:D:103:LEU:HD11	2.36	0.59
1:C:22:TYR:CE2	1:C:75:PHE:HB3	2.37	0.59
1:B:19:ILE:HG12	1:B:20:THR:N	2.18	0.59
1:C:6:ILE:CG2	1:C:7:SER:H	2.10	0.59
2:E:153:TYR:HB3	2:E:154:PRO:CD	2.28	0.59
2:E:22:GLU:HG2	2:E:76:THR:CG2	2.32	0.59
2:F:17:THR:H	2:F:81:SER:CB	2.15	0.59
1:B:55:MET:HB3	1:B:59:ALA:HB3	1.85	0.58
1:C:49:TYR:CZ	1:C:82:THR:HG22	2.37	0.58
1:C:124:LYS:NZ	1:C:131:GLU:OE1	2.32	0.58
1:A:75:PHE:C	1:A:75:PHE:CD1	2.76	0.58
1:B:78:LEU:HD12	2:F:52:GLY:O	2.03	0.58
1:C:158:ILE:HB	1:C:170:ILE:HB	1.85	0.58
1:C:50:TYR:CZ	1:C:83:GLY:HA3	2.38	0.58
2:E:153:TYR:O	2:E:154:PRO:C	2.40	0.58
1:A:79:ASN:HB2	2:E:30:THR:CG2	2.34	0.58
2:F:36:ARG:CG	2:F:37:GLN:H	2.02	0.58
1:C:27:CYS:O	1:C:69:VAL:HG12	2.04	0.58
1:D:9:VAL:O	1:D:13:LEU:HD12	2.03	0.58
1:D:13:LEU:HD13	1:D:147:TYR:CE1	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:6:ILE:HG13	1:D:10:LYS:HG3	1.86	0.58
1:A:22:TYR:CE2	1:A:84:GLU:HB3	2.39	0.58
1:B:4:LYS:HB3	1:B:4:LYS:NZ	2.19	0.58
2:E:25:SER:O	2:E:73:THR:HG23	2.03	0.58
2:E:87:SER:OG	2:E:116:VAL:HG22	2.04	0.58
1:C:157:ARG:NE	1:C:157:ARG:N	2.51	0.58
1:D:184:ILE:HD11	1:D:187:LYS:NZ	2.18	0.58
2:E:97:GLY:O	2:E:98:SER:CB	2.52	0.58
1:C:108:ILE:O	1:C:110:GLY:N	2.35	0.58
1:B:42:GLN:HA	1:B:46:GLY:O	2.02	0.58
2:E:165:GLY:C	2:E:166:LYS:HD2	2.24	0.57
2:E:71:SER:C	2:E:73:THR:H	2.08	0.57
1:C:77:ILE:HG12	1:C:78:LEU:N	2.20	0.57
1:C:117:ASN:O	1:C:118:ASN:HB2	2.04	0.57
2:E:62:LYS:C	2:E:64:LYS:H	2.06	0.57
1:A:81:HIS:CG	1:A:81:HIS:O	2.58	0.57
1:B:154:VAL:HG12	1:B:207:GLU:O	2.03	0.57
2:E:95:LEU:HD23	2:E:106:GLN:HB2	1.86	0.57
1:A:28:ARG:N	1:A:28:ARG:HD3	2.15	0.57
2:E:201:THR:O	2:E:202:PHE:CB	2.51	0.57
2:E:208:ASN:C	2:E:208:ASN:ND2	2.57	0.57
1:B:103:LEU:HD11	1:D:201:HIS:HB3	1.87	0.57
1:A:102:LEU:HD11	1:A:122:LEU:HG	1.87	0.57
2:E:219:LEU:HD13	2:E:220:SER:HB2	1.87	0.57
1:A:190:ASP:O	1:A:191:ASN:C	2.42	0.57
2:F:71:SER:OG	2:F:72:LEU:HD23	2.04	0.57
2:F:44:MET:O	2:F:45:LEU:HD13	2.04	0.57
2:E:127:VAL:HG21	2:E:214:VAL:CG2	2.34	0.57
1:D:45:ARG:NH1	1:D:45:ARG:HG2	2.14	0.57
2:E:68:ASN:N	2:E:68:ASN:HD22	2.03	0.57
1:D:129:PHE:CA	1:D:132:ILE:HG22	2.35	0.57
2:E:64:LYS:N	2:E:64:LYS:HD2	2.20	0.57
1:A:122:LEU:HD13	1:A:127:VAL:HG11	1.86	0.57
1:B:76:TYR:CA	1:B:181:ARG:HB3	2.29	0.57
1:A:139:TYR:O	1:A:140:LEU:HG	2.05	0.57
2:F:192:LEU:H	2:F:192:LEU:HD12	1.67	0.57
1:D:11:SER:C	1:D:13:LEU:H	2.06	0.57
1:A:104:GLY:H	1:A:117:ASN:ND2	2.03	0.57
1:C:101:LYS:HD3	1:C:118:ASN:OD1	2.05	0.57
2:F:69:HIS:HA	2:F:75:SER:HB3	1.87	0.56
1:C:39:ILE:HG12	1:C:69:VAL:HG11	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:5:SER:O	2:F:23:CYS:HA	2.05	0.56
1:B:36:THR:HA	1:B:53:SER:O	2.05	0.56
2:E:43:LEU:HD23	2:E:43:LEU:N	2.20	0.56
1:D:120:ILE:O	1:D:120:ILE:HG22	2.05	0.56
2:F:236:ILE:HG12	2:F:237:VAL:N	2.20	0.56
2:E:98:SER:O	2:E:99:GLY:C	2.43	0.56
1:C:51:ILE:HD13	1:C:84:GLU:HB2	1.87	0.56
1:C:136:ILE:O	1:C:139:TYR:HB3	2.05	0.56
2:E:43:LEU:CD1	2:E:108:PHE:HZ	2.03	0.56
1:A:54:GLU:OE2	1:A:189:LYS:HE3	2.06	0.56
2:E:73:THR:O	2:E:73:THR:HG22	2.05	0.56
2:E:209:HIS:NE2	2:E:211:ARG:HB3	2.19	0.56
1:D:81:HIS:C	1:D:81:HIS:ND1	2.58	0.56
1:A:13:LEU:O	1:A:16:ALA:N	2.38	0.56
2:F:36:ARG:NH1	2:F:65:PHE:HE1	2.04	0.56
2:E:125:PRO:HG2	2:E:237:VAL:HG21	1.88	0.56
2:E:143:ALA:O	2:E:197:ARG:HA	2.05	0.56
1:B:36:THR:HG22	1:B:54:GLU:HA	1.86	0.56
2:F:238:SER:OG	2:F:239:ALA:N	2.39	0.56
1:A:9:VAL:C	1:A:11:SER:N	2.57	0.56
1:D:39:ILE:CD1	1:D:90:ILE:HD12	2.35	0.56
2:E:27(A):PHE:HE1	2:E:94:ALA:CB	2.19	0.56
1:C:9:VAL:C	1:C:11:SER:H	2.09	0.56
2:E:10:ARG:HG3	2:E:11:VAL:HG23	1.88	0.56
2:E:227:GLN:CG	2:E:231:LYS:HD2	2.36	0.56
1:D:129:PHE:CE2	1:D:194:ILE:HD11	2.41	0.56
1:D:28:ARG:HB3	1:D:68:HIS:CE1	2.40	0.56
2:E:10:ARG:HD2	2:E:217:TYR:HB3	1.88	0.56
2:E:26:LEU:O	2:E:27:ASP:C	2.44	0.56
2:F:147:CYS:SG	2:F:148:LEU:N	2.79	0.56
1:B:10:LYS:HZ1	1:B:151:SER:HB3	1.70	0.55
1:C:18:THR:HG22	1:C:18:THR:O	2.06	0.55
1:B:10:LYS:HZ3	1:B:151:SER:HB3	1.71	0.55
2:E:87:SER:HA	2:E:114:LEU:O	2.07	0.55
2:E:64:LYS:CE	2:E:64:LYS:HA	2.28	0.55
1:A:14:LEU:O	1:A:14:LEU:HD23	2.06	0.55
1:A:55:MET:CG	1:A:60:SER:HB3	2.37	0.55
2:F:234:THR:O	2:F:235:GLN:CB	2.54	0.55
2:E:68:ASN:ND2	2:E:76:THR:OG1	2.32	0.55
1:D:3:LYS:CD	1:D:4:LYS:H	2.19	0.55
1:C:29:VAL:HG11	1:C:37:LEU:HD11	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:94:GLN:NE2	1:D:125:ASP:H	2.03	0.55
1:B:37:LEU:HD23	1:B:90:ILE:HG12	1.89	0.55
1:B:201:HIS:CB	1:D:103:LEU:HD11	2.36	0.55
2:E:118:GLU:HG3	2:E:119:ASP:N	2.22	0.55
1:D:72:PHE:CE2	1:D:131:GLU:HG3	2.42	0.55
1:B:60:SER:C	1:B:62:LYS:N	2.60	0.55
1:C:7:SER:C	1:C:9:VAL:N	2.60	0.55
2:F:69:HIS:HA	2:F:75:SER:CB	2.36	0.55
2:E:206:PRO:C	2:E:208:ASN:N	2.59	0.55
1:A:79:ASN:HB2	2:E:30:THR:CB	2.37	0.55
1:D:72:PHE:C	1:D:72:PHE:CD1	2.80	0.55
1:B:130:GLN:O	1:B:133:ASP:HB3	2.06	0.55
1:B:107:PHE:CD2	1:B:205:TYR:CE1	2.95	0.54
1:D:10:LYS:HB3	1:D:147:TYR:O	2.07	0.54
1:C:21:PRO:HG3	1:C:134:PHE:HE2	1.71	0.54
1:B:164:ASP:OD1	1:B:164:ASP:N	2.40	0.54
1:B:60:SER:O	1:B:62:LYS:N	2.39	0.54
1:B:72:PHE:C	1:B:72:PHE:CD1	2.79	0.54
2:F:50:ALA:O	2:F:51:GLU:C	2.45	0.54
1:C:63:PHE:C	1:C:64:LYS:HG3	2.24	0.54
2:F:237:VAL:HG13	2:F:238:SER:N	2.21	0.54
2:E:142:LYS:HD3	2:E:197:ARG:HE	1.72	0.54
1:B:29:VAL:HA	1:B:39:ILE:HA	1.89	0.54
1:B:90:ILE:CG1	1:B:90:ILE:O	2.54	0.54
1:A:191:ASN:HD22	1:A:191:ASN:C	2.09	0.54
1:A:73:GLY:HA2	1:A:130:GLN:OE1	2.06	0.54
2:E:50:ALA:O	2:E:52:GLY:N	2.41	0.54
1:D:6:ILE:CG1	1:D:10:LYS:HD2	2.38	0.54
2:F:207:ARG:O	2:F:208:ASN:O	2.26	0.54
1:A:139:TYR:O	1:A:140:LEU:HB2	2.06	0.54
1:D:39:ILE:HD13	1:D:69:VAL:HG11	1.89	0.54
1:D:6:ILE:HG13	1:D:10:LYS:CD	2.37	0.54
1:B:65:ARG:HG3	1:B:66:ASP:H	1.71	0.54
2:F:233:VAL:HG12	2:F:234:THR:HG23	1.87	0.54
2:E:153:TYR:O	2:E:155:ASP:N	2.41	0.54
1:B:67:ASP:O	1:B:69:VAL:HG12	2.08	0.54
1:C:19:ILE:HD11	1:C:75:PHE:CD2	2.43	0.54
1:B:8:ASN:N	1:B:8:ASN:HD22	2.05	0.54
2:E:27(A):PHE:O	2:E:28:GLN:CB	2.55	0.54
1:A:56:SER:HA	1:A:189:LYS:HE2	1.90	0.54
2:E:20:LYS:N	2:E:20:LYS:HD2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:223:ASP:O	2:E:224:GLU:HB2	2.07	0.53
2:E:23:CYS:SG	2:E:32:MET:HE3	2.49	0.53
2:F:12:ILE:HG12	2:F:217:TYR:O	2.08	0.53
1:B:181:ARG:HH11	2:F:52(A):SER:CB	2.21	0.53
1:C:129:PHE:CE2	1:C:160:ILE:HG13	2.44	0.53
1:B:150:THR:O	1:B:151:SER:HB2	2.09	0.53
1:C:106:LEU:HD11	1:C:144:TYR:CE2	2.43	0.53
1:A:180:THR:HG21	2:E:53:LYS:NZ	2.24	0.53
1:D:45:ARG:NH2	1:D:84:GLU:OE2	2.40	0.53
1:B:157:ARG:HH11	1:B:157:ARG:CG	2.17	0.53
1:A:77:ILE:HG22	2:E:51:GLU:HG3	1.90	0.53
2:E:89:PHE:CE2	2:E:113:ARG:HG2	2.43	0.53
1:D:140:LEU:O	1:D:146:ILE:HG12	2.08	0.53
1:B:160:ILE:HG23	1:B:199:PHE:CE1	2.39	0.53
1:A:168:GLU:OE1	1:A:192:ARG:NH1	2.41	0.53
1:A:3:LYS:O	1:A:5:ASP:OD2	2.26	0.53
2:F:10:ARG:HA	2:F:113:ARG:H	1.73	0.53
1:A:50:TYR:HD1	1:A:82:THR:HG22	1.73	0.53
1:A:115:ASN:O	1:A:116:LEU:HB2	2.08	0.53
1:A:76:TYR:HD1	1:A:77:ILE:HG12	1.73	0.53
2:E:120:LEU:HD21	2:E:220:SER:OG	2.08	0.53
1:D:6:ILE:HG13	1:D:10:LYS:CG	2.39	0.53
2:F:194:SER:O	2:F:195:ARG:CB	2.57	0.53
1:D:98:VAL:HG22	1:D:99:ASN:N	2.22	0.53
1:B:146:ILE:HG13	1:B:147:TYR:N	2.23	0.53
1:A:168:GLU:CD	1:A:192:ARG:NH1	2.62	0.53
1:D:69:VAL:CG2	1:D:90:ILE:HG23	2.27	0.53
1:D:4:LYS:O	1:D:5:ASP:O	2.27	0.53
2:E:60:VAL:O	2:E:61:GLU:CG	2.56	0.53
2:E:9:SER:O	2:E:10:ARG:HB3	2.09	0.53
1:A:31:PHE:CD1	1:A:32:SER:N	2.77	0.53
1:A:9:VAL:O	1:A:11:SER:N	2.42	0.53
2:E:174:THR:HG22	2:E:194:SER:OG	2.08	0.53
1:D:42:GLN:O	1:D:43:LYS:CB	2.56	0.53
1:B:19:ILE:HG12	1:B:20:THR:H	1.74	0.52
2:E:10:ARG:C	2:E:11:VAL:HG23	2.29	0.52
1:D:45:ARG:CG	1:D:45:ARG:NH1	2.71	0.52
1:C:102:LEU:HD11	1:C:122:LEU:CG	2.38	0.52
2:E:138:SER:O	2:E:139:HIS:CB	2.57	0.52
2:E:54:ALA:C	2:E:55:THR:HG22	2.29	0.52
2:F:129:VAL:O	2:F:130:PHE:CD1	2.62	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:102:LEU:HD22	1:B:199:PHE:CE2	2.43	0.52
2:E:153:TYR:CB	2:E:154:PRO:HD3	2.33	0.52
1:C:45:ARG:HG3	1:C:45:ARG:NH1	2.23	0.52
1:B:4:LYS:NZ	1:B:4:LYS:CB	2.73	0.52
2:E:233:VAL:O	2:E:235:GLN:N	2.42	0.52
2:E:172:VAL:HG12	2:E:196:LEU:CD1	2.38	0.52
2:E:122:ASN:O	2:E:123:PHE:CB	2.56	0.52
1:A:10:LYS:HZ1	1:A:151:SER:HB3	1.73	0.52
1:A:43:LYS:HE3	1:A:44:TYR:CE2	2.45	0.52
1:D:39:ILE:HD13	1:D:69:VAL:CG1	2.40	0.52
1:B:63:PHE:CD2	1:B:90:ILE:HD11	2.45	0.52
2:E:14:LYS:HG3	2:E:15:SER:H	1.74	0.52
1:D:129:PHE:HA	1:D:132:ILE:CG2	2.39	0.52
1:B:131:GLU:CG	1:B:135:LYS:HE3	2.40	0.52
1:C:154:VAL:O	1:C:154:VAL:HG22	2.10	0.52
1:C:87:TYR:CD2	1:C:186:ALA:HA	2.44	0.52
2:E:62:LYS:HA	2:E:62:LYS:CE	2.25	0.52
1:B:30:ASN:N	1:B:38:ASN:O	2.42	0.52
2:F:234:THR:O	2:F:235:GLN:HB2	2.09	0.52
1:A:109:SER:OG	1:A:207:GLU:HA	2.10	0.52
2:F:17:THR:N	2:F:81:SER:OG	2.43	0.52
1:B:195:ASN:ND2	1:B:197:LYS:H	2.08	0.52
1:B:65:ARG:O	1:B:66:ASP:C	2.47	0.52
2:E:168:VAL:HG22	2:E:169:HIS:N	2.25	0.52
1:D:39:ILE:HD11	1:D:90:ILE:HD12	1.92	0.51
1:B:85:TYR:O	1:B:86:ILE:HG23	2.10	0.51
1:B:10:LYS:HE2	1:B:146:ILE:O	2.10	0.51
2:E:80:THR:O	2:E:81:SER:O	2.28	0.51
2:F:87:SER:O	2:F:88:SER:OG	2.28	0.51
1:D:156:GLY:O	1:D:157:ARG:NH1	2.44	0.51
1:C:7:SER:O	1:C:8:ASN:HB2	2.09	0.51
2:E:30:THR:O	2:E:30:THR:OG1	2.19	0.51
2:F:65:PHE:HD2	2:F:79:VAL:HG12	1.76	0.51
1:D:77:ILE:CG1	1:D:78:LEU:N	2.74	0.51
2:F:48:THR:OG1	2:F:49:SER:N	2.44	0.51
1:A:94:GLN:NE2	1:A:125:ASP:N	2.48	0.51
1:D:13:LEU:HD22	1:D:147:TYR:CZ	2.45	0.51
1:A:55:MET:HE2	1:A:191:ASN:HB2	1.92	0.51
2:F:14:LYS:O	2:F:17:THR:HB	2.11	0.51
2:E:136:GLU:OE1	2:E:144:THR:HG22	2.10	0.51
2:E:97:GLY:O	2:E:98:SER:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:19:VAL:HG12	2:F:21:ILE:HG13	1.93	0.51
1:A:160:ILE:HG23	1:A:199:PHE:CE1	2.46	0.51
2:E:83:HIS:O	2:E:84:PRO:C	2.49	0.51
1:A:181:ARG:NH1	2:E:52(A):SER:OG	2.43	0.51
2:E:153:TYR:CB	2:E:154:PRO:CD	2.89	0.51
1:B:70:ASP:CG	1:B:93:ALA:HA	2.31	0.51
2:E:186:ASN:O	2:E:187:ASP:HB3	2.10	0.51
1:B:197:LYS:HA	1:D:163:LYS:HE3	1.92	0.51
1:C:152:PRO:O	1:C:208:LYS:HG2	2.11	0.51
1:B:50:TYR:HE1	1:B:82:THR:HG1	1.58	0.51
1:C:6:ILE:HD13	1:C:7:SER:N	2.26	0.51
2:E:21:ILE:HD12	2:E:77:LEU:CD1	2.41	0.51
1:B:176:PRO:HD2	1:B:184:ILE:HG13	1.93	0.51
2:E:14:LYS:NZ	2:E:223:ASP:OD2	2.45	0.50
1:B:106:LEU:HD21	1:B:108:ILE:HG13	1.93	0.50
1:C:157:ARG:NE	1:C:205:TYR:HB2	2.26	0.50
2:E:186:ASN:O	2:E:188:SER:N	2.43	0.50
1:D:102:LEU:HD12	1:D:120:ILE:CG2	2.28	0.50
1:B:78:LEU:HD12	2:F:52:GLY:C	2.31	0.50
2:F:11:VAL:HG22	2:F:12:ILE:N	2.26	0.50
2:E:233:VAL:HG23	2:E:234:THR:N	2.25	0.50
1:D:9:VAL:C	1:D:11:SER:H	2.14	0.50
2:F:74:LEU:CG	2:F:75:SER:N	2.74	0.50
1:A:13:LEU:O	1:A:14:LEU:C	2.49	0.50
1:A:16:ALA:HA	1:A:181:ARG:HE	1.74	0.50
1:C:19:ILE:HD11	1:C:75:PHE:CE2	2.46	0.50
1:C:141:MET:CE	1:C:147:TYR:HD2	2.24	0.50
2:E:180:LYS:HE3	2:E:188:SER:CB	2.41	0.50
1:D:108:ILE:HG12	1:D:206:LEU:HB2	1.93	0.50
2:F:73:THR:HG22	2:F:74:LEU:N	2.26	0.50
1:A:178:GLU:HB3	1:A:183:ASP:OD2	2.11	0.50
1:A:181:ARG:N	2:E:53:LYS:O	2.41	0.50
1:D:39:ILE:CD1	1:D:69:VAL:HG11	2.42	0.50
2:E:166:LYS:HB3	2:E:167:GLU:OE1	2.12	0.50
2:F:22:GLU:O	2:F:24:ARG:HG3	2.10	0.50
2:E:135:ALA:O	2:E:138:SER:O	2.30	0.50
2:E:63:ASP:OD1	2:E:64:LYS:HD2	2.10	0.50
1:A:78:LEU:HD22	2:E:52:GLY:CA	2.39	0.50
2:F:20:LYS:C	2:F:21:ILE:HG13	2.32	0.50
2:E:37:GLN:HG3	2:E:42:SER:HA	1.93	0.50
2:F:17:THR:H	2:F:81:SER:HB2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:PHE:CD1	1:A:185:PHE:N	2.79	0.50
1:B:168:GLU:CD	1:B:192:ARG:HH12	2.15	0.50
2:E:71:SER:C	2:E:73:THR:N	2.63	0.50
2:E:3:VAL:HG22	2:E:4:VAL:N	2.27	0.50
2:E:65:PHE:HE1	2:E:79:VAL:HG23	1.77	0.50
1:B:69:VAL:HG22	1:B:70:ASP:N	2.27	0.50
1:A:101:LYS:HD3	1:A:118:ASN:OD1	2.12	0.50
1:D:5:ASP:C	1:D:7:SER:H	2.15	0.50
1:B:106:LEU:HD12	1:B:204:ILE:HD11	1.94	0.49
2:E:226:THR:CG2	2:E:227:GLN:N	2.60	0.49
2:E:98:SER:O	2:E:100:SER:N	2.45	0.49
1:D:42:GLN:O	1:D:43:LYS:CG	2.59	0.49
1:C:17:TYR:O	1:C:19:ILE:HG22	2.12	0.49
2:F:71:SER:C	2:F:73:THR:N	2.63	0.49
2:E:182:GLN:O	2:E:185:LEU:CD2	2.60	0.49
1:C:77:ILE:HG12	1:C:78:LEU:H	1.76	0.49
1:B:94:GLN:HG3	1:B:96:ASN:O	2.12	0.49
1:C:39:ILE:HG22	1:C:40:ASP:N	2.27	0.49
2:E:125:PRO:HB3	2:E:152:PHE:CB	2.38	0.49
2:E:10:ARG:O	2:E:11:VAL:HG23	2.13	0.49
1:D:132:ILE:HG23	1:D:133:ASP:N	2.27	0.49
2:F:30:THR:CG2	2:F:31:THR:H	2.13	0.49
2:E:159:LEU:HD22	2:E:174:THR:CG2	2.40	0.49
1:D:10:LYS:HB3	1:D:147:TYR:HA	1.94	0.49
2:E:8:PRO:CG	2:E:21:ILE:HA	2.43	0.49
1:B:64:LYS:HD3	1:B:65:ARG:N	2.27	0.49
1:C:106:LEU:CD1	1:C:144:TYR:CZ	2.95	0.49
2:F:13:ALA:O	2:F:115:THR:O	2.30	0.49
1:B:64:LYS:HD3	1:B:65:ARG:O	2.11	0.49
1:C:97:LYS:O	1:C:98:VAL:CG1	2.61	0.49
1:A:114:GLN:NE2	1:A:115:ASN:N	2.61	0.49
1:C:177:ASN:HB2	1:C:183:ASP:OD1	2.12	0.49
1:C:85:TYR:CD1	1:C:85:TYR:N	2.80	0.49
2:E:62:LYS:C	2:E:64:LYS:N	2.65	0.49
1:A:69:VAL:HG22	1:A:70:ASP:N	2.26	0.49
1:C:6:ILE:CG2	1:C:7:SER:N	2.69	0.49
2:E:113:ARG:NH2	2:E:155:ASP:OD2	2.46	0.49
1:C:132:ILE:O	1:C:133:ASP:C	2.50	0.49
1:A:6:ILE:HG23	1:A:7:SER:N	2.27	0.49
1:A:23:ASP:HA	1:A:71:VAL:O	2.13	0.49
1:D:100:HIS:N	1:D:122:LEU:O	2.22	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:SER:O	1:B:59:ALA:HB3	2.11	0.49
1:B:69:VAL:CG2	1:B:90:ILE:CD1	2.89	0.49
1:C:141:MET:O	1:C:145:LYS:HD3	2.12	0.49
2:E:107:TYR:O	2:E:108:PHE:HD1	1.94	0.49
2:E:8:PRO:HG3	2:E:22:GLU:H	1.77	0.49
1:A:79:ASN:OD1	2:E:97:GLY:N	2.45	0.49
2:F:41:GLN:O	2:F:42:SER:HB3	2.12	0.49
1:B:89:GLY:HA3	1:B:130:GLN:NE2	2.27	0.49
2:E:72:LEU:H	2:E:72:LEU:HD23	1.77	0.49
1:C:65:ARG:HG3	1:C:66:ASP:N	2.27	0.49
1:D:70:ASP:OD1	1:D:93:ALA:HA	2.12	0.49
2:E:219:LEU:HD21	2:E:232:PRO:O	2.13	0.49
2:E:227:GLN:HE21	2:E:231:LYS:HZ3	1.60	0.49
1:D:11:SER:C	1:D:13:LEU:N	2.66	0.49
1:B:64:LYS:HE2	1:B:65:ARG:H	1.77	0.49
1:A:137:ARG:NH2	1:A:187:LYS:NZ	2.61	0.49
1:C:22:TYR:O	1:C:72:PHE:HA	2.13	0.49
1:B:164:ASP:OD1	1:B:198:ASN:OD1	2.31	0.49
1:C:170:ILE:HG22	1:C:170:ILE:O	2.13	0.49
1:A:184:ILE:C	1:A:186:ALA:N	2.66	0.49
1:A:4:LYS:NZ	1:A:154:VAL:HG22	2.28	0.49
2:E:240:GLU:OE2	2:E:242:TRP:HZ3	1.95	0.49
1:A:94:GLN:NE2	1:A:124:LYS:HA	2.18	0.49
1:B:10:LYS:HZ1	1:B:151:SER:CB	2.25	0.49
1:B:4:LYS:HB3	1:B:4:LYS:HZ3	1.77	0.49
2:F:33:PHE:CD1	2:F:33:PHE:N	2.79	0.49
1:D:77:ILE:CG1	1:D:78:LEU:H	2.25	0.48
1:C:76:TYR:CE1	1:C:77:ILE:HG22	2.48	0.48
2:E:84:PRO:HA	2:E:116:VAL:HG23	1.94	0.48
2:E:172:VAL:HA	2:E:195:ARG:O	2.13	0.48
1:D:75:PHE:CD1	1:D:75:PHE:C	2.87	0.48
1:B:195:ASN:ND2	1:B:197:LYS:N	2.61	0.48
2:E:52:GLY:O	2:E:52(A):SER:CB	2.57	0.48
2:F:234:THR:O	2:F:235:GLN:HG2	2.12	0.48
1:A:100:HIS:O	1:A:121:ILE:HG23	2.13	0.48
1:C:202:PHE:CD1	1:C:202:PHE:O	2.67	0.48
2:E:84:PRO:O	2:E:85:GLU:C	2.52	0.48
2:F:12:ILE:HD12	2:F:234:THR:H	1.78	0.48
1:A:102:LEU:HD12	1:A:120:ILE:CG2	2.40	0.48
1:A:17:TYR:O	1:A:19:ILE:HG22	2.13	0.48
1:A:102:LEU:HD22	1:A:199:PHE:CE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:SER:O	1:B:59:ALA:N	2.46	0.48
2:E:27(A):PHE:C	2:E:27(A):PHE:CD2	2.85	0.48
1:B:196:MET:C	1:B:198:ASN:H	2.16	0.48
1:B:19:ILE:HD12	1:B:181:ARG:CZ	2.43	0.48
2:E:8:PRO:HG2	2:E:21:ILE:HA	1.95	0.48
1:A:202:PHE:O	1:A:202:PHE:CD1	2.66	0.48
1:B:76:TYR:HA	1:B:181:ARG:CB	2.31	0.48
1:B:37:LEU:HB2	1:B:55:MET:CE	2.44	0.48
2:E:68:ASN:N	2:E:68:ASN:ND2	2.61	0.48
1:D:72:PHE:HD1	1:D:72:PHE:C	2.17	0.48
1:A:9:VAL:C	1:A:11:SER:H	2.17	0.48
2:F:12:ILE:CD1	2:F:234:THR:H	2.27	0.48
1:D:27:CYS:O	1:D:69:VAL:N	2.44	0.48
1:B:77:ILE:C	2:F:52:GLY:HA3	2.33	0.48
1:A:114:GLN:CD	1:A:115:ASN:N	2.67	0.48
2:E:23:CYS:SG	2:E:32:MET:CE	3.02	0.48
1:C:154:VAL:HG13	1:C:155:SER:OG	2.13	0.48
1:A:39:ILE:CD1	1:A:90:ILE:HD13	2.44	0.48
2:E:83:HIS:O	2:E:116:VAL:HG21	2.14	0.47
1:B:19:ILE:HD11	1:B:75:PHE:CE2	2.49	0.47
1:B:29:VAL:HG11	1:B:37:LEU:HD11	1.95	0.47
1:B:157:ARG:NE	1:B:159:GLU:OE2	2.47	0.47
1:A:50:TYR:CD1	1:A:82:THR:HG22	2.49	0.47
1:B:89:GLY:CA	1:B:130:GLN:NE2	2.77	0.47
2:E:33:PHE:HD1	2:E:93:SER:OG	1.96	0.47
2:E:36:ARG:HB2	2:E:46:MET:SD	2.54	0.47
2:F:72:LEU:HD23	2:F:72:LEU:H	1.79	0.47
1:D:94:GLN:HE22	1:D:125:ASP:H	1.62	0.47
2:E:31:THR:HG23	2:E:49:SER:O	2.14	0.47
2:F:86:ASP:OD2	2:F:116:VAL:HG23	2.14	0.47
1:B:106:LEU:HD23	1:B:106:LEU:C	2.35	0.47
2:E:40:LYS:O	2:E:41:GLN:CB	2.62	0.47
1:D:130:GLN:HA	1:D:188:TYR:CE1	2.49	0.47
2:F:116:VAL:HG12	2:F:116:VAL:O	2.13	0.47
2:F:12:ILE:HD12	2:F:233:VAL:CA	2.44	0.47
1:D:146:ILE:O	1:D:147:TYR:C	2.53	0.47
1:B:168:GLU:OE2	1:B:192:ARG:NH1	2.47	0.47
2:F:74:LEU:HG	2:F:75:SER:H	1.78	0.47
1:B:30:ASN:HB2	1:B:38:ASN:OD1	2.15	0.47
1:B:163:LYS:HD3	1:B:163:LYS:HA	1.71	0.47
1:B:72:PHE:C	1:B:72:PHE:HD1	2.17	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:ASP:OD2	1:B:188:TYR:OH	2.18	0.47
1:C:87:TYR:CE2	1:C:186:ALA:HA	2.49	0.47
1:C:180:THR:H	1:C:183:ASP:HB2	1.79	0.47
2:E:33:PHE:HD1	2:E:93:SER:HG	1.62	0.47
2:E:226:THR:CG2	2:E:227:GLN:HG3	2.44	0.47
2:F:72:LEU:HD23	2:F:72:LEU:N	2.29	0.47
1:B:131:GLU:HG3	1:B:135:LYS:HE3	1.95	0.47
2:E:110:PRO:O	2:E:111:GLY:O	2.33	0.47
2:E:118:GLU:HG3	2:E:119:ASP:H	1.80	0.47
2:E:83:HIS:C	2:E:116:VAL:HG21	2.34	0.47
2:E:14:LYS:HE2	2:E:222:ASN:N	2.30	0.47
1:A:30:ASN:ND2	1:A:30:ASN:C	2.66	0.47
1:B:181:ARG:NH1	2:F:52(A):SER:OG	2.48	0.47
1:B:195:ASN:HD22	1:B:197:LYS:N	2.13	0.47
1:B:7:SER:O	1:B:9:VAL:N	2.47	0.47
1:B:164:ASP:O	1:B:165:GLY:C	2.53	0.47
1:B:119:LYS:O	1:B:120:ILE:HG13	2.15	0.47
2:E:15:SER:HB3	2:E:83:HIS:CE1	2.50	0.47
2:E:172:VAL:HG12	2:E:196:LEU:HD13	1.96	0.47
2:E:60:VAL:O	2:E:61:GLU:HG2	2.15	0.47
1:B:75:PHE:CE1	1:B:181:ARG:NH1	2.83	0.47
1:B:75:PHE:C	1:B:75:PHE:CD1	2.88	0.47
1:C:157:ARG:HH21	1:C:205:TYR:C	2.18	0.47
2:E:180:LYS:NZ	2:E:184:ALA:HA	2.30	0.47
1:D:155:SER:HA	1:D:173:PHE:CD1	2.50	0.47
2:F:194:SER:OG	2:F:195:ARG:N	2.45	0.47
2:E:56:TYR:CD2	2:E:57:GLU:N	2.76	0.47
2:E:62:LYS:CA	2:E:62:LYS:HE2	2.29	0.47
2:F:12:ILE:CD1	2:F:234:THR:N	2.78	0.47
2:E:125:PRO:HB3	2:E:152:PHE:CD1	2.49	0.47
2:F:205:ASN:OD1	2:F:206:PRO:HD2	2.14	0.47
1:C:24:TYR:CE2	1:C:51:ILE:HD11	2.47	0.47
1:C:22:TYR:CE1	1:C:84:GLU:OE2	2.68	0.47
1:D:76:TYR:HB2	1:D:182:SER:HB2	1.96	0.47
1:C:14:LEU:HD23	1:C:14:LEU:C	2.34	0.46
1:A:10:LYS:O	1:A:14:LEU:HB2	2.15	0.46
2:E:125:PRO:CB	2:E:152:PHE:HB3	2.40	0.46
2:E:142:LYS:CD	2:E:197:ARG:HE	2.28	0.46
1:B:6:ILE:HG13	1:B:7:SER:H	1.78	0.46
2:F:205:ASN:CG	2:F:206:PRO:HD2	2.35	0.46
1:C:202:PHE:C	1:C:202:PHE:CD1	2.87	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:69:VAL:HG22	1:D:70:ASP:N	2.30	0.46
2:F:62:LYS:HD2	2:F:65:PHE:CE1	2.51	0.46
1:A:39:ILE:HD12	1:A:39:ILE:N	2.30	0.46
1:A:63:PHE:HB3	1:A:67:ASP:OD2	2.14	0.46
2:F:129:VAL:CG2	2:F:239:ALA:HB1	2.46	0.46
1:B:37:LEU:HB2	1:B:55:MET:HE1	1.97	0.46
1:D:41:THR:CG2	1:D:51:ILE:HG12	2.45	0.46
2:E:236:ILE:HG23	2:E:236:ILE:O	2.14	0.46
1:D:195:ASN:ND2	1:D:197:LYS:HB3	2.29	0.46
1:B:74:LEU:CB	1:B:185:PHE:CE2	2.99	0.46
1:B:200:SER:O	1:B:201:HIS:CB	2.61	0.46
1:D:22:TYR:O	1:D:72:PHE:HA	2.15	0.46
1:A:130:GLN:HG3	1:A:188:TYR:CE2	2.51	0.46
1:B:72:PHE:CZ	1:B:131:GLU:HG3	2.50	0.46
2:E:219:LEU:CD1	2:E:220:SER:HB2	2.45	0.46
1:D:29:VAL:HG11	1:D:64:LYS:C	2.36	0.46
1:B:60:SER:C	1:B:62:LYS:H	2.18	0.46
1:C:34:THR:CG2	1:C:34:THR:O	2.63	0.46
2:E:95:LEU:HD22	2:E:96:ALA:H	1.81	0.46
1:D:100:HIS:O	1:D:122:LEU:N	2.42	0.46
2:E:214:VAL:HB	2:E:237:VAL:CG2	2.36	0.46
1:D:85:TYR:CD1	1:D:85:TYR:N	2.83	0.46
1:A:201:HIS:HB3	1:C:103:LEU:CD1	2.46	0.46
1:B:80:SER:O	1:B:81:HIS:HB2	2.16	0.46
1:A:69:VAL:HG23	1:A:91:THR:O	2.15	0.46
1:C:9:VAL:C	1:C:11:SER:N	2.68	0.46
2:E:227:GLN:HG2	2:E:231:LYS:CD	2.39	0.46
1:B:29:VAL:HG22	1:B:39:ILE:HG12	1.98	0.46
1:D:104:GLY:H	1:D:117:ASN:HD22	1.64	0.46
1:A:28:ARG:CD	1:A:28:ARG:H	2.14	0.46
1:C:115:ASN:O	1:C:116:LEU:HD23	2.16	0.46
2:E:137:ILE:O	2:E:141:GLN:NE2	2.48	0.46
2:E:82:ALA:HB1	2:E:116:VAL:HG12	1.98	0.46
1:A:77:ILE:C	1:A:78:LEU:CD1	2.81	0.46
1:A:53:SER:HB2	1:A:90:ILE:CD1	2.45	0.46
1:B:21:PRO:HB3	1:B:74:LEU:HD23	1.98	0.46
2:E:136:GLU:OE2	2:E:144:THR:HG23	2.16	0.46
2:F:22:GLU:HB2	2:F:74:LEU:CD1	2.46	0.46
1:A:138:LYS:NZ	1:A:142:ASP:OD2	2.49	0.46
1:A:63:PHE:CE1	1:A:92:PRO:HG3	2.51	0.45
2:E:120:LEU:HD21	2:E:220:SER:CA	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:206:PRO:O	2:E:208:ASN:N	2.48	0.45
2:E:20:LYS:H	2:E:20:LYS:CD	2.26	0.45
2:F:6:GLN:NE2	2:F:90:TYR:O	2.34	0.45
2:E:14:LYS:HG3	2:E:15:SER:N	2.32	0.45
2:F:20:LYS:O	2:F:21:ILE:HG13	2.16	0.45
2:F:37:GLN:O	2:F:88:SER:OG	2.35	0.45
1:D:120:ILE:HD11	1:D:139:TYR:HB2	1.97	0.45
1:A:139:TYR:O	1:A:140:LEU:CG	2.64	0.45
2:E:120:LEU:HD21	2:E:220:SER:CB	2.46	0.45
2:E:59:GLY:O	2:E:60:VAL:HB	2.16	0.45
1:B:24:TYR:CD2	1:B:41:THR:HG21	2.50	0.45
1:C:55:MET:CE	1:C:60:SER:HA	2.47	0.45
1:B:148:ASP:O	1:B:149:ALA:C	2.55	0.45
1:B:140:LEU:HD21	1:B:204:ILE:HD12	1.98	0.45
1:D:108:ILE:O	1:D:111:GLU:O	2.34	0.45
1:C:144:TYR:O	1:C:145:LYS:C	2.54	0.45
1:C:108:ILE:H	1:C:112:SER:HA	1.82	0.45
1:A:3:LYS:NZ	1:D:61:GLN:CB	2.80	0.45
2:E:225:TRP:O	2:E:226:THR:O	2.35	0.45
2:F:9:SER:O	2:F:112:THR:HA	2.16	0.45
1:C:75:PHE:CZ	1:C:181:ARG:NH1	2.85	0.45
1:C:97:LYS:C	1:C:98:VAL:HG13	2.37	0.45
1:A:28:ARG:NH1	1:A:28:ARG:HG3	2.29	0.45
1:B:75:PHE:HA	1:B:86:ILE:HG22	1.98	0.45
1:D:178:GLU:O	1:D:180:THR:HG23	2.16	0.45
1:A:79:ASN:CB	2:E:30:THR:HG21	2.44	0.45
1:C:90:ILE:H	1:C:191:ASN:HD21	1.65	0.45
1:B:75:PHE:O	1:B:185:PHE:CE2	2.69	0.45
2:E:19:VAL:H	2:E:79:VAL:HG12	1.82	0.45
1:B:102:LEU:HD11	1:B:122:LEU:HD21	1.99	0.45
2:E:14:LYS:HG2	2:E:223:ASP:HB2	1.99	0.45
2:E:125:PRO:HB3	2:E:152:PHE:CG	2.52	0.45
1:A:98:VAL:HG21	1:A:100:HIS:CE1	2.52	0.45
1:B:87:TYR:CD2	1:B:185:PHE:O	2.70	0.44
2:E:230:ALA:O	2:E:231:LYS:C	2.56	0.44
2:E:68:ASN:HD21	2:E:76:THR:HG1	1.62	0.44
2:F:42:SER:O	2:F:44:MET:N	2.49	0.44
1:C:192:ARG:HE	1:C:192:ARG:HB3	1.58	0.44
2:F:12:ILE:HD12	2:F:234:THR:N	2.33	0.44
1:B:8:ASN:HD22	1:B:8:ASN:H	1.62	0.44
1:D:43:LYS:HG3	1:D:43:LYS:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:LEU:HB3	1:C:146:ILE:HD12	2.00	0.44
1:C:28:ARG:HA	1:C:67:ASP:O	2.17	0.44
1:C:9:VAL:O	1:C:13:LEU:HD12	2.16	0.44
1:D:84:GLU:C	1:D:85:TYR:HD1	2.21	0.44
1:D:64:LYS:HZ3	1:D:65:ARG:CG	2.31	0.44
2:F:5:SER:OG	2:F:6:GLN:N	2.51	0.44
1:C:162:THR:HG21	1:C:164:ASP:OD2	2.18	0.44
1:D:55:MET:HE3	1:D:60:SER:HA	1.99	0.44
1:A:57:TYR:C	1:A:59:ALA:H	2.20	0.44
2:E:16:GLY:H	2:E:82:ALA:HB3	1.80	0.44
1:B:157:ARG:CG	1:B:157:ARG:NH1	2.78	0.44
1:A:79:ASN:C	1:A:81:HIS:N	2.56	0.44
2:F:192:LEU:CD1	2:F:192:LEU:N	2.78	0.44
1:B:196:MET:C	1:B:198:ASN:N	2.71	0.44
1:B:104:GLY:H	1:B:117:ASN:ND2	2.16	0.44
1:D:7:SER:O	1:D:8:ASN:HB2	2.17	0.44
1:A:115:ASN:HB3	1:C:115:ASN:HD21	1.82	0.44
1:C:76:TYR:HB2	1:C:182:SER:HA	1.99	0.44
1:A:46:GLY:O	1:A:49:TYR:HD1	2.00	0.44
1:A:85:TYR:N	1:A:85:TYR:CD1	2.85	0.44
1:B:144:TYR:O	1:B:145:LYS:O	2.36	0.44
1:B:50:TYR:CD1	1:B:82:THR:O	2.71	0.44
1:C:91:THR:HB	1:C:92:PRO:CD	2.46	0.44
2:E:162:TRP:CB	2:E:211:ARG:HG2	2.48	0.44
1:B:102:LEU:HD11	1:B:122:LEU:HD23	1.96	0.44
1:D:156:GLY:C	1:D:157:ARG:HH11	2.21	0.44
2:E:92:CYS:O	2:E:93:SER:HB3	2.17	0.44
1:B:14:LEU:HD23	1:B:14:LEU:C	2.35	0.44
2:F:36:ARG:NH1	2:F:65:PHE:CE1	2.86	0.44
1:B:19:ILE:CG1	1:B:20:THR:N	2.80	0.44
1:A:31:PHE:CE1	1:A:33:THR:HG23	2.31	0.44
2:E:19:VAL:O	2:E:78:THR:HA	2.18	0.44
2:F:209:HIS:HB3	2:F:240:GLU:HG3	2.00	0.44
2:E:173:SER:O	2:E:194:SER:HA	2.18	0.43
2:E:136:GLU:HG2	2:E:140:THR:HG21	2.00	0.43
1:D:75:PHE:CE1	1:D:181:ARG:NH1	2.86	0.43
1:B:119:LYS:O	1:B:120:ILE:CG1	2.66	0.43
2:E:42:SER:O	2:E:43:LEU:HB2	2.18	0.43
2:E:113:ARG:HD3	2:E:156:HIS:HD1	1.78	0.43
1:D:184:ILE:HD12	1:D:184:ILE:O	2.18	0.43
2:E:201:THR:HA	2:E:204:GLN:CG	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:PHE:CD1	1:C:75:PHE:C	2.92	0.43
1:C:140:LEU:HD11	1:C:204:ILE:HG21	2.00	0.43
1:C:127:VAL:CG1	1:C:132:ILE:HG13	2.49	0.43
1:A:55:MET:HG3	1:A:60:SER:CB	2.48	0.43
1:A:124:LYS:HB3	1:A:126:ILE:O	2.19	0.43
1:B:77:ILE:HA	2:F:52(A):SER:H	1.83	0.43
1:B:14:LEU:HD23	1:B:15:TYR:H	1.75	0.43
1:D:127:VAL:HG12	1:D:128:THR:O	2.18	0.43
2:E:37:GLN:HG2	2:E:37:GLN:O	2.19	0.43
1:C:110:GLY:O	1:C:111:GLU:HB3	2.18	0.43
2:E:52(A):SER:C	2:E:54:ALA:N	2.67	0.43
1:C:69:VAL:HG23	1:C:91:THR:O	2.19	0.43
2:F:47:ALA:HB3	2:F:67:ILE:CG2	2.40	0.43
1:B:146:ILE:HD11	1:B:147:TYR:CZ	2.54	0.43
2:E:203:TRP:O	2:E:243:GLY:HA3	2.19	0.43
1:A:114:GLN:NE2	1:A:115:ASN:HB2	2.34	0.43
1:B:71:VAL:HG12	1:B:72:PHE:N	2.34	0.43
1:A:154:VAL:O	1:A:155:SER:OG	2.32	0.43
1:D:50:TYR:CZ	1:D:83:GLY:HA3	2.53	0.43
1:A:160:ILE:CG2	1:A:199:PHE:CE1	3.01	0.43
1:B:87:TYR:CD2	1:B:185:PHE:C	2.92	0.43
1:D:64:LYS:HG2	1:D:65:ARG:N	2.33	0.43
1:B:157:ARG:HB2	1:B:170:ILE:O	2.19	0.43
1:A:55:MET:HA	1:A:189:LYS:O	2.18	0.43
1:B:178:GLU:HB3	1:B:183:ASP:OD2	2.19	0.43
2:E:87:SER:OG	2:E:115:THR:HA	2.18	0.43
2:F:234:THR:O	2:F:235:GLN:CG	2.67	0.43
1:D:129:PHE:CE1	1:D:192:ARG:HG2	2.54	0.43
2:E:163:VAL:HG22	2:E:210:PHE:HE1	1.84	0.43
1:B:60:SER:O	1:B:62:LYS:HB2	2.18	0.43
1:D:75:PHE:CZ	1:D:181:ARG:NH1	2.87	0.43
2:F:20:LYS:O	2:F:21:ILE:CG1	2.67	0.43
2:E:180:LYS:HZ3	2:E:184:ALA:HA	1.83	0.43
2:F:127:VAL:HG23	2:F:128:ALA:N	2.32	0.43
1:B:144:TYR:O	1:B:145:LYS:C	2.57	0.43
1:A:163:LYS:HG2	1:A:198:ASN:HA	1.99	0.43
1:B:69:VAL:HG23	1:B:70:ASP:N	2.34	0.43
1:D:180:THR:O	1:D:184:ILE:HG22	2.19	0.43
1:B:150:THR:O	1:B:151:SER:CB	2.66	0.43
1:A:4:LYS:HE3	1:A:154:VAL:HG22	2.00	0.43
1:A:122:LEU:HD13	1:A:127:VAL:HG21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:SER:HB2	1:A:90:ILE:HD11	2.01	0.42
1:B:106:LEU:CG	1:B:204:ILE:HD11	2.49	0.42
1:B:11:SER:CA	1:B:14:LEU:HD22	2.45	0.42
2:E:159:LEU:HD22	2:E:174:THR:OG1	2.19	0.42
1:A:104:GLY:CA	1:A:202:PHE:O	2.67	0.42
1:A:79:ASN:O	1:A:79:ASN:CG	2.57	0.42
1:C:129:PHE:O	1:C:133:ASP:N	2.44	0.42
2:F:127:VAL:HA	2:F:150:THR:O	2.19	0.42
1:D:28:ARG:CZ	1:D:68:HIS:CE1	3.02	0.42
1:B:50:TYR:O	1:B:84:GLU:HG3	2.18	0.42
1:B:106:LEU:CD2	1:B:108:ILE:HG13	2.49	0.42
1:B:116:LEU:HD11	1:B:204:ILE:CD1	2.49	0.42
1:C:127:VAL:HG11	1:C:132:ILE:HG13	2.00	0.42
1:A:184:ILE:O	1:A:186:ALA:N	2.52	0.42
1:C:177:ASN:O	1:C:179:GLY:N	2.52	0.42
1:C:33:THR:OG1	1:C:34:THR:N	2.51	0.42
1:B:74:LEU:HB2	1:B:185:PHE:CZ	2.54	0.42
1:C:72:PHE:CD1	1:C:72:PHE:C	2.91	0.42
2:E:82:ALA:HB1	2:E:116:VAL:CG1	2.50	0.42
1:A:199:PHE:O	1:C:163:LYS:HE3	2.19	0.42
1:B:16:ALA:HB1	1:B:181:ARG:HE	1.85	0.42
2:E:229:ARG:C	2:E:231:LYS:H	2.23	0.42
1:C:17:TYR:C	1:C:19:ILE:N	2.71	0.42
2:F:148:LEU:HD23	2:F:149:ALA:H	1.84	0.42
1:C:130:GLN:HA	1:C:188:TYR:CE1	2.55	0.42
1:B:130:GLN:HG3	1:B:188:TYR:CG	2.54	0.42
1:C:177:ASN:O	1:C:178:GLU:C	2.58	0.42
1:B:126:ILE:N	1:B:126:ILE:HD12	2.34	0.42
1:B:138:LYS:O	1:B:139:TYR:C	2.58	0.42
2:E:118:GLU:OE2	2:E:224:GLU:HG2	2.19	0.42
1:B:8:ASN:ND2	1:B:8:ASN:H	2.17	0.42
1:B:21:PRO:HD3	1:B:134:PHE:CE2	2.55	0.42
1:D:85:TYR:HD1	1:D:85:TYR:N	2.17	0.42
1:D:167:HIS:ND1	1:D:167:HIS:C	2.72	0.42
1:D:168:GLU:OE1	1:D:192:ARG:NH1	2.53	0.42
1:C:160:ILE:HB	1:C:168:GLU:HB2	2.02	0.42
1:C:29:VAL:CG1	1:C:37:LEU:HD11	2.49	0.42
1:B:94:GLN:NE2	1:B:125:ASP:H	2.17	0.42
1:C:138:LYS:NZ	1:C:142:ASP:OD2	2.53	0.42
1:A:181:ARG:NH2	2:E:69:HIS:O	2.36	0.42
2:E:27(A):PHE:CE1	2:E:94:ALA:CB	3.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3:LYS:HD3	1:B:177:ASN:N	2.34	0.42
1:A:26:ASP:N	1:A:70:ASP:OD1	2.50	0.42
1:D:102:LEU:HD11	1:D:122:LEU:CG	2.36	0.42
1:B:28:ARG:CG	1:B:66:ASP:OD1	2.63	0.42
1:B:175:SER:HA	1:B:176:PRO:HD2	1.89	0.42
1:A:190:ASP:CG	1:A:192:ARG:HB2	2.40	0.42
1:B:186:ALA:C	1:B:188:TYR:H	2.22	0.42
1:C:61:GLN:HE21	1:C:61:GLN:HB3	1.70	0.42
2:E:17:THR:O	2:E:81:SER:O	2.38	0.42
1:A:9:VAL:O	1:A:10:LYS:C	2.57	0.42
1:D:6:ILE:HD12	1:D:6:ILE:HA	1.90	0.42
2:E:21:ILE:HD12	2:E:77:LEU:HD12	2.02	0.42
1:D:106:LEU:HD22	1:D:108:ILE:HG13	2.01	0.42
2:E:32:MET:O	2:E:49:SER:N	2.43	0.42
1:D:139:TYR:CE1	1:D:143:ASN:ND2	2.88	0.42
1:B:122:LEU:HA	1:B:122:LEU:HD13	1.80	0.42
1:A:6:ILE:CG2	1:A:7:SER:N	2.83	0.42
2:E:168:VAL:CG2	2:E:169:HIS:N	2.83	0.42
1:D:154:VAL:HG12	1:D:207:GLU:O	2.19	0.42
2:E:176:PRO:O	2:E:177:GLN:HB3	2.20	0.42
2:E:79:VAL:O	2:E:80:THR:CG2	2.68	0.42
1:B:69:VAL:CG2	1:B:90:ILE:HD12	2.50	0.42
1:D:147:TYR:HE1	1:D:172:LEU:O	2.03	0.42
1:D:9:VAL:C	1:D:11:SER:N	2.74	0.42
1:D:29:VAL:HG11	1:D:64:LYS:CA	2.50	0.42
1:D:132:ILE:CG2	1:D:133:ASP:N	2.83	0.42
1:D:55:MET:CE	1:D:60:SER:HA	2.50	0.42
2:F:88:SER:O	2:F:89:PHE:C	2.58	0.41
1:A:39:ILE:HD11	1:A:90:ILE:HD13	2.01	0.41
1:B:76:TYR:CE1	1:B:85:TYR:HD2	2.38	0.41
2:E:227:GLN:HE21	2:E:231:LYS:HZ2	1.67	0.41
1:B:55:MET:CB	1:B:59:ALA:HB3	2.48	0.41
1:A:10:LYS:HZ2	1:A:151:SER:HB3	1.84	0.41
1:B:21:PRO:HD3	1:B:134:PHE:CZ	2.55	0.41
2:E:142:LYS:CD	2:E:197:ARG:HH11	2.32	0.41
2:E:67:ILE:HA	2:E:76:THR:O	2.19	0.41
1:A:98:VAL:CG2	1:A:100:HIS:CE1	3.03	0.41
2:E:90:TYR:O	2:E:112:THR:HG22	2.21	0.41
1:B:141:MET:O	1:B:142:ASP:C	2.58	0.41
1:C:163:LYS:HD3	1:C:163:LYS:HA	1.89	0.41
1:D:100:HIS:CD2	1:D:196:MET:HG3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:TYR:HA	1:B:82:THR:O	2.20	0.41
1:D:64:LYS:NZ	1:D:65:ARG:HG2	2.35	0.41
2:E:199:SER:HB2	2:E:201:THR:O	2.20	0.41
2:F:125:PRO:HB2	2:F:126:GLU:H	1.53	0.41
2:F:40:LYS:O	2:F:41:GLN:HB2	2.20	0.41
1:B:119:LYS:C	1:B:120:ILE:HG13	2.40	0.41
2:F:86:ASP:CG	2:F:116:VAL:HG23	2.41	0.41
1:A:64:LYS:O	1:A:67:ASP:OD1	2.38	0.41
1:D:129:PHE:C	1:D:132:ILE:HG22	2.40	0.41
2:E:26:LEU:C	2:E:26:LEU:HD23	2.39	0.41
1:A:191:ASN:ND2	1:A:191:ASN:C	2.74	0.41
1:C:151:SER:HA	1:C:152:PRO:HD3	1.61	0.41
1:C:61:GLN:HG2	1:C:61:GLN:H	1.72	0.41
2:E:79:VAL:CG1	2:E:80:THR:N	2.69	0.41
2:E:107:TYR:O	2:E:108:PHE:CD1	2.73	0.41
1:B:19:ILE:CG1	1:B:20:THR:H	2.33	0.41
1:B:28:ARG:O	1:B:40:ASP:N	2.51	0.41
2:E:122:ASN:HB3	2:E:123:PHE:H	1.54	0.41
1:A:150:THR:O	1:A:150:THR:OG1	2.33	0.41
2:E:81:SER:O	2:E:82:ALA:HB2	2.21	0.41
2:F:115:THR:OG1	2:F:116:VAL:N	2.49	0.41
2:F:77:LEU:C	2:F:77:LEU:HD23	2.40	0.41
1:B:64:LYS:HZ1	1:B:65:ARG:HB3	1.80	0.41
2:E:208:ASN:HD22	2:E:209:HIS:N	2.18	0.41
1:B:196:MET:O	1:B:198:ASN:N	2.54	0.41
1:A:9:VAL:HG12	1:A:10:LYS:N	2.35	0.41
2:F:61:GLU:O	2:F:62:LYS:HB2	2.20	0.41
1:B:16:ALA:HA	1:B:181:ARG:HH21	1.84	0.41
1:A:72:PHE:O	1:A:89:GLY:HA3	2.21	0.41
1:C:64:LYS:O	1:C:65:ARG:C	2.59	0.41
1:A:55:MET:O	1:A:56:SER:C	2.59	0.41
2:F:74:LEU:CG	2:F:75:SER:H	2.32	0.41
1:A:119:LYS:HE2	1:A:139:TYR:CE1	2.56	0.41
1:A:76:TYR:HE1	1:A:77:ILE:HD11	1.86	0.41
2:F:38:PHE:HB3	2:F:39:PRO:HD2	2.01	0.41
1:C:64:LYS:O	1:C:65:ARG:O	2.39	0.41
1:A:122:LEU:HA	1:A:122:LEU:HD23	1.84	0.41
1:A:53:SER:CB	1:A:90:ILE:HD12	2.50	0.41
1:A:91:THR:O	1:A:92:PRO:C	2.59	0.41
2:E:172:VAL:HG12	2:E:196:LEU:HD12	2.02	0.41
1:C:16:ALA:HA	1:C:181:ARG:HE	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:ASP:OD2	1:A:188:TYR:OH	2.31	0.41
1:D:98:VAL:CG2	1:D:99:ASN:N	2.84	0.41
1:C:47:LYS:HE2	1:C:48:ASP:OD1	2.20	0.41
1:B:191:ASN:HD22	1:B:191:ASN:HA	1.54	0.41
2:E:68:ASN:H	2:E:68:ASN:HD22	1.66	0.41
1:B:10:LYS:HG2	1:B:147:TYR:HA	2.03	0.41
2:F:72:LEU:CD2	2:F:72:LEU:H	2.34	0.41
2:F:40:LYS:HE2	2:F:40:LYS:HB3	1.72	0.41
2:E:205:ASN:O	2:E:205:ASN:CG	2.59	0.41
2:E:14:LYS:O	2:E:82:ALA:HB3	2.21	0.40
1:D:29:VAL:CG1	1:D:64:LYS:C	2.89	0.40
1:A:186:ALA:O	1:A:189:LYS:HB2	2.20	0.40
1:B:94:GLN:HE22	1:B:125:ASP:H	1.68	0.40
1:A:17:TYR:O	1:A:19:ILE:N	2.54	0.40
2:E:110:PRO:C	2:E:111:GLY:O	2.58	0.40
1:A:97:LYS:NZ	1:A:123:GLU:OE1	2.54	0.40
2:E:17:THR:O	2:E:82:ALA:HB2	2.20	0.40
1:B:69:VAL:HG23	1:B:70:ASP:H	1.86	0.40
1:D:42:GLN:O	1:D:43:LYS:HB3	2.21	0.40
1:D:60:SER:O	1:D:61:GLN:C	2.60	0.40
1:B:3:LYS:HD3	1:B:177:ASN:H	1.86	0.40
1:D:14:LEU:O	1:D:18:THR:OG1	2.31	0.40
2:E:83:HIS:O	2:E:85:GLU:N	2.54	0.40
1:D:28:ARG:CZ	1:D:68:HIS:HE1	2.35	0.40
2:F:130:PHE:O	2:F:131:GLU:CB	2.70	0.40
2:E:27(A):PHE:O	2:E:28:GLN:HB2	2.21	0.40
1:C:106:LEU:CD2	1:C:106:LEU:C	2.90	0.40
1:A:12:ASP:N	1:A:12:ASP:OD1	2.54	0.40
2:E:95:LEU:HA	2:E:95:LEU:HD23	1.93	0.40
1:A:70:ASP:OD2	1:A:94:GLN:N	2.47	0.40
2:E:235:GLN:NE2	2:E:237:VAL:CG1	2.85	0.40
1:B:108:ILE:HG12	1:B:206:LEU:CB	2.35	0.40
1:D:4:LYS:O	1:D:5:ASP:C	2.60	0.40
2:F:27(A):PHE:CE2	2:F:28:GLN:O	2.75	0.40
1:A:75:PHE:C	1:A:75:PHE:HD1	2.22	0.40
2:E:215:GLN:HG2	2:E:217:TYR:CD2	2.56	0.40
2:E:228:ASP:O	2:E:229:ARG:HB2	2.22	0.40
2:E:140:THR:HG22	2:E:142:LYS:N	2.34	0.40
2:E:198:VAL:HG23	2:E:199:SER:N	2.35	0.40
1:B:154:VAL:CG1	1:B:155:SER:H	2.27	0.40
1:B:31:PHE:C	1:B:31:PHE:CD1	2.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:LYS:O	1:D:48:ASP:CB	2.69	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:141:GLN:OE1	2:E:223:ASP:OD2[1_655]	2.18	0.02

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	197/208 (95%)	145 (74%)	33 (17%)	19 (10%)	1	3
1	B	196/208 (94%)	146 (74%)	32 (16%)	18 (9%)	1	4
1	C	206/208 (99%)	152 (74%)	37 (18%)	17 (8%)	1	5
1	D	190/208 (91%)	147 (77%)	25 (13%)	18 (10%)	1	3
2	E	245/247 (99%)	143 (58%)	42 (17%)	60 (24%)	0	0
2	F	122/247 (49%)	59 (48%)	31 (25%)	32 (26%)	0	0
All	All	1156/1326 (87%)	792 (68%)	200 (17%)	164 (14%)	0	1

All (164) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	ILE
1	A	9	VAL
1	A	65	ARG
1	A	66	ASP
1	A	80	SER
1	A	115	ASN
1	B	4	LYS

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Mol	Chain	Res	Type
1	B	7	SER
1	B	81	HIS
1	B	177	ASN
1	C	65	ARG
1	C	79	ASN
1	C	81	HIS
1	D	5	ASP
1	D	6	ILE
1	D	31	PHE
1	D	61	GLN
1	D	79	ASN
1	D	81	HIS
1	D	111	GLU
1	D	112	SER
1	D	120	ILE
1	D	146	ILE
1	D	177	ASN
1	D	179	GLY
2	E	8	PRO
2	E	27	ASP
2	E	39	PRO
2	E	42	SER
2	E	51	GLU
2	E	52(A)	SER
2	E	60	VAL
2	E	79	VAL
2	E	81	SER
2	E	98	SER
2	E	99	GLY
2	E	107	TYR
2	E	120	LEU
2	E	122	ASN
2	E	123	PHE
2	E	139	HIS
2	E	153	TYR
2	E	155	ASP
2	E	220	SER
2	E	223	ASP
2	E	224	GLU
2	E	226	THR
2	E	234	THR
2	F	9	SER

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Mol	Chain	Res	Type
2	F	27	ASP
2	F	41	GLN
2	F	42	SER
2	F	43	LEU
2	F	75	SER
2	F	87	SER
2	F	125	PRO
2	F	131	GLU
2	F	195	ARG
2	F	207	ARG
2	F	208	ASN
2	F	235	GLN
2	F	236	ILE
2	F	237	VAL
1	A	4	LYS
1	A	64	LYS
1	A	140	LEU
1	A	145	LYS
1	A	165	GLY
1	B	8	ASN
1	B	61	GLN
1	B	66	ASP
1	B	145	LYS
1	B	165	GLY
1	B	201	HIS
1	C	109	SER
1	C	113	GLN
1	C	178	GLU
1	D	165	GLY
2	E	11	VAL
2	E	28	GLN
2	E	64	LYS
2	E	80	THR
2	E	82	ALA
2	E	140	THR
2	E	154	PRO
2	E	167	GLU
2	E	197	ARG
2	E	227	GLN
2	E	229	ARG
2	F	7	HIS
2	F	37	GLN

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Mol	Chain	Res	Type
2	F	81	SER
2	F	88	SER
2	F	110	PRO
2	F	115	THR
2	F	126	GLU
1	A	33	THR
1	A	79	ASN
1	B	77	ILE
1	C	6	ILE
1	C	47	LYS
1	C	112	SER
1	C	184	ILE
1	D	43	LYS
1	D	117	ASN
2	E	31	THR
2	E	41	GLN
2	E	43	LEU
2	E	62	LYS
2	E	101	SER
2	E	159	LEU
2	E	160	SER
2	E	185	LEU
2	E	206	PRO
2	F	8	PRO
2	F	48	THR
2	F	188	SER
1	A	77	ILE
1	A	150	THR
1	A	177	ASN
1	B	5	ASP
1	B	14	LEU
1	B	151	SER
1	C	80	SER
1	D	145	LYS
2	E	29	ALA
2	E	55	THR
2	E	86	ASP
2	E	103	ASP
2	E	110	PRO
2	E	169	HIS
2	E	188	SER
2	F	30	THR

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Mol	Chain	Res	Type
2	F	51	GLU
2	F	238	SER
1	A	185	PHE
1	B	30	ASN
1	B	35	HIS
1	C	18	THR
1	C	110	GLY
1	C	134	PHE
1	D	110	GLY
2	E	10	ARG
2	E	12	ILE
2	E	40	LYS
2	E	125	PRO
2	E	216	PHE
2	F	21	ILE
2	F	206	PRO
1	A	113	GLN
1	B	197	LYS
1	C	177	ASN
2	E	93	SER
2	E	231	LYS
2	F	239	ALA
1	B	86	ILE
1	D	77	ILE
2	E	111	GLY
1	A	152	PRO
1	C	170	ILE
2	E	233	VAL
2	F	84	PRO
1	C	120	ILE
2	E	232	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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	183/192 (95%)	153 (84%)	30 (16%)	3 14
1	B	175/192 (91%)	156 (89%)	19 (11%)	8 30
1	C	186/192 (97%)	166 (89%)	20 (11%)	8 30
1	D	171/192 (89%)	157 (92%)	14 (8%)	14 46
2	E	201/213 (94%)	162 (81%)	39 (19%)	2 9
2	F	108/213 (51%)	87 (81%)	21 (19%)	2 9
All	All	1024/1194 (86%)	881 (86%)	143 (14%)	4 19

All (143) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	7	SER
1	A	8	ASN
1	A	12	ASP
1	A	14	LEU
1	A	25	LYS
1	A	28	ARG
1	A	29	VAL
1	A	30	ASN
1	A	31	PHE
1	A	32	SER
1	A	51	ILE
1	A	63	PHE
1	A	65	ARG
1	A	77	ILE
1	A	85	TYR
1	A	99	ASN
1	A	106	LEU
1	A	108	ILE
1	A	112	SER
1	A	127	VAL
1	A	128	THR
1	A	150	THR
1	A	157	ARG
1	A	164	ASP
1	A	166	LYS
1	A	168	GLU

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Mol	Chain	Res	Type
1	A	191	ASN
1	A	195	ASN
1	A	207	GLU
1	B	4	LYS
1	B	14	LEU
1	B	64	LYS
1	B	69	VAL
1	B	72	PHE
1	B	78	LEU
1	B	79	ASN
1	B	90	ILE
1	B	98	VAL
1	B	128	THR
1	B	143	ASN
1	B	148	ASP
1	B	157	ARG
1	B	164	ASP
1	B	168	GLU
1	B	171	ASP
1	B	191	ASN
1	B	193	ILE
1	B	197	LYS
1	C	1	ASP
1	C	5	ASP
1	C	6	ILE
1	C	13	LEU
1	C	20	THR
1	C	34	THR
1	C	45	ARG
1	C	58	GLU
1	C	65	ARG
1	C	85	TYR
1	C	106	LEU
1	C	146	ILE
1	C	155	SER
1	C	157	ARG
1	C	175	SER
1	C	191	ASN
1	C	195	ASN
1	C	197	LYS
1	C	200	SER
1	C	207	GLU

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Mol	Chain	Res	Type
1	D	13	LEU
1	D	41	THR
1	D	45	ARG
1	D	55	MET
1	D	58	GLU
1	D	63	PHE
1	D	66	ASP
1	D	72	PHE
1	D	85	TYR
1	D	106	LEU
1	D	111	GLU
1	D	157	ARG
1	D	167	HIS
1	D	191	ASN
2	E	10	ARG
2	E	14	LYS
2	E	27(A)	PHE
2	E	39	PRO
2	E	43	LEU
2	E	44	MET
2	E	51	GLU
2	E	55	THR
2	E	58	GLN
2	E	61	GLU
2	E	67	ILE
2	E	68	ASN
2	E	77	LEU
2	E	78	THR
2	E	95	LEU
2	E	102	THR
2	E	108	PHE
2	E	113	ARG
2	E	116	VAL
2	E	125	PRO
2	E	144	THR
2	E	148	LEU
2	E	150	THR
2	E	155	ASP
2	E	169	HIS
2	E	185	LEU
2	E	195	ARG
2	E	207	ARG

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Mol	Chain	Res	Type
2	E	208	ASN
2	E	210	PHE
2	E	211	ARG
2	E	215	GLN
2	E	222	ASN
2	E	224	GLU
2	E	226	THR
2	E	228	ASP
2	E	229	ARG
2	E	232	PRO
2	E	235	GLN
2	F	5	SER
2	F	7	HIS
2	F	10	ARG
2	F	20	LYS
2	F	33	PHE
2	F	35	TYR
2	F	61	GLU
2	F	62	LYS
2	F	67	ILE
2	F	76	THR
2	F	77	LEU
2	F	83	HIS
2	F	108	PHE
2	F	125	PRO
2	F	126	GLU
2	F	130	PHE
2	F	146	VAL
2	F	147	CYS
2	F	148	LEU
2	F	187	ASP
2	F	192	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	ASN
1	A	94	GLN
1	A	114	GLN
1	A	117	ASN
1	A	195	ASN
1	B	8	ASN

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Mol	Chain	Res	Type
1	B	94	GLN
1	B	100	HIS
1	B	117	ASN
1	B	130	GLN
1	B	191	ASN
1	B	195	ASN
1	C	8	ASN
1	C	30	ASN
1	C	42	GLN
1	C	61	GLN
1	C	81	HIS
1	C	94	GLN
1	C	167	HIS
1	C	191	ASN
1	D	68	HIS
1	D	94	GLN
1	D	117	ASN
1	D	167	HIS
1	D	177	ASN
1	D	191	ASN
1	D	195	ASN
2	E	28	GLN
2	E	37	GLN
2	E	68	ASN
2	E	122	ASN
2	E	141	GLN
2	E	156	HIS
2	E	169	HIS
2	E	208	ASN
2	E	215	GLN
2	E	227	GLN
2	F	68	ASN

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 [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	203/208 (97%)	0.39	7 (3%)	49	21	29, 56, 87, 119	0
1	B	200/208 (96%)	0.54	13 (6%)	22	8	49, 81, 103, 124	0
1	C	208/208 (100%)	0.42	7 (3%)	49	21	34, 57, 84, 104	0
1	D	198/208 (95%)	0.58	16 (8%)	15	5	50, 74, 110, 130	0
2	E	247/247 (100%)	0.69	22 (8%)	12	4	42, 80, 119, 130	0
2	F	144/247 (58%)	1.29	28 (19%)	1	1	69, 112, 137, 149	0
All	All	1200/1326 (90%)	0.62	93 (7%)	16	6	29, 74, 123, 149	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	89	PHE	9.3
2	F	151	GLY	8.9
1	D	29	VAL	7.7
2	F	150	THR	7.2
2	F	147	CYS	5.8
1	D	66	ASP	5.4
2	E	128	ALA	5.1
2	F	15	SER	4.7
2	F	18	SER	4.6
2	F	146	VAL	4.5
1	B	177	ASN	4.1
1	A	3	LYS	4.1
1	C	114	GLN	4.0
2	E	16	GLY	4.0
2	F	237	VAL	4.0
1	B	5	ASP	4.0
2	F	204	GLN	4.0
2	E	225	TRP	3.9
2	F	130	PHE	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	30	ASN	3.6
1	D	82	THR	3.5
2	F	42	SER	3.5
1	B	35	HIS	3.4
2	E	100	SER	3.4
2	E	223	ASP	3.4
1	D	185	PHE	3.4
2	F	55	THR	3.3
2	E	115	THR	3.3
1	C	152	PRO	3.3
2	E	232	PRO	3.3
1	B	15	TYR	3.1
1	D	28	ARG	3.1
1	D	58	GLU	3.1
1	D	81	HIS	3.1
1	C	179	GLY	2.9
1	B	41	THR	2.9
1	C	81	HIS	2.9
2	E	102	THR	2.9
2	E	228	ASP	2.8
2	E	99	GLY	2.8
1	B	22	TYR	2.7
1	D	30	ASN	2.7
2	F	107	TYR	2.7
1	B	176	PRO	2.7
2	E	81	SER	2.7
2	F	92	CYS	2.6
2	F	215	GLN	2.6
1	A	57	TYR	2.6
1	B	34	THR	2.6
1	B	147	TYR	2.6
2	E	28	GLN	2.5
2	F	64	LYS	2.5
1	C	2	SER	2.5
2	F	17	THR	2.5
1	B	178	GLU	2.5
2	F	189	ARG	2.5
2	E	12	ILE	2.5
2	F	59	GLY	2.4
2	F	209	HIS	2.4
2	E	218	GLY	2.4
1	D	4	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
2	F	66	LEU	2.4
2	F	152	PHE	2.4
1	D	86	ILE	2.4
1	D	7	SER	2.3
1	D	16	ALA	2.3
2	F	90	TYR	2.3
2	F	11	VAL	2.3
1	B	202	PHE	2.2
2	F	210	PHE	2.2
1	A	60	SER	2.2
2	E	203	TRP	2.2
1	B	42	GLN	2.1
2	F	52	GLY	2.1
2	E	14	LYS	2.1
1	B	36	THR	2.1
2	E	55	THR	2.1
1	D	161	GLY	2.1
1	C	153	TYR	2.1
1	C	61	GLN	2.1
2	F	129	VAL	2.1
1	D	104	GLY	2.1
2	E	25	SER	2.1
2	E	221	GLU	2.1
1	D	85	TYR	2.1
1	A	96	ASN	2.1
2	E	215	GLN	2.0
1	A	162	THR	2.0
1	D	167	HIS	2.0
2	E	30	THR	2.0
2	E	224	GLU	2.0
1	A	175	SER	2.0
2	F	190	TYR	2.0

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

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

6.3 Carbohydrates ⓘ

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.