



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:09 PM UTC

PDB ID : 3FMV / pdb_00003fmv
Title : Crystal structure of the serine phosphatase of RNA polymerase II CTD (SSU72 superfamily) from *Drosophila melanogaster*. Monoclinic crystal form. Northeast Structural Genomics Consortium target FR253.
Authors : Kuzin, A.P.; Chen, Y.; Seetharaman, J.; Forouhar, F.; Chinag, Y.; Fang, Y.; Cunningham, K.; Ma, L.-C.; Xiao, R.; Liu, J.; Baran, M.C.; Acton, T.B.; Rost, B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2008-12-22
Resolution : 3.31 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

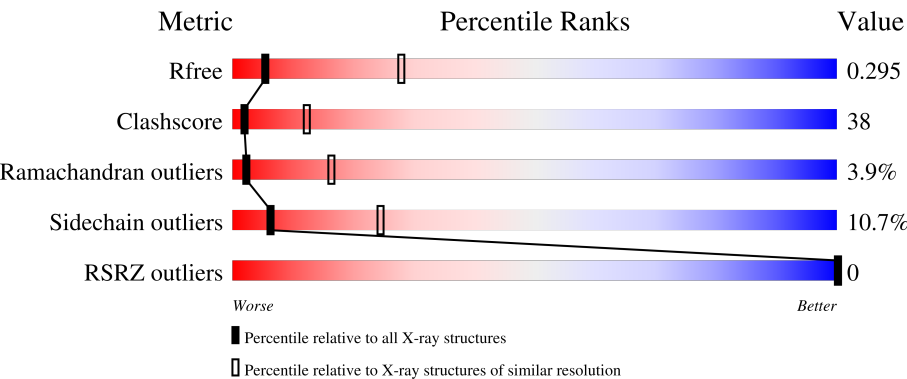
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.31 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}	180053	1153 (3.34-3.30)
Clashscore	190562	1193 (3.34-3.30)
Ramachandran outliers	187476	1172 (3.34-3.30)
Sidechain outliers	187428	1171 (3.34-3.30)
RSRZ outliers	180081	1153 (3.34-3.30)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	195	33%53%11%..
1	B	195	37%45%15%..
1	C	195	36%49%11%..

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
1	D	195	39%49%9%
1	E	195	34%47%15%
1	F	195	38%49%9%
1	G	195	43%45%9%
1	H	195	39%47%10%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12432 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.

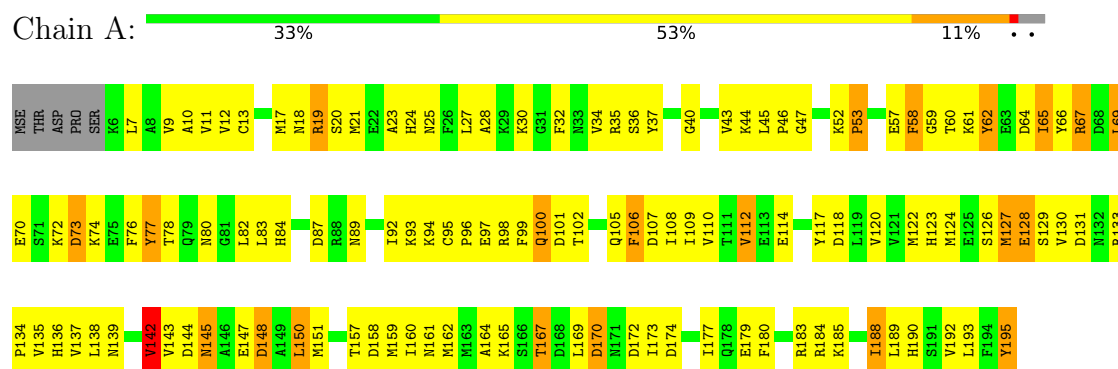
- Molecule 1 is a protein called Serine phosphatase of RNA polymerase II CTD.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	190	Total	C	N	O	S	Se	0	0	0
			1554	975	268	298	2	11			
1	B	190	Total	C	N	O	S	Se	0	0	0
			1554	975	268	298	2	11			
1	C	190	Total	C	N	O	S	Se	0	0	0
			1554	975	268	298	2	11			
1	D	190	Total	C	N	O	S	Se	0	0	0
			1554	975	268	298	2	11			
1	E	190	Total	C	N	O	S	Se	0	0	0
			1554	975	268	298	2	11			
1	F	190	Total	C	N	O	S	Se	0	0	0
			1554	975	268	298	2	11			
1	G	190	Total	C	N	O	S	Se	0	0	0
			1554	975	268	298	2	11			
1	H	190	Total	C	N	O	S	Se	0	0	0
			1554	975	268	298	2	11			

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

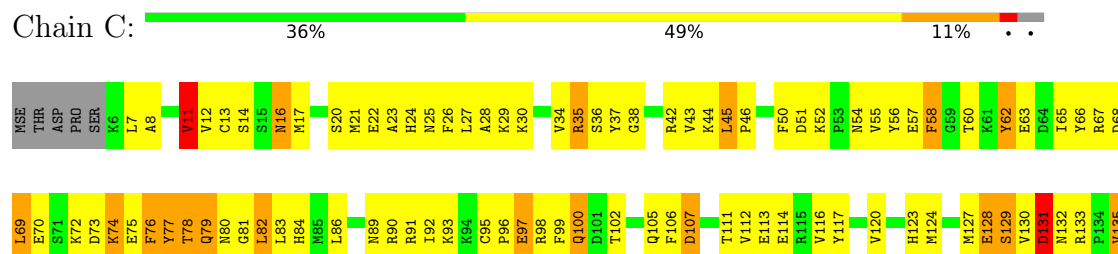
• Molecule 1: Serine phosphatase of RNA polymerase II CTD



• Molecule 1: Serine phosphatase of RNA polymerase II CTD

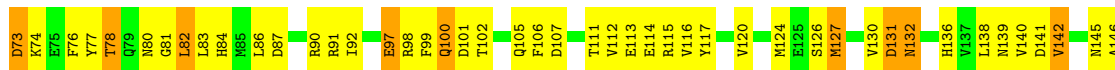
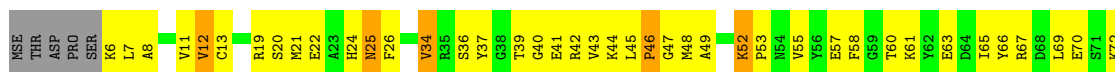


• Molecule 1: Serine phosphatase of RNA polymerase II CTD

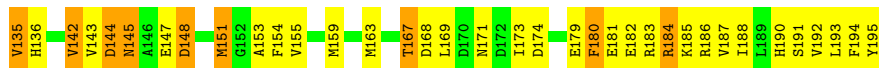
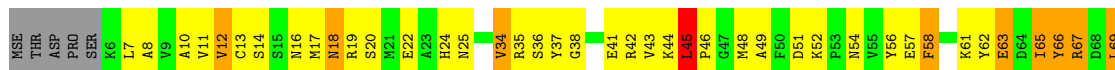
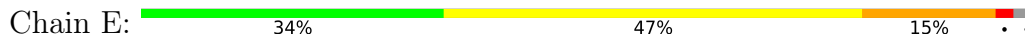




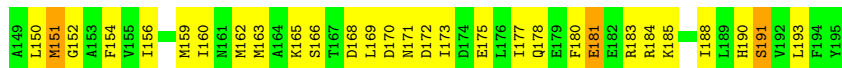
- Molecule 1: Serine phosphatase of RNA polymerase II CTD



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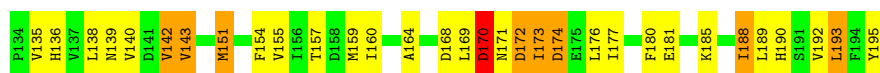
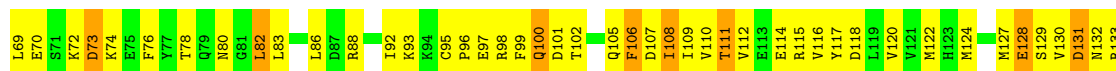
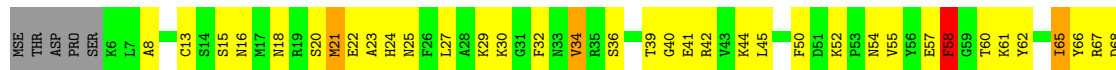
- Molecule 1: Serine phosphatase of RNA polymerase II CTD





• Molecule 1: Serine phosphatase of RNA polymerase II CTD

Chain H: 39% 47% 10% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.98Å 99.00Å 158.12Å 90.00° 90.87° 90.00°	Depositor
Resolution (Å)	19.93 – 3.31 19.93 – 3.31	Depositor EDS
% Data completeness (in resolution range)	87.5 (19.93-3.31) 91.0 (19.93-3.31)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.73 (at 3.31Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.228 , 0.280 0.245 , 0.295	Depositor DCC
R_{free} test set	2701 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	70.5	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.117 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12432	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	0.76	1/1568 (0.1%)	1.26	14/2088 (0.7%)
1	B	0.74	0/1568	1.20	8/2088 (0.4%)
1	C	0.74	0/1568	1.16	10/2088 (0.5%)
1	D	0.63	0/1568	1.09	7/2088 (0.3%)
1	E	0.75	0/1568	1.24	13/2088 (0.6%)
1	F	0.58	0/1568	1.08	10/2088 (0.5%)
1	G	0.63	0/1568	1.12	11/2088 (0.5%)
1	H	0.67	0/1568	1.15	9/2088 (0.4%)
All	All	0.69	1/12544 (0.0%)	1.16	82/16704 (0.5%)

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	C	0	1
1	E	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	142	VAL	CA-CB	5.26	1.61	1.54

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	ARG	CA-C-N	12.72	132.89	119.78
1	A	133	ARG	C-N-CA	12.72	132.89	119.78
1	C	62	TYR	N-CA-C	-9.46	99.48	111.02
1	D	169	LEU	N-CA-C	9.26	121.30	111.03
1	C	34	VAL	N-CA-C	9.02	121.47	108.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	65	ILE	N-CA-C	-8.82	101.81	110.72
1	E	180	PHE	N-CA-C	-8.63	102.30	113.17
1	H	34	VAL	N-CA-C	8.19	119.58	108.11
1	B	34	VAL	N-CA-C	7.90	120.23	108.46
1	H	78	THR	N-CA-C	-7.88	103.45	113.23
1	A	112	VAL	N-CA-C	7.81	119.59	112.17
1	A	62	TYR	N-CA-C	-7.71	102.88	111.82
1	E	187	VAL	N-CA-C	7.44	118.60	109.30
1	B	133	ARG	N-CA-C	-7.29	100.61	109.72
1	H	110	VAL	N-CA-C	7.20	117.77	108.12
1	E	72	LYS	N-CA-C	-7.17	101.87	108.75
1	F	78	THR	N-CA-C	-7.08	103.62	112.90
1	H	192	VAL	N-CA-C	7.03	117.78	107.37
1	C	11	VAL	N-CA-C	-7.00	98.31	108.11
1	D	192	VAL	N-CA-C	6.88	118.04	107.99
1	A	34	VAL	N-CA-C	6.88	118.63	108.45
1	H	65	ILE	N-CA-C	-6.75	103.90	110.72
1	B	104	GLU	N-CA-C	6.74	119.74	110.24
1	E	12	VAL	N-CA-C	6.71	117.97	108.17
1	G	91	ARG	N-CA-C	-6.66	105.69	113.88
1	A	23	ALA	N-CA-C	-6.56	104.21	111.36
1	G	181	GLU	N-CA-C	-6.53	104.79	112.89
1	G	192	VAL	N-CA-C	6.46	117.51	110.21
1	H	106	PHE	N-CA-C	6.42	117.91	108.86
1	A	77	TYR	N-CA-C	6.38	120.33	112.54
1	E	95	CYS	CA-C-N	6.31	126.26	119.76
1	E	95	CYS	C-N-CA	6.31	126.26	119.76
1	G	65	ILE	N-CA-C	-6.30	104.35	110.72
1	D	78	THR	N-CA-C	-6.24	103.06	112.04
1	B	78	THR	N-CA-C	-6.19	105.22	112.89
1	G	62	TYR	N-CA-C	-6.14	104.66	111.36
1	D	34	VAL	N-CA-C	6.13	117.42	108.53
1	A	12	VAL	N-CA-C	6.11	116.89	107.78
1	G	52	LYS	CA-C-N	6.11	126.62	120.14
1	G	52	LYS	C-N-CA	6.11	126.62	120.14
1	G	12	VAL	N-CA-C	6.06	116.81	107.78
1	E	78	THR	N-CA-C	-5.97	104.34	111.69
1	H	21	MSE	N-CA-C	5.93	117.83	111.36
1	C	77	TYR	N-CA-C	5.88	118.64	111.82
1	G	18	ASN	N-CA-C	5.83	120.02	111.34
1	F	18	ASN	N-CA-C	5.78	118.01	108.48
1	D	194	PHE	N-CA-C	5.77	118.95	110.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	14	SER	N-CA-C	5.76	118.43	111.40
1	E	34	VAL	N-CA-C	5.74	117.61	108.89
1	F	48	MSE	N-CA-C	-5.71	105.14	111.36
1	C	78	THR	N-CA-C	-5.67	106.32	113.18
1	B	110	VAL	CB-CA-C	-5.59	103.48	111.31
1	C	107	ASP	N-CA-C	-5.59	107.01	113.88
1	B	173	ILE	N-CA-C	-5.58	105.09	110.72
1	D	177	ILE	N-CA-C	-5.55	104.95	111.00
1	F	30	LYS	N-CA-C	-5.54	106.56	113.38
1	C	151	MSE	N-CA-C	-5.54	105.16	111.14
1	F	82	LEU	N-CA-C	-5.47	105.23	111.14
1	A	133	ARG	CB-CA-C	5.46	115.92	109.47
1	C	181	GLU	N-CA-C	-5.45	106.47	113.23
1	H	174	ASP	N-CA-C	5.43	119.01	112.38
1	E	48	MSE	N-CA-C	-5.43	104.39	111.02
1	C	129	SER	N-CA-C	5.41	117.06	110.41
1	A	67	ARG	N-CA-C	-5.40	105.29	111.07
1	H	188	ILE	N-CA-C	5.38	115.38	107.15
1	A	65	ILE	N-CA-C	-5.37	105.14	110.62
1	G	185	LYS	N-CA-C	5.33	117.14	110.91
1	F	21	MSE	N-CA-C	5.31	117.15	111.36
1	A	106	PHE	N-CA-C	5.23	117.23	109.69
1	F	52	LYS	CA-C-N	5.23	125.69	120.14
1	F	52	LYS	C-N-CA	5.23	125.69	120.14
1	G	35	ARG	N-CA-C	-5.22	101.42	109.52
1	E	65	ILE	N-CA-C	-5.17	105.34	110.62
1	B	23	ALA	N-CA-C	-5.17	105.26	112.45
1	A	192	VAL	N-CA-C	5.14	115.49	107.99
1	D	12	VAL	N-CA-C	5.12	115.28	108.27
1	B	65	ILE	N-CA-C	-5.11	104.59	111.44
1	F	181	GLU	N-CA-C	-5.08	106.93	113.23
1	E	104	GLU	N-CA-C	5.08	117.26	110.35
1	E	45	LEU	CA-C-N	5.07	125.05	120.03
1	E	45	LEU	C-N-CA	5.07	125.05	120.03
1	A	134	PRO	N-CA-C	5.00	119.16	111.21

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	37	TYR	Sidechain
1	E	66	TYR	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	1554	0	1529	138	0
1	B	1554	0	1529	131	0
1	C	1554	0	1529	139	0
1	D	1554	0	1529	113	0
1	E	1554	0	1529	134	0
1	F	1554	0	1529	102	0
1	G	1554	0	1529	106	0
1	H	1554	0	1529	118	0
All	All	12432	0	12232	946	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 38.

All (946) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:100:GLN:H	1:G:100:GLN:NE2	1.53	1.04
1:E:51:ASP:O	1:E:52:LYS:HE3	1.56	1.04
1:C:100:GLN:HE21	1:C:100:GLN:N	1.59	0.99
1:C:13:CYS:SG	1:C:20:SER:HB2	2.01	0.99
1:D:100:GLN:H	1:D:100:GLN:NE2	1.61	0.99
1:B:100:GLN:HE21	1:B:100:GLN:N	1.62	0.98
1:F:78:THR:HG23	1:F:83:LEU:HD12	1.46	0.98
1:G:100:GLN:HE21	1:G:100:GLN:N	1.62	0.96
1:F:100:GLN:H	1:F:100:GLN:NE2	1.62	0.96
1:D:100:GLN:HE21	1:D:100:GLN:N	1.62	0.96
1:A:57:GLU:HG2	1:A:59:GLY:H	1.30	0.95
1:A:100:GLN:H	1:A:100:GLN:HE21	1.11	0.95
1:E:115:ARG:O	1:E:119:LEU:HD13	1.66	0.94
1:F:61:LYS:HE3	1:F:94:LYS:HE3	1.47	0.94
1:C:21:MSE:HE3	1:C:92:ILE:HD12	1.47	0.94
1:D:78:THR:HG22	1:D:83:LEU:HD12	1.49	0.93
1:H:112:VAL:HB	1:H:142:VAL:HG13	1.49	0.92
1:F:100:GLN:HE21	1:F:100:GLN:N	1.67	0.92
1:B:100:GLN:H	1:B:100:GLN:NE2	1.67	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:LYS:O	1:B:65:ILE:HD13	1.71	0.91
1:C:100:GLN:H	1:C:100:GLN:NE2	1.67	0.90
1:E:130:VAL:HG23	1:E:131:ASP:H	1.36	0.89
1:A:45:LEU:HD23	1:A:82:LEU:HD12	1.51	0.89
1:D:112:VAL:HB	1:D:142:VAL:CG1	2.03	0.89
1:F:61:LYS:HA	1:F:95:CYS:HB3	1.54	0.89
1:B:90:ARG:HB2	1:B:90:ARG:HH11	1.35	0.88
1:F:100:GLN:H	1:F:100:GLN:HE21	0.91	0.87
1:G:78:THR:HG23	1:G:83:LEU:HD12	1.56	0.87
1:F:61:LYS:HA	1:F:95:CYS:CB	2.05	0.86
1:E:99:PHE:O	1:E:102:THR:HG22	1.76	0.86
1:A:100:GLN:H	1:A:100:GLN:NE2	1.72	0.86
1:A:61:LYS:HB2	1:A:64:ASP:OD2	1.75	0.85
1:E:67:ARG:NH1	1:E:67:ARG:HB2	1.91	0.85
1:F:57:GLU:O	1:F:60:THR:HG23	1.77	0.85
1:B:112:VAL:HB	1:B:142:VAL:CG1	2.06	0.85
1:A:112:VAL:HB	1:A:142:VAL:CG1	2.07	0.84
1:E:159:MSE:HE1	1:E:188:ILE:HD13	1.57	0.84
1:G:99:PHE:CE2	1:G:120:VAL:HG13	2.13	0.84
1:A:73:ASP:HB3	1:A:76:PHE:HB3	1.58	0.84
1:A:112:VAL:HB	1:A:142:VAL:HG13	1.60	0.84
1:E:100:GLN:H	1:E:100:GLN:NE2	1.75	0.84
1:B:73:ASP:HB3	1:B:76:PHE:HB3	1.60	0.83
1:E:61:LYS:HA	1:E:95:CYS:HB3	1.57	0.83
1:C:45:LEU:HD23	1:C:82:LEU:HD12	1.61	0.83
1:H:107:ASP:C	1:H:108:ILE:HD12	2.04	0.83
1:B:33:ASN:HD22	1:B:33:ASN:C	1.87	0.83
1:B:87:ASP:O	1:B:90:ARG:HG2	1.79	0.82
1:C:99:PHE:O	1:C:102:THR:HG22	1.77	0.82
1:B:112:VAL:HB	1:B:142:VAL:HG13	1.61	0.82
1:H:100:GLN:H	1:H:100:GLN:HE21	1.25	0.82
1:B:78:THR:HG22	1:B:83:LEU:HD12	1.60	0.82
1:C:113:GLU:HB3	1:C:116:VAL:HG23	1.60	0.81
1:C:155:VAL:HG22	1:C:184:ARG:HH12	1.44	0.81
1:H:80:ASN:OD1	1:H:82:LEU:HB2	1.81	0.80
1:D:159:MSE:HE1	1:D:188:ILE:HG12	1.64	0.80
1:C:159:MSE:HB2	1:C:180:PHE:CZ	2.17	0.80
1:F:73:ASP:HB3	1:F:76:PHE:HB3	1.61	0.80
1:E:127:MSE:H	1:E:127:MSE:SE	2.14	0.79
1:B:45:LEU:HD23	1:B:82:LEU:CD1	2.12	0.79
1:D:99:PHE:O	1:D:102:THR:HG22	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:85:MSE:HG3	1:G:88:ARG:NH2	1.99	0.78
1:C:13:CYS:SG	1:C:20:SER:CB	2.72	0.78
1:F:7:LEU:HB2	1:F:107:ASP:OD2	1.83	0.78
1:C:100:GLN:HE21	1:C:100:GLN:H	0.81	0.78
1:A:7:LEU:H	1:A:7:LEU:HD23	1.49	0.77
1:D:111:THR:HG21	1:D:117:TYR:HA	1.67	0.77
1:G:100:GLN:H	1:G:100:GLN:HE21	0.79	0.77
1:B:7:LEU:HD23	1:B:7:LEU:H	1.50	0.77
1:E:67:ARG:CG	1:E:67:ARG:HH11	1.98	0.77
1:B:66:TYR:CD1	1:B:83:LEU:HD22	2.20	0.76
1:A:106:PHE:HB2	1:A:109:ILE:HD11	1.67	0.76
1:C:111:THR:HG21	1:C:117:TYR:HA	1.66	0.75
1:D:67:ARG:HH11	1:D:67:ARG:HG3	1.49	0.75
1:B:99:PHE:O	1:B:102:THR:HG22	1.87	0.75
1:B:80:ASN:OD1	1:B:82:LEU:HD23	1.85	0.75
1:G:99:PHE:O	1:G:102:THR:HG22	1.86	0.75
1:D:73:ASP:HB3	1:D:76:PHE:HB3	1.69	0.75
1:A:100:GLN:HE21	1:A:100:GLN:N	1.84	0.75
1:A:120:VAL:O	1:A:124:MSE:HG2	1.86	0.75
1:A:78:THR:CG2	1:A:83:LEU:HD12	2.16	0.74
1:C:116:VAL:O	1:C:120:VAL:HG23	1.87	0.74
1:H:107:ASP:HB2	1:H:108:ILE:HD12	1.70	0.74
1:D:100:GLN:H	1:D:100:GLN:HE21	0.81	0.74
1:B:61:LYS:CE	1:B:94:LYS:HE3	2.18	0.74
1:E:24:HIS:HD2	1:E:36:SER:OG	1.71	0.74
1:A:99:PHE:O	1:A:102:THR:HG22	1.87	0.73
1:C:45:LEU:N	1:C:45:LEU:HD12	2.03	0.73
1:D:78:THR:CG2	1:D:83:LEU:HD12	2.19	0.73
1:B:150:LEU:HD23	1:B:150:LEU:H	1.53	0.73
1:F:44:LYS:C	1:F:45:LEU:HD12	2.14	0.73
1:A:158:ASP:CG	1:A:184:ARG:HH21	1.95	0.73
1:A:67:ARG:HG3	1:A:67:ARG:HH11	1.52	0.73
1:H:112:VAL:HB	1:H:142:VAL:CG1	2.19	0.73
1:A:107:ASP:C	1:A:108:ILE:HD12	2.14	0.72
1:D:112:VAL:HB	1:D:142:VAL:HG13	1.69	0.72
1:B:117:TYR:O	1:B:121:VAL:HG23	1.90	0.72
1:C:183:ARG:HG3	1:C:183:ARG:HH11	1.55	0.72
1:B:90:ARG:HB2	1:B:90:ARG:NH1	2.05	0.72
1:F:51:ASP:O	1:F:52:LYS:HE3	1.90	0.72
1:F:13:CYS:SG	1:F:20:SER:HB2	2.30	0.71
1:E:112:VAL:HB	1:E:142:VAL:HG13	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:MSE:HE2	1:B:151:MSE:O	1.89	0.71
1:F:61:LYS:CE	1:F:94:LYS:HE3	2.18	0.71
1:G:13:CYS:SG	1:G:20:SER:HB2	2.30	0.71
1:C:67:ARG:HH22	1:D:189:LEU:HD13	1.56	0.71
1:D:159:MSE:HE3	1:D:180:PHE:CD2	2.26	0.71
1:F:66:TYR:HE1	1:F:83:LEU:HB3	1.53	0.71
1:G:8:ALA:O	1:G:106:PHE:HB3	1.90	0.71
1:B:7:LEU:HD23	1:B:7:LEU:N	2.05	0.70
1:C:73:ASP:HB3	1:C:76:PHE:HB3	1.71	0.70
1:G:99:PHE:HE2	1:G:120:VAL:HG13	1.56	0.70
1:A:159:MSE:HE1	1:A:188:ILE:HG12	1.72	0.70
1:B:100:GLN:HE21	1:B:100:GLN:H	0.81	0.70
1:D:72:LYS:O	1:D:74:LYS:N	2.25	0.70
1:G:78:THR:CG2	1:G:83:LEU:HD12	2.21	0.70
1:C:112:VAL:HB	1:C:142:VAL:HG13	1.74	0.70
1:E:111:THR:HG21	1:E:117:TYR:HA	1.71	0.70
1:F:13:CYS:SG	1:F:20:SER:CB	2.79	0.70
1:C:162:MSE:CE	1:C:183:ARG:HH21	2.05	0.70
1:C:159:MSE:HB2	1:C:180:PHE:CE2	2.27	0.70
1:F:67:ARG:HG3	1:F:67:ARG:HH11	1.56	0.69
1:A:66:TYR:CD1	1:A:83:LEU:HD22	2.26	0.69
1:C:44:LYS:C	1:C:45:LEU:HD12	2.17	0.69
1:F:21:MSE:HE3	1:F:92:ILE:HD12	1.75	0.69
1:C:159:MSE:HE1	1:C:188:ILE:HG21	1.75	0.68
1:E:78:THR:CG2	1:E:83:LEU:HD12	2.23	0.68
1:E:136:HIS:CD2	1:E:173:ILE:HD13	2.28	0.68
1:F:159:MSE:HE1	1:F:188:ILE:HG21	1.75	0.68
1:B:70:GLU:OE2	1:B:74:LYS:HD3	1.93	0.68
1:E:185:LYS:C	1:E:186:ARG:HG3	2.18	0.68
1:E:67:ARG:HH11	1:E:67:ARG:HG3	1.58	0.68
1:F:162:MSE:HA	1:F:165:LYS:NZ	2.08	0.68
1:H:100:GLN:H	1:H:100:GLN:NE2	1.92	0.68
1:A:165:LYS:HB2	1:C:151:MSE:HE3	1.76	0.68
1:C:78:THR:CG2	1:C:83:LEU:HD12	2.24	0.68
1:C:67:ARG:HG3	1:C:67:ARG:HH11	1.59	0.68
1:B:61:LYS:HA	1:B:95:CYS:HB3	1.76	0.68
1:H:13:CYS:SG	1:H:20:SER:HB2	2.34	0.68
1:H:45:LEU:HD23	1:H:82:LEU:HD11	1.76	0.68
1:B:159:MSE:HE1	1:B:188:ILE:HG12	1.75	0.68
1:F:88:ARG:HA	1:F:91:ARG:HD2	1.76	0.68
1:C:130:VAL:HG23	1:C:131:ASP:N	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:THR:CG2	1:B:83:LEU:HD12	2.23	0.67
1:D:98:ARG:HD3	1:D:101:ASP:OD2	1.94	0.67
1:H:13:CYS:SG	1:H:20:SER:CB	2.82	0.67
1:C:67:ARG:NH1	1:D:114:GLU:HG3	2.09	0.67
1:E:135:VAL:HG12	1:E:193:LEU:O	1.95	0.67
1:E:184:ARG:O	1:E:186:ARG:HG3	1.95	0.67
1:H:66:TYR:HE1	1:H:83:LEU:HD13	1.58	0.67
1:G:145:ASN:HB3	1:G:148:ASP:HB2	1.77	0.67
1:B:77:TYR:HD1	1:B:80:ASN:HD21	1.39	0.66
1:D:87:ASP:OD1	1:E:167:THR:HG21	1.95	0.66
1:H:61:LYS:HA	1:H:95:CYS:HB3	1.77	0.66
1:D:13:CYS:SG	1:D:20:SER:HB2	2.35	0.66
1:D:151:MSE:O	1:D:155:VAL:HG23	1.95	0.66
1:C:45:LEU:HB3	1:C:46:PRO:HD2	1.78	0.66
1:H:120:VAL:O	1:H:124:MSE:HG2	1.95	0.66
1:A:66:TYR:HD1	1:A:83:LEU:HD22	1.60	0.66
1:B:66:TYR:HD1	1:B:83:LEU:HD22	1.60	0.66
1:A:45:LEU:HD23	1:A:82:LEU:CD1	2.25	0.66
1:D:80:ASN:OD1	1:D:82:LEU:HD23	1.96	0.66
1:F:99:PHE:O	1:F:102:THR:HG22	1.95	0.66
1:F:147:GLU:HG3	1:F:150:LEU:HD12	1.75	0.66
1:H:130:VAL:O	1:H:132:ASN:N	2.29	0.66
1:E:80:ASN:OD1	1:E:82:LEU:HB2	1.95	0.66
1:H:159:MSE:HE1	1:H:188:ILE:HG21	1.78	0.66
1:C:17:MSE:HE3	1:C:43:VAL:HG11	1.78	0.65
1:E:67:ARG:NH1	1:E:67:ARG:CB	2.58	0.65
1:H:108:ILE:HD12	1:H:108:ILE:N	2.09	0.65
1:F:159:MSE:HB2	1:F:180:PHE:CE2	2.31	0.65
1:H:67:ARG:HG3	1:H:67:ARG:HH11	1.62	0.65
1:A:57:GLU:HG2	1:A:59:GLY:N	2.07	0.65
1:A:188:ILE:HD12	1:A:188:ILE:N	2.11	0.65
1:C:130:VAL:HG23	1:C:131:ASP:H	1.61	0.65
1:H:105:GLN:HB2	1:H:195:TYR:CZ	2.32	0.65
1:C:159:MSE:HE3	1:C:180:PHE:CD2	2.32	0.65
1:D:66:TYR:HE1	1:D:83:LEU:HD13	1.62	0.65
1:G:21:MSE:HE3	1:G:92:ILE:HD12	1.79	0.65
1:H:133:ARG:HG2	1:H:195:TYR:HB2	1.78	0.65
1:E:7:LEU:HB2	1:E:107:ASP:OD2	1.97	0.65
1:F:120:VAL:O	1:F:124:MSE:HG2	1.96	0.65
1:H:21:MSE:HE3	1:H:92:ILE:HD12	1.78	0.65
1:A:150:LEU:H	1:A:150:LEU:HD23	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:THR:HG22	1:C:83:LEU:HD12	1.79	0.64
1:D:172:ASP:O	1:D:176:LEU:HG	1.97	0.64
1:E:62:TYR:CE1	1:E:96:PRO:HD3	2.32	0.64
1:A:78:THR:HG23	1:A:83:LEU:HD12	1.77	0.64
1:F:44:LYS:O	1:F:45:LEU:HD12	1.98	0.64
1:A:27:LEU:HD23	1:A:157:THR:HG23	1.79	0.64
1:F:24:HIS:HD2	1:F:36:SER:OG	1.81	0.64
1:G:8:ALA:HB1	1:G:106:PHE:HD1	1.62	0.64
1:A:151:MSE:HA	1:A:151:MSE:HE2	1.80	0.64
1:B:69:LEU:HD12	1:B:77:TYR:CE2	2.33	0.64
1:H:45:LEU:HD23	1:H:82:LEU:CD1	2.28	0.64
1:H:68:ASP:OD1	1:H:72:LYS:HE2	1.97	0.64
1:B:87:ASP:OD1	1:B:90:ARG:HD3	1.98	0.63
1:E:100:GLN:H	1:E:100:GLN:HE21	1.45	0.63
1:H:30:LYS:HB3	1:H:32:PHE:CD2	2.33	0.63
1:E:78:THR:HG22	1:E:83:LEU:HD12	1.80	0.63
1:B:61:LYS:HE3	1:B:94:LYS:HE3	1.80	0.63
1:F:60:THR:O	1:F:95:CYS:HB2	1.98	0.63
1:E:133:ARG:HG3	1:E:195:TYR:HB2	1.79	0.63
1:G:24:HIS:HD2	1:G:36:SER:OG	1.81	0.63
1:D:87:ASP:O	1:D:90:ARG:HG3	1.99	0.63
1:F:111:THR:CG2	1:F:120:VAL:HG21	2.28	0.63
1:H:25:ASN:HD21	1:H:29:LYS:HE3	1.64	0.63
1:H:65:ILE:O	1:H:69:LEU:HD23	1.99	0.63
1:E:87:ASP:O	1:E:90:ARG:HG2	1.99	0.63
1:G:51:ASP:O	1:G:52:LYS:HE3	1.98	0.63
1:G:116:VAL:O	1:G:120:VAL:HG23	1.99	0.63
1:A:165:LYS:CE	1:C:151:MSE:HG2	2.29	0.62
1:A:78:THR:HG22	1:A:83:LEU:HD12	1.80	0.62
1:E:107:ASP:O	1:E:108:ILE:HD13	2.00	0.62
1:E:143:VAL:C	1:E:145:ASN:H	2.06	0.62
1:B:19:ARG:HD3	1:B:143:VAL:O	1.99	0.62
1:B:147:GLU:HG3	1:D:154:PHE:CD1	2.33	0.62
1:E:10:ALA:HA	1:E:35:ARG:O	1.98	0.62
1:E:136:HIS:HD2	1:E:190:HIS:CE1	2.17	0.62
1:F:67:ARG:HH11	1:F:67:ARG:CG	2.12	0.62
1:G:159:MSE:HB2	1:G:180:PHE:CE2	2.33	0.62
1:A:143:VAL:HG12	1:A:145:ASN:H	1.63	0.62
1:F:80:ASN:OD1	1:F:82:LEU:HB2	1.98	0.62
1:H:99:PHE:O	1:H:102:THR:HG22	2.00	0.62
1:B:124:MSE:HE1	1:B:135:VAL:HG11	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:45:LEU:HD23	1:C:82:LEU:CD1	2.28	0.62
1:D:66:TYR:CD1	1:D:83:LEU:HD22	2.34	0.62
1:D:151:MSE:HA	1:D:151:MSE:HE2	1.82	0.62
1:C:89:ASN:O	1:C:91:ARG:N	2.33	0.62
1:B:9:VAL:HG12	1:B:10:ALA:N	2.15	0.61
1:A:80:ASN:OD1	1:A:82:LEU:HD23	1.99	0.61
1:G:44:LYS:C	1:G:45:LEU:HD12	2.25	0.61
1:D:39:THR:HA	1:D:100:GLN:HE22	1.66	0.61
1:H:169:LEU:HD22	1:H:173:ILE:HB	1.82	0.61
1:B:33:ASN:C	1:B:33:ASN:ND2	2.55	0.61
1:F:19:ARG:HD3	1:F:143:VAL:O	2.00	0.61
1:B:131:ASP:HB2	1:B:195:TYR:OXT	2.01	0.61
1:G:115:ARG:O	1:G:119:LEU:HD13	2.00	0.61
1:G:124:MSE:HE1	1:G:135:VAL:HG11	1.82	0.61
1:C:82:LEU:O	1:C:86:LEU:HG	2.01	0.61
1:H:41:GLU:C	1:H:42:ARG:HG3	2.25	0.61
1:D:91:ARG:HH21	1:E:167:THR:HG23	1.65	0.61
1:E:75:GLU:HG3	1:E:79:GLN:OE1	2.01	0.61
1:A:147:GLU:OE2	1:H:151:MSE:HE1	2.00	0.60
1:B:39:THR:HA	1:B:100:GLN:HE22	1.66	0.60
1:C:89:ASN:C	1:C:91:ARG:H	2.09	0.60
1:B:7:LEU:N	1:B:7:LEU:CD2	2.64	0.60
1:D:169:LEU:HD11	1:D:173:ILE:HD12	1.83	0.60
1:G:13:CYS:SG	1:G:20:SER:CB	2.89	0.60
1:C:136:HIS:CD2	1:C:173:ILE:HD13	2.37	0.60
1:D:105:GLN:HB2	1:D:195:TYR:CE2	2.36	0.60
1:B:77:TYR:HA	1:B:80:ASN:ND2	2.16	0.60
1:H:159:MSE:HE1	1:H:188:ILE:HD12	1.83	0.60
1:F:61:LYS:HA	1:F:95:CYS:HB2	1.83	0.60
1:C:42:ARG:HB3	1:C:56:TYR:O	2.02	0.60
1:E:124:MSE:HE1	1:E:135:VAL:HG11	1.84	0.60
1:G:80:ASN:OD1	1:G:82:LEU:HB2	2.02	0.60
1:H:107:ASP:HB2	1:H:108:ILE:CD1	2.32	0.60
1:A:129:SER:HB3	1:A:195:TYR:O	2.02	0.60
1:B:162:MSE:O	1:B:165:LYS:HG2	2.02	0.60
1:H:109:ILE:HD12	1:H:124:MSE:HE2	1.83	0.60
1:B:123:HIS:O	1:B:126:SER:HB3	2.02	0.59
1:D:66:TYR:CE1	1:D:83:LEU:HD22	2.37	0.59
1:G:45:LEU:HB3	1:G:46:PRO:HD2	1.84	0.59
1:H:73:ASP:HB3	1:H:76:PHE:HB3	1.84	0.59
1:E:159:MSE:HG3	1:E:163:MSE:HE3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:HIS:HD2	1:A:36:SER:HB3	1.68	0.59
1:A:159:MSE:HE1	1:A:188:ILE:HG21	1.84	0.59
1:A:46:PRO:HG2	1:A:82:LEU:HD21	1.85	0.59
1:E:45:LEU:HB3	1:E:46:PRO:HD2	1.85	0.59
1:H:60:THR:OG1	1:H:65:ILE:HD11	2.02	0.59
1:A:106:PHE:HB2	1:A:109:ILE:CD1	2.32	0.59
1:G:112:VAL:HB	1:G:142:VAL:CG1	2.33	0.59
1:A:136:HIS:CD2	1:A:190:HIS:HE1	2.20	0.59
1:D:105:GLN:HB2	1:D:195:TYR:CZ	2.38	0.59
1:E:25:ASN:C	1:E:25:ASN:HD22	2.09	0.59
1:B:145:ASN:ND2	1:B:148:ASP:HB2	2.18	0.58
1:F:175:GLU:O	1:F:178:GLN:HB3	2.03	0.58
1:A:46:PRO:CG	1:A:82:LEU:HD21	2.33	0.58
1:F:13:CYS:SG	1:F:20:SER:HB3	2.44	0.58
1:E:130:VAL:HG23	1:E:131:ASP:N	2.15	0.58
1:G:7:LEU:HB2	1:G:107:ASP:OD2	2.02	0.58
1:D:43:VAL:O	1:D:55:VAL:HG13	2.03	0.58
1:D:159:MSE:CE	1:D:188:ILE:HG12	2.34	0.58
1:H:13:CYS:SG	1:H:20:SER:HB3	2.44	0.58
1:B:121:VAL:HG13	1:B:193:LEU:HD21	1.84	0.58
1:C:21:MSE:HE1	1:C:92:ILE:HB	1.84	0.58
1:C:111:THR:HG22	1:C:120:VAL:HG21	1.86	0.58
1:G:112:VAL:HG23	1:G:112:VAL:O	2.04	0.58
1:F:111:THR:HG22	1:F:120:VAL:HG21	1.85	0.57
1:G:184:ARG:HB3	1:G:186:ARG:NH1	2.19	0.57
1:A:159:MSE:CE	1:A:188:ILE:HG12	2.34	0.57
1:A:124:MSE:CB	1:A:193:LEU:HG	2.34	0.57
1:A:145:ASN:ND2	1:A:148:ASP:H	2.02	0.57
1:C:162:MSE:CE	1:C:183:ARG:NH2	2.67	0.57
1:G:173:ILE:HD11	1:G:177:ILE:HD11	1.86	0.57
1:B:151:MSE:CE	1:B:151:MSE:HA	2.34	0.57
1:C:183:ARG:HD2	1:C:184:ARG:HD3	1.85	0.57
1:E:151:MSE:HE2	1:E:154:PHE:HB2	1.86	0.57
1:C:45:LEU:N	1:C:45:LEU:CD1	2.68	0.57
1:C:51:ASP:O	1:C:52:LYS:HE3	2.04	0.57
1:G:136:HIS:HB3	1:G:190:HIS:CE1	2.38	0.57
1:A:185:LYS:HD2	1:A:185:LYS:N	2.19	0.57
1:H:114:GLU:O	1:H:117:TYR:HB3	2.05	0.57
1:A:44:LYS:O	1:A:44:LYS:HG3	2.04	0.57
1:B:66:TYR:HE1	1:B:83:LEU:HD13	1.70	0.57
1:C:130:VAL:O	1:C:131:ASP:C	2.47	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:GLU:CD	1:H:151:MSE:HE1	2.30	0.56
1:A:7:LEU:HD23	1:A:7:LEU:N	2.20	0.56
1:A:13:CYS:SG	1:A:20:SER:HB3	2.45	0.56
1:A:136:HIS:HD2	1:A:190:HIS:HE1	1.52	0.56
1:E:54:ASN:HB3	1:E:56:TYR:HE1	1.70	0.56
1:C:67:ARG:HH12	1:D:189:LEU:CD1	2.18	0.56
1:F:79:GLN:C	1:F:81:GLY:H	2.13	0.56
1:B:42:ARG:CZ	1:B:55:VAL:HG11	2.35	0.56
1:E:54:ASN:HB3	1:E:56:TYR:CE1	2.40	0.56
1:E:145:ASN:HD21	1:E:147:GLU:HB3	1.70	0.56
1:C:100:GLN:HG3	1:C:123:HIS:CD2	2.41	0.56
1:E:100:GLN:HE21	1:E:100:GLN:N	2.04	0.56
1:H:159:MSE:HB2	1:H:180:PHE:CZ	2.40	0.56
1:A:136:HIS:HD2	1:A:190:HIS:CE1	2.23	0.56
1:C:113:GLU:HB3	1:C:116:VAL:CG2	2.33	0.56
1:E:24:HIS:HD2	1:E:36:SER:CB	2.19	0.56
1:G:93:LYS:HD3	1:G:97:GLU:HG3	1.88	0.56
1:E:22:GLU:HG3	1:E:153:ALA:HB2	1.87	0.56
1:D:159:MSE:HB2	1:D:180:PHE:CZ	2.42	0.55
1:E:17:MSE:HG3	1:E:45:LEU:HD11	1.86	0.55
1:C:105:GLN:HB2	1:C:195:TYR:CE2	2.41	0.55
1:C:35:ARG:HH11	1:C:35:ARG:HG2	1.71	0.55
1:E:67:ARG:NH1	1:E:67:ARG:CG	2.63	0.55
1:H:24:HIS:HD2	1:H:36:SER:HB3	1.71	0.55
1:C:25:ASN:HD21	1:C:29:LYS:HE3	1.71	0.55
1:C:27:LEU:O	1:C:28:ALA:C	2.50	0.55
1:E:63:GLU:HB2	1:E:90:ARG:HH11	1.72	0.55
1:F:64:ASP:OD1	1:F:67:ARG:NH2	2.38	0.55
1:G:192:VAL:C	1:G:193:LEU:HD22	2.31	0.55
1:H:54:ASN:ND2	1:H:72:LYS:HZ1	2.05	0.55
1:F:70:GLU:HG2	1:F:74:LYS:HD3	1.87	0.55
1:F:147:GLU:HG3	1:F:150:LEU:CD1	2.36	0.55
1:G:17:MSE:CE	1:G:62:TYR:HE1	2.20	0.55
1:B:74:LYS:O	1:B:78:THR:HG23	2.07	0.55
1:B:151:MSE:HE2	1:B:151:MSE:HA	1.89	0.55
1:E:116:VAL:O	1:E:120:VAL:HG23	2.05	0.55
1:A:70:GLU:OE2	1:A:74:LYS:HD3	2.06	0.55
1:C:70:GLU:OE2	1:C:74:LYS:HD3	2.07	0.55
1:A:165:LYS:HE3	1:C:151:MSE:HG2	1.88	0.55
1:F:95:CYS:HB2	1:F:96:PRO:HD2	1.89	0.55
1:H:169:LEU:O	1:H:171:ASN:N	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:145:ASN:HB3	1:C:148:ASP:HB2	1.89	0.54
1:E:185:LYS:O	1:E:186:ARG:HG3	2.07	0.54
1:A:24:HIS:CD2	1:A:36:SER:HB3	2.42	0.54
1:E:130:VAL:O	1:E:132:ASN:N	2.39	0.54
1:F:145:ASN:ND2	1:F:147:GLU:H	2.05	0.54
1:H:105:GLN:HB2	1:H:195:TYR:CE2	2.42	0.54
1:B:147:GLU:HG3	1:D:154:PHE:CE1	2.43	0.54
1:H:42:ARG:CZ	1:H:55:VAL:HG11	2.37	0.54
1:A:93:LYS:NZ	1:A:97:GLU:OE2	2.40	0.54
1:B:19:ARG:HD3	1:B:144:ASP:HA	1.88	0.54
1:G:159:MSE:HE3	1:G:180:PHE:CD2	2.42	0.54
1:C:21:MSE:CE	1:C:92:ILE:HD12	2.32	0.54
1:G:7:LEU:O	1:G:9:VAL:HG23	2.08	0.54
1:G:21:MSE:HE2	1:G:89:ASN:HB3	1.89	0.54
1:H:25:ASN:ND2	1:H:29:LYS:HE3	2.23	0.54
1:D:169:LEU:C	1:D:169:LEU:HD13	2.33	0.54
1:G:73:ASP:O	1:G:74:LYS:C	2.50	0.54
1:G:171:ASN:C	1:G:173:ILE:H	2.14	0.54
1:C:73:ASP:O	1:C:75:GLU:N	2.41	0.54
1:F:112:VAL:HB	1:F:142:VAL:CG1	2.38	0.54
1:B:111:THR:OG1	1:B:139:ASN:HA	2.07	0.54
1:B:66:TYR:CE1	1:B:83:LEU:HD22	2.42	0.53
1:E:133:ARG:CG	1:E:195:TYR:HB2	2.38	0.53
1:G:129:SER:N	1:G:195:TYR:O	2.40	0.53
1:H:135:VAL:HG12	1:H:193:LEU:O	2.09	0.53
1:C:57:GLU:HB3	1:C:60:THR:HG23	1.90	0.53
1:F:162:MSE:HA	1:F:165:LYS:HZ3	1.71	0.53
1:G:17:MSE:HE1	1:G:62:TYR:CE1	2.43	0.53
1:B:151:MSE:HE1	1:D:147:GLU:HG3	1.90	0.53
1:C:173:ILE:HG23	1:C:174:ASP:N	2.24	0.53
1:E:41:GLU:C	1:E:42:ARG:HG3	2.33	0.53
1:B:23:ALA:O	1:B:27:LEU:HG	2.08	0.53
1:G:173:ILE:HD13	1:G:173:ILE:C	2.34	0.53
1:A:128:GLU:OE1	1:A:129:SER:O	2.27	0.53
1:D:67:ARG:HG3	1:D:67:ARG:NH1	2.22	0.53
1:F:116:VAL:O	1:F:117:TYR:C	2.51	0.53
1:G:73:ASP:HB3	1:G:76:PHE:HB3	1.91	0.53
1:H:66:TYR:CE1	1:H:83:LEU:HD13	2.42	0.53
1:A:62:TYR:CE1	1:A:96:PRO:HD3	2.44	0.53
1:A:145:ASN:HD21	1:A:147:GLU:HB3	1.73	0.53
1:C:8:ALA:HB3	1:C:106:PHE:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:123:HIS:O	1:E:126:SER:HB3	2.09	0.53
1:G:89:ASN:C	1:G:91:ARG:H	2.16	0.53
1:B:90:ARG:HH11	1:B:90:ARG:CB	2.13	0.53
1:C:65:ILE:HB	1:C:86:LEU:HD13	1.91	0.53
1:E:54:ASN:CG	1:E:69:LEU:HD11	2.34	0.53
1:G:138:LEU:HD13	1:G:163:MSE:HE1	1.91	0.53
1:H:130:VAL:O	1:H:131:ASP:C	2.52	0.52
1:A:11:VAL:HG11	1:A:20:SER:HA	1.92	0.52
1:A:137:VAL:HG21	1:A:193:LEU:HD23	1.91	0.52
1:A:169:LEU:HD13	1:A:169:LEU:C	2.35	0.52
1:D:40:GLY:O	1:D:98:ARG:NH1	2.43	0.52
1:E:78:THR:HG23	1:E:83:LEU:HD12	1.90	0.52
1:G:151:MSE:HE2	1:G:154:PHE:HB2	1.91	0.52
1:H:168:ASP:OD1	1:H:168:ASP:O	2.28	0.52
1:A:37:TYR:CD1	1:A:97:GLU:HB2	2.44	0.52
1:E:159:MSE:HB2	1:E:180:PHE:CZ	2.43	0.52
1:B:111:THR:HG21	1:B:117:TYR:HA	1.91	0.52
1:C:62:TYR:O	1:C:63:GLU:C	2.53	0.52
1:E:25:ASN:C	1:E:25:ASN:ND2	2.67	0.52
1:A:58:PHE:HE1	1:A:97:GLU:O	1.92	0.52
1:E:35:ARG:HG2	1:E:35:ARG:HH11	1.75	0.52
1:G:48:MSE:SE	1:G:73:ASP:OD2	2.78	0.52
1:C:124:MSE:CE	1:C:135:VAL:HG11	2.38	0.52
1:G:100:GLN:NE2	1:G:100:GLN:N	2.37	0.52
1:A:102:THR:HG23	1:A:102:THR:O	2.09	0.52
1:B:45:LEU:HB3	1:B:82:LEU:HD11	1.91	0.52
1:B:151:MSE:HE1	1:D:147:GLU:CG	2.40	0.51
1:D:49:ALA:HB3	1:D:52:LYS:HB2	1.91	0.51
1:E:124:MSE:CE	1:E:135:VAL:HG11	2.40	0.51
1:G:77:TYR:HA	1:G:80:ASN:HD21	1.75	0.51
1:H:107:ASP:CB	1:H:108:ILE:HD12	2.37	0.51
1:D:67:ARG:HH11	1:D:67:ARG:CG	2.20	0.51
1:D:116:VAL:O	1:D:120:VAL:HG23	2.11	0.51
1:F:156:ILE:O	1:F:160:ILE:HD13	2.10	0.51
1:H:57:GLU:HB3	1:H:60:THR:HG23	1.92	0.51
1:B:47:GLY:HA3	1:B:53:PRO:HA	1.93	0.51
1:H:22:GLU:OE1	1:H:22:GLU:HA	2.10	0.51
1:H:140:VAL:O	1:H:142:VAL:HG12	2.10	0.51
1:F:162:MSE:HA	1:F:165:LYS:HZ2	1.75	0.51
1:H:30:LYS:HB3	1:H:32:PHE:CE2	2.46	0.51
1:A:172:ASP:HB3	1:C:30:LYS:NZ	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:GLU:O	1:C:76:PHE:C	2.52	0.51
1:F:80:ASN:O	1:F:82:LEU:N	2.43	0.51
1:G:192:VAL:O	1:G:193:LEU:HD22	2.10	0.51
1:C:17:MSE:HE2	1:C:62:TYR:HE1	1.76	0.51
1:C:62:TYR:CE1	1:C:96:PRO:HD3	2.45	0.51
1:H:151:MSE:HE2	1:H:151:MSE:HA	1.93	0.51
1:B:162:MSE:HE1	1:B:183:ARG:HE	1.75	0.51
1:F:44:LYS:NZ	1:F:53:PRO:HG3	2.26	0.51
1:G:66:TYR:O	1:G:67:ARG:C	2.54	0.51
1:H:120:VAL:O	1:H:120:VAL:HG12	2.10	0.51
1:B:9:VAL:CG1	1:B:10:ALA:N	2.73	0.51
1:F:12:VAL:HG13	1:F:37:TYR:O	2.10	0.51
1:F:25:ASN:O	1:F:28:ALA:N	2.43	0.51
1:F:173:ILE:O	1:F:177:ILE:HG13	2.11	0.51
1:H:111:THR:CG2	1:H:120:VAL:HG21	2.41	0.51
1:B:61:LYS:HD3	1:B:94:LYS:HE3	1.93	0.51
1:C:190:HIS:ND1	1:C:191:SER:N	2.57	0.51
1:C:100:GLN:HA	1:C:123:HIS:CD2	2.46	0.51
1:G:145:ASN:ND2	1:G:148:ASP:H	2.08	0.51
1:D:140:VAL:O	1:D:142:VAL:HG12	2.10	0.50
1:E:136:HIS:HD2	1:E:190:HIS:HE1	1.55	0.50
1:C:79:GLN:HG3	1:H:143:VAL:CG1	2.42	0.50
1:E:44:LYS:C	1:E:45:LEU:HD12	2.35	0.50
1:B:39:THR:O	1:B:40:GLY:O	2.28	0.50
1:B:145:ASN:HD22	1:B:148:ASP:HB2	1.76	0.50
1:D:136:HIS:CE1	1:D:169:LEU:HD12	2.46	0.50
1:A:105:GLN:HB2	1:A:195:TYR:CE2	2.47	0.50
1:B:13:CYS:SG	1:B:20:SER:CB	3.00	0.50
1:D:24:HIS:HA	1:D:34:VAL:HG21	1.93	0.50
1:B:63:GLU:O	1:B:66:TYR:HB3	2.12	0.50
1:C:190:HIS:O	1:C:191:SER:HB3	2.12	0.50
1:D:102:THR:HG23	1:D:102:THR:O	2.11	0.50
1:D:182:GLU:O	1:D:185:LYS:HE3	2.10	0.50
1:E:24:HIS:CD2	1:E:36:SER:OG	2.60	0.50
1:E:193:LEU:N	1:E:193:LEU:HD22	2.27	0.50
1:F:147:GLU:HA	1:F:150:LEU:CD1	2.41	0.50
1:F:181:GLU:HG3	1:F:188:ILE:HD12	1.93	0.50
1:G:183:ARG:HG3	1:G:183:ARG:HH11	1.75	0.50
1:C:93:LYS:NZ	1:C:97:GLU:OE2	2.44	0.50
1:D:105:GLN:HA	1:D:195:TYR:OH	2.12	0.50
1:F:57:GLU:O	1:F:59:GLY:N	2.34	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:66:TYR:CE1	1:F:83:LEU:HB3	2.41	0.50
1:A:145:ASN:HD22	1:A:148:ASP:HB2	1.77	0.50
1:A:165:LYS:HD2	1:C:151:MSE:HG2	1.94	0.50
1:B:145:ASN:ND2	1:B:148:ASP:H	2.09	0.50
1:B:151:MSE:CE	1:D:147:GLU:HG3	2.42	0.50
1:B:61:LYS:HB2	1:B:64:ASP:OD2	2.11	0.50
1:B:61:LYS:CD	1:B:94:LYS:HE3	2.42	0.50
1:C:136:HIS:CD2	1:C:192:VAL:HG12	2.47	0.50
1:A:67:ARG:HG3	1:A:67:ARG:NH1	2.23	0.50
1:B:66:TYR:CE1	1:B:83:LEU:HD13	2.47	0.50
1:C:100:GLN:N	1:C:100:GLN:NE2	2.42	0.50
1:D:6:LYS:O	1:D:6:LYS:HG2	2.12	0.50
1:D:183:ARG:HG3	1:D:183:ARG:HH11	1.77	0.50
1:C:183:ARG:HG3	1:C:183:ARG:NH1	2.26	0.49
1:F:135:VAL:O	1:F:135:VAL:HG13	2.11	0.49
1:A:11:VAL:CG1	1:A:20:SER:HA	2.43	0.49
1:B:159:MSE:HB2	1:B:180:PHE:CZ	2.47	0.49
1:C:11:VAL:HG11	1:C:23:ALA:HB3	1.93	0.49
1:C:106:PHE:O	1:C:195:TYR:HE2	1.95	0.49
1:E:128:GLU:OE1	1:E:129:SER:O	2.30	0.49
1:G:181:GLU:HG2	1:G:188:ILE:HG12	1.94	0.49
1:A:169:LEU:HD22	1:A:173:ILE:HB	1.94	0.49
1:B:116:VAL:O	1:B:120:VAL:HG23	2.12	0.49
1:D:138:LEU:HA	1:D:189:LEU:O	2.13	0.49
1:G:85:MSE:CG	1:G:88:ARG:NH2	2.74	0.49
1:A:10:ALA:HA	1:A:35:ARG:O	2.11	0.49
1:A:139:ASN:HB3	1:A:189:LEU:HB2	1.93	0.49
1:C:46:PRO:HB3	1:H:50:PHE:HD2	1.77	0.49
1:F:138:LEU:HD13	1:F:163:MSE:HE1	1.94	0.49
1:G:140:VAL:HG22	1:G:188:ILE:HD12	1.93	0.49
1:A:24:HIS:HD2	1:A:36:SER:CB	2.25	0.49
1:B:27:LEU:HD21	1:B:157:THR:HA	1.94	0.49
1:C:89:ASN:C	1:C:91:ARG:N	2.71	0.49
1:B:130:VAL:O	1:B:131:ASP:C	2.55	0.49
1:C:67:ARG:HH11	1:C:67:ARG:CG	2.25	0.49
1:C:78:THR:HG23	1:C:83:LEU:HD12	1.94	0.49
1:D:46:PRO:HG2	1:D:82:LEU:HD21	1.93	0.49
1:D:114:GLU:O	1:D:117:TYR:HB3	2.11	0.49
1:F:67:ARG:CG	1:F:67:ARG:NH1	2.72	0.49
1:H:40:GLY:O	1:H:98:ARG:NH1	2.43	0.49
1:A:93:LYS:HD3	1:A:97:GLU:HG3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:84:HIS:ND1	1:B:84:HIS:C	2.71	0.49
1:D:73:ASP:O	1:D:74:LYS:C	2.53	0.49
1:G:169:LEU:O	1:G:171:ASN:N	2.46	0.49
1:B:143:VAL:HG12	1:B:144:ASP:N	2.28	0.49
1:D:81:GLY:O	1:D:82:LEU:C	2.56	0.49
1:E:136:HIS:CD2	1:E:190:HIS:HE1	2.31	0.49
1:B:147:GLU:HG3	1:D:154:PHE:CG	2.48	0.49
1:D:57:GLU:HB3	1:D:60:THR:HG23	1.93	0.49
1:D:120:VAL:O	1:D:124:MSE:HG2	2.13	0.49
1:D:130:VAL:O	1:D:131:ASP:C	2.55	0.49
1:B:63:GLU:O	1:B:66:TYR:N	2.44	0.49
1:B:91:ARG:NH2	1:E:174:ASP:OD2	2.44	0.49
1:F:66:TYR:CD1	1:F:83:LEU:HD22	2.48	0.49
1:F:99:PHE:O	1:F:100:GLN:C	2.55	0.49
1:H:8:ALA:O	1:H:106:PHE:HB3	2.13	0.49
1:H:173:ILE:HD13	1:H:173:ILE:C	2.38	0.49
1:B:40:GLY:O	1:B:98:ARG:NH1	2.46	0.48
1:B:152:GLY:O	1:B:156:ILE:HG13	2.13	0.48
1:C:58:PHE:CG	1:C:98:ARG:HB2	2.48	0.48
1:E:130:VAL:CG2	1:E:131:ASP:H	2.17	0.48
1:F:159:MSE:HB2	1:F:180:PHE:CZ	2.47	0.48
1:H:24:HIS:CD2	1:H:36:SER:HB3	2.48	0.48
1:C:50:PHE:HB3	1:H:44:LYS:NZ	2.27	0.48
1:C:55:VAL:C	1:C:56:TYR:CD1	2.92	0.48
1:C:143:VAL:C	1:C:145:ASN:H	2.22	0.48
1:D:7:LEU:HD23	1:D:7:LEU:N	2.28	0.48
1:D:8:ALA:O	1:D:106:PHE:HB3	2.13	0.48
1:E:8:ALA:HB1	1:E:106:PHE:HD1	1.78	0.48
1:E:179:GLU:HA	1:E:182:GLU:HB3	1.94	0.48
1:F:184:ARG:O	1:F:185:LYS:HB2	2.12	0.48
1:G:98:ARG:NH2	1:G:100:GLN:HG2	2.29	0.48
1:H:173:ILE:HG23	1:H:174:ASP:N	2.28	0.48
1:D:90:ARG:NH1	1:D:90:ARG:HB2	2.28	0.48
1:F:78:THR:CG2	1:F:83:LEU:HD12	2.30	0.48
1:H:133:ARG:CG	1:H:195:TYR:HB2	2.41	0.48
1:H:136:HIS:HD2	1:H:190:HIS:CE1	2.32	0.48
1:G:52:LYS:H	1:G:53:PRO:HD3	1.79	0.48
1:H:151:MSE:O	1:H:155:VAL:HG23	2.13	0.48
1:C:184:ARG:O	1:C:186:ARG:HG3	2.13	0.48
1:E:143:VAL:C	1:E:145:ASN:N	2.72	0.48
1:E:16:ASN:OD1	1:E:93:LYS:HE3	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:67:ARG:HH11	1:E:67:ARG:CB	2.24	0.48
1:G:136:HIS:HB3	1:G:190:HIS:HE1	1.77	0.48
1:D:173:ILE:HG23	1:D:174:ASP:N	2.29	0.48
1:F:21:MSE:HE2	1:F:89:ASN:HB3	1.95	0.48
1:B:150:LEU:HD12	1:D:150:LEU:HD12	1.96	0.48
1:C:17:MSE:CE	1:C:62:TYR:HE1	2.27	0.48
1:C:128:GLU:OE1	1:C:129:SER:O	2.32	0.48
1:B:130:VAL:O	1:B:132:ASN:N	2.47	0.48
1:C:67:ARG:HG3	1:D:114:GLU:CD	2.38	0.48
1:G:159:MSE:HB2	1:G:180:PHE:CZ	2.49	0.48
1:C:24:HIS:HD2	1:C:36:SER:OG	1.96	0.47
1:E:159:MSE:CE	1:E:188:ILE:HD13	2.38	0.47
1:B:13:CYS:SG	1:B:20:SER:HB2	2.54	0.47
1:E:99:PHE:CE2	1:E:120:VAL:HG13	2.49	0.47
1:G:39:THR:HA	1:G:100:GLN:HE22	1.79	0.47
1:H:111:THR:HG22	1:H:116:VAL:HG12	1.95	0.47
1:A:73:ASP:O	1:A:74:LYS:C	2.55	0.47
1:C:54:ASN:HB3	1:C:56:TYR:HE1	1.78	0.47
1:E:13:CYS:SG	1:E:20:SER:CB	3.03	0.47
1:H:23:ALA:O	1:H:24:HIS:C	2.56	0.47
1:B:66:TYR:HE1	1:B:83:LEU:HB3	1.79	0.47
1:B:159:MSE:HB2	1:B:180:PHE:CE1	2.49	0.47
1:D:159:MSE:HE1	1:D:188:ILE:HG21	1.96	0.47
1:G:17:MSE:HE2	1:G:62:TYR:HE1	1.79	0.47
1:B:168:ASP:OD1	1:B:171:ASN:ND2	2.47	0.47
1:B:169:LEU:C	1:B:169:LEU:HD13	2.40	0.47
1:F:61:LYS:HE3	1:F:94:LYS:CE	2.34	0.47
1:H:54:ASN:ND2	1:H:72:LYS:NZ	2.63	0.47
1:C:24:HIS:CD2	1:C:36:SER:HB3	2.50	0.47
1:E:131:ASP:HB2	1:E:133:ARG:HG2	1.97	0.47
1:E:168:ASP:OD1	1:E:171:ASN:HB2	2.15	0.47
1:C:130:VAL:O	1:C:132:ASN:N	2.47	0.47
1:F:45:LEU:HB3	1:F:46:PRO:HD2	1.97	0.47
1:F:183:ARG:HG3	1:F:183:ARG:HH11	1.79	0.47
1:G:77:TYR:HA	1:G:80:ASN:ND2	2.29	0.47
1:G:169:LEU:O	1:G:173:ILE:HB	2.13	0.47
1:G:173:ILE:O	1:G:177:ILE:HG13	2.15	0.47
1:G:173:ILE:CD1	1:G:177:ILE:HD11	2.44	0.47
1:H:15:SER:O	1:H:16:ASN:C	2.56	0.47
1:H:76:PHE:CE1	1:H:80:ASN:ND2	2.83	0.47
1:A:118:ASP:O	1:A:122:MSE:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:VAL:HA	1:B:138:LEU:O	2.15	0.47
1:E:95:CYS:HB2	1:E:96:PRO:HD2	1.96	0.47
1:A:136:HIS:CD2	1:A:190:HIS:CE1	3.01	0.47
1:E:24:HIS:HD1	1:E:24:HIS:C	2.21	0.47
1:A:124:MSE:HB3	1:A:193:LEU:HG	1.97	0.47
1:D:45:LEU:HD23	1:D:82:LEU:HD12	1.96	0.47
1:F:25:ASN:O	1:F:26:PHE:C	2.58	0.47
1:H:159:MSE:HA	1:H:180:PHE:CE1	2.50	0.47
1:B:133:ARG:O	1:B:133:ARG:HG3	2.14	0.46
1:B:136:HIS:HD2	1:B:190:HIS:HE1	1.63	0.46
1:C:130:VAL:CG2	1:C:131:ASP:N	2.77	0.46
1:G:17:MSE:CE	1:G:62:TYR:CE1	2.98	0.46
1:H:100:GLN:HE21	1:H:100:GLN:N	2.02	0.46
1:H:151:MSE:HE2	1:H:154:PHE:CD2	2.50	0.46
1:H:169:LEU:O	1:H:170:ASP:C	2.58	0.46
1:A:21:MSE:O	1:A:24:HIS:HB3	2.15	0.46
1:E:192:VAL:C	1:E:193:LEU:HD22	2.40	0.46
1:G:52:LYS:N	1:G:53:PRO:CD	2.77	0.46
1:G:151:MSE:HE2	1:G:151:MSE:HA	1.98	0.46
1:A:60:THR:O	1:A:95:CYS:HB2	2.16	0.46
1:A:135:VAL:HG13	1:A:135:VAL:O	2.14	0.46
1:B:93:LYS:HD3	1:B:97:GLU:HG2	1.97	0.46
1:E:124:MSE:C	1:E:126:SER:H	2.23	0.46
1:A:57:GLU:HB3	1:A:60:THR:HG23	1.97	0.46
1:C:105:GLN:HB2	1:C:195:TYR:CZ	2.51	0.46
1:D:173:ILE:HG23	1:D:174:ASP:H	1.81	0.46
1:F:22:GLU:OE1	1:F:22:GLU:HA	2.14	0.46
1:A:66:TYR:HE1	1:A:83:LEU:HD13	1.81	0.46
1:A:66:TYR:O	1:A:70:GLU:HB2	2.16	0.46
1:B:143:VAL:HG12	1:B:145:ASN:N	2.31	0.46
1:B:30:LYS:HD2	1:B:30:LYS:HA	1.82	0.46
1:A:70:GLU:C	1:A:72:LYS:H	2.24	0.46
1:A:162:MSE:HE1	1:A:183:ARG:HH21	1.81	0.46
1:E:49:ALA:C	1:E:51:ASP:H	2.22	0.46
1:G:17:MSE:HE1	1:G:62:TYR:CD1	2.51	0.46
1:G:117:TYR:O	1:G:121:VAL:HG23	2.15	0.46
1:H:177:ILE:O	1:H:181:GLU:HG3	2.16	0.46
1:B:143:VAL:CG1	1:B:144:ASP:N	2.79	0.46
1:B:173:ILE:HG23	1:B:174:ASP:N	2.31	0.46
1:C:95:CYS:O	1:C:95:CYS:SG	2.73	0.46
1:C:190:HIS:CG	1:C:191:SER:N	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:73:ASP:OD2	1:E:76:PHE:HB2	2.16	0.46
1:F:169:LEU:O	1:F:171:ASN:N	2.49	0.46
1:A:123:HIS:ND1	1:A:123:HIS:C	2.73	0.46
1:G:21:MSE:HE1	1:G:92:ILE:HB	1.98	0.46
1:H:61:LYS:HA	1:H:95:CYS:CB	2.44	0.46
1:B:143:VAL:C	1:B:145:ASN:H	2.24	0.46
1:E:159:MSE:CG	1:E:163:MSE:HE3	2.46	0.46
1:G:25:ASN:C	1:G:25:ASN:HD22	2.22	0.46
1:G:107:ASP:O	1:G:135:VAL:HG23	2.16	0.46
1:H:8:ALA:HB1	1:H:106:PHE:HD1	1.81	0.46
1:H:111:THR:HG21	1:H:117:TYR:HA	1.96	0.46
1:H:118:ASP:O	1:H:122:MSE:HB2	2.16	0.46
1:E:13:CYS:SG	1:E:20:SER:HB3	2.56	0.45
1:E:24:HIS:O	1:E:24:HIS:ND1	2.41	0.45
1:G:65:ILE:HB	1:G:86:LEU:HD13	1.98	0.45
1:A:173:ILE:O	1:A:177:ILE:HG13	2.16	0.45
1:C:62:TYR:O	1:C:65:ILE:N	2.49	0.45
1:E:16:ASN:HA	1:E:20:SER:OG	2.17	0.45
1:E:128:GLU:OE1	1:E:128:GLU:C	2.59	0.45
1:F:159:MSE:CE	1:F:188:ILE:HD13	2.46	0.45
1:C:112:VAL:HA	1:C:140:VAL:O	2.17	0.45
1:D:181:GLU:HG2	1:D:186:ARG:O	2.15	0.45
1:E:130:VAL:O	1:E:131:ASP:C	2.58	0.45
1:F:115:ARG:O	1:F:119:LEU:HD13	2.16	0.45
1:G:67:ARG:HH11	1:G:67:ARG:CG	2.29	0.45
1:A:19:ARG:HD3	1:A:144:ASP:HA	1.99	0.45
1:A:137:VAL:CG2	1:A:193:LEU:HD23	2.46	0.45
1:C:77:TYR:HD1	1:C:80:ASN:HD21	1.62	0.45
1:E:98:ARG:HG2	1:E:100:GLN:NE2	2.31	0.45
1:E:155:VAL:HG21	1:E:186:ARG:HH22	1.81	0.45
1:F:43:VAL:O	1:F:56:TYR:N	2.50	0.45
1:A:124:MSE:CE	1:A:135:VAL:HG11	2.45	0.45
1:D:41:GLU:C	1:D:42:ARG:HG3	2.42	0.45
1:G:7:LEU:HD23	1:G:7:LEU:N	2.31	0.45
1:A:37:TYR:HD1	1:A:97:GLU:HB2	1.81	0.45
1:A:179:GLU:HB3	1:A:183:ARG:NH2	2.32	0.45
1:C:162:MSE:HE2	1:C:183:ARG:NH2	2.32	0.45
1:D:25:ASN:O	1:D:26:PHE:C	2.58	0.45
1:D:113:GLU:O	1:D:114:GLU:C	2.60	0.45
1:E:136:HIS:CD2	1:E:173:ILE:CD1	2.98	0.45
1:A:28:ALA:C	1:A:30:LYS:H	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:37:TYR:CD1	1:G:97:GLU:HB2	2.52	0.45
1:G:61:LYS:HA	1:G:95:CYS:HB3	1.99	0.45
1:G:169:LEU:O	1:G:170:ASP:C	2.59	0.45
1:H:95:CYS:HB2	1:H:96:PRO:HD2	1.99	0.45
1:H:171:ASN:C	1:H:173:ILE:H	2.24	0.45
1:C:73:ASP:HB3	1:C:76:PHE:CB	2.44	0.45
1:D:21:MSE:HE1	1:D:92:ILE:HB	1.99	0.45
1:C:130:VAL:CG2	1:C:131:ASP:H	2.27	0.45
1:D:69:LEU:HD12	1:D:77:TYR:CE2	2.52	0.45
1:D:100:GLN:NE2	1:D:100:GLN:N	2.40	0.45
1:E:114:GLU:O	1:E:117:TYR:HB3	2.17	0.45
1:E:117:TYR:OH	1:E:191:SER:HB3	2.17	0.45
1:B:172:ASP:O	1:B:176:LEU:HD12	2.16	0.45
1:C:50:PHE:HB3	1:H:44:LYS:HZ2	1.81	0.45
1:D:11:VAL:O	1:D:36:SER:HA	2.17	0.45
1:H:24:HIS:HD2	1:H:36:SER:CB	2.29	0.45
1:C:68:ASP:OD1	1:C:68:ASP:C	2.60	0.44
1:H:124:MSE:HE3	1:H:135:VAL:HG11	1.98	0.44
1:B:45:LEU:HD23	1:B:82:LEU:HD12	1.97	0.44
1:E:168:ASP:OD1	1:E:168:ASP:O	2.35	0.44
1:E:185:LYS:HD2	1:E:185:LYS:N	2.33	0.44
1:F:93:LYS:HD3	1:F:97:GLU:HG3	1.99	0.44
1:C:26:PHE:O	1:C:27:LEU:C	2.60	0.44
1:D:63:GLU:O	1:D:66:TYR:HB3	2.17	0.44
1:E:135:VAL:CG1	1:E:193:LEU:O	2.64	0.44
1:F:151:MSE:O	1:F:152:GLY:C	2.60	0.44
1:B:151:MSE:HE1	1:D:147:GLU:CD	2.42	0.44
1:C:155:VAL:HG22	1:C:184:ARG:NH1	2.22	0.44
1:E:75:GLU:CG	1:E:79:GLN:OE1	2.63	0.44
1:F:111:THR:HG21	1:F:117:TYR:HA	1.98	0.44
1:F:181:GLU:O	1:F:185:LYS:HA	2.18	0.44
1:A:7:LEU:N	1:A:7:LEU:CD2	2.81	0.44
1:B:45:LEU:HD12	1:B:45:LEU:N	2.32	0.44
1:C:24:HIS:HD2	1:C:36:SER:CB	2.31	0.44
1:G:18:ASN:C	1:G:18:ASN:ND2	2.76	0.44
1:A:183:ARG:HG3	1:A:183:ARG:HH11	1.82	0.44
1:C:107:ASP:OD1	1:C:133:ARG:NH2	2.51	0.44
1:E:76:PHE:HD1	1:E:77:TYR:CE1	2.36	0.44
1:F:37:TYR:CD1	1:F:97:GLU:HB2	2.53	0.44
1:G:185:LYS:N	1:G:185:LYS:HD2	2.33	0.44
1:H:139:ASN:HB3	1:H:189:LEU:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:ASN:O	1:A:19:ARG:C	2.59	0.44
1:B:88:ARG:O	1:B:88:ARG:HG2	2.18	0.44
1:G:24:HIS:HD1	1:G:24:HIS:C	2.25	0.44
1:H:130:VAL:C	1:H:132:ASN:N	2.76	0.44
1:A:32:PHE:HZ	1:A:161:ASN:HA	1.82	0.44
1:E:17:MSE:CE	1:E:62:TYR:HE1	2.31	0.44
1:E:57:GLU:HG2	1:E:58:PHE:N	2.33	0.44
1:E:93:LYS:HD3	1:E:97:GLU:HG2	2.00	0.44
1:E:169:LEU:O	1:E:173:ILE:HB	2.18	0.44
1:H:67:ARG:HH11	1:H:67:ARG:CG	2.27	0.44
1:H:181:GLU:O	1:H:185:LYS:HA	2.18	0.44
1:C:70:GLU:C	1:C:72:LYS:H	2.26	0.44
1:D:37:TYR:HA	1:D:97:GLU:O	2.18	0.44
1:A:21:MSE:HE2	1:A:89:ASN:HB3	1.99	0.43
1:A:62:TYR:CD2	1:A:95:CYS:HA	2.53	0.43
1:A:66:TYR:CE1	1:A:83:LEU:HD22	2.53	0.43
1:B:80:ASN:OD1	1:B:80:ASN:C	2.61	0.43
1:E:145:ASN:ND2	1:E:148:ASP:H	2.16	0.43
1:E:181:GLU:O	1:E:185:LYS:HA	2.17	0.43
1:H:88:ARG:O	1:H:92:ILE:HG13	2.18	0.43
1:H:129:SER:HB2	1:H:195:TYR:O	2.17	0.43
1:A:57:GLU:C	1:A:59:GLY:H	2.26	0.43
1:F:17:MSE:HG3	1:F:45:LEU:HD11	2.00	0.43
1:G:51:ASP:O	1:G:52:LYS:HB2	2.18	0.43
1:H:73:ASP:O	1:H:74:LYS:C	2.61	0.43
1:A:169:LEU:HD11	1:A:173:ILE:HD12	2.00	0.43
1:C:172:ASP:O	1:C:173:ILE:C	2.61	0.43
1:D:87:ASP:O	1:D:90:ARG:CG	2.66	0.43
1:H:27:LEU:HD21	1:H:157:THR:HA	2.00	0.43
1:H:70:GLU:C	1:H:72:LYS:H	2.26	0.43
1:A:61:LYS:O	1:A:65:ILE:HG13	2.19	0.43
1:A:180:PHE:CE2	1:A:184:ARG:HG3	2.53	0.43
1:E:106:PHE:O	1:E:195:TYR:HE2	2.01	0.43
1:F:44:LYS:C	1:F:45:LEU:CD1	2.87	0.43
1:H:52:LYS:HD3	1:H:52:LYS:HA	1.86	0.43
1:A:110:VAL:HA	1:A:138:LEU:O	2.19	0.43
1:B:13:CYS:SG	1:B:20:SER:HB3	2.57	0.43
1:B:168:ASP:CG	1:B:171:ASN:HD22	2.26	0.43
1:E:127:MSE:SE	1:E:127:MSE:N	2.95	0.43
1:A:124:MSE:HB2	1:A:193:LEU:HG	2.00	0.43
1:A:172:ASP:HB3	1:C:30:LYS:HZ1	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:52:LYS:HD3	1:D:52:LYS:HA	1.88	0.43
1:D:130:VAL:O	1:D:132:ASN:N	2.51	0.43
1:F:11:VAL:HG12	1:F:12:VAL:N	2.32	0.43
1:F:143:VAL:HG12	1:F:144:ASP:N	2.33	0.43
1:H:58:PHE:CG	1:H:98:ARG:HG3	2.53	0.43
1:A:124:MSE:HE1	1:A:135:VAL:HG11	1.99	0.43
1:E:11:VAL:HG12	1:E:12:VAL:N	2.34	0.43
1:G:52:LYS:N	1:G:53:PRO:HD3	2.33	0.43
1:D:61:LYS:O	1:D:65:ILE:HG13	2.19	0.43
1:D:67:ARG:NH1	1:D:67:ARG:CG	2.77	0.43
1:E:183:ARG:HH11	1:E:183:ARG:HG3	1.84	0.43
1:G:171:ASN:O	1:G:173:ILE:N	2.52	0.43
1:C:133:ARG:O	1:C:133:ARG:HG3	2.18	0.43
1:C:159:MSE:CG	1:C:163:MSE:HE3	2.49	0.43
1:E:67:ARG:CB	1:E:67:ARG:CZ	2.97	0.43
1:E:143:VAL:O	1:E:145:ASN:N	2.43	0.43
1:H:61:LYS:O	1:H:65:ILE:HG12	2.19	0.43
1:B:70:GLU:C	1:B:72:LYS:H	2.27	0.43
1:D:105:GLN:CB	1:D:195:TYR:CZ	3.01	0.43
1:D:131:ASP:O	1:D:132:ASN:C	2.62	0.43
1:E:80:ASN:OD1	1:E:80:ASN:C	2.62	0.43
1:E:115:ARG:O	1:E:119:LEU:CD1	2.52	0.43
1:G:180:PHE:O	1:G:184:ARG:HB2	2.19	0.43
1:H:193:LEU:HD13	1:H:193:LEU:HA	1.85	0.43
1:A:28:ALA:C	1:A:30:LYS:N	2.77	0.42
1:G:24:HIS:HD2	1:G:36:SER:CB	2.31	0.42
1:G:25:ASN:C	1:G:25:ASN:ND2	2.77	0.42
1:H:108:ILE:HG21	1:H:160:ILE:CD1	2.49	0.42
1:A:47:GLY:HA3	1:A:52:LYS:O	2.19	0.42
1:A:160:ILE:HD13	1:A:160:ILE:HA	1.86	0.42
1:A:161:ASN:O	1:A:164:ALA:HB3	2.19	0.42
1:D:45:LEU:HD21	1:D:86:LEU:HD21	1.99	0.42
1:E:11:VAL:O	1:E:36:SER:HA	2.20	0.42
1:F:8:ALA:HB1	1:F:106:PHE:HD1	1.84	0.42
1:F:22:GLU:O	1:F:25:ASN:HB3	2.18	0.42
1:G:19:ARG:HD2	1:G:112:VAL:HG21	2.02	0.42
1:G:100:GLN:O	1:G:123:HIS:NE2	2.52	0.42
1:G:112:VAL:HB	1:G:142:VAL:HG12	1.99	0.42
1:H:128:GLU:C	1:H:128:GLU:CD	2.87	0.42
1:B:18:ASN:O	1:B:19:ARG:C	2.61	0.42
1:D:114:GLU:O	1:D:117:TYR:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:17:MSE:HG3	1:E:45:LEU:CD1	2.49	0.42
1:F:37:TYR:HD1	1:F:97:GLU:HB2	1.83	0.42
1:B:20:SER:OG	1:B:36:SER:HB2	2.19	0.42
1:B:159:MSE:HA	1:B:180:PHE:CE1	2.54	0.42
1:A:108:ILE:HD12	1:A:108:ILE:N	2.35	0.42
1:C:155:VAL:HG21	1:C:186:ARG:NH1	2.34	0.42
1:D:47:GLY:HA3	1:D:52:LYS:O	2.19	0.42
1:D:159:MSE:HE3	1:D:180:PHE:CE2	2.53	0.42
1:F:9:VAL:HG13	1:F:108:ILE:HB	2.01	0.42
1:F:13:CYS:O	1:F:38:GLY:HA2	2.19	0.42
1:F:44:LYS:HE3	1:F:53:PRO:HB2	2.01	0.42
1:G:42:ARG:NE	1:G:55:VAL:HG11	2.33	0.42
1:G:61:LYS:HA	1:G:95:CYS:CB	2.49	0.42
1:H:173:ILE:HA	1:H:176:LEU:HD12	2.02	0.42
1:A:69:LEU:HD12	1:A:77:TYR:CZ	2.55	0.42
1:A:130:VAL:O	1:A:131:ASP:C	2.62	0.42
1:A:167:THR:HG21	1:C:158:ASP:CG	2.45	0.42
1:C:16:ASN:HD22	1:C:16:ASN:HA	1.65	0.42
1:D:70:GLU:C	1:D:72:LYS:H	2.28	0.42
1:A:20:SER:O	1:A:24:HIS:HB2	2.19	0.42
1:A:127:MSE:SE	1:A:127:MSE:H	2.53	0.42
1:B:151:MSE:HE2	1:B:151:MSE:CA	2.49	0.42
1:C:105:GLN:HE21	1:C:105:GLN:HB3	1.68	0.42
1:F:24:HIS:CD2	1:F:36:SER:OG	2.69	0.42
1:F:68:ASP:OD1	1:F:72:LYS:HE2	2.19	0.42
1:G:171:ASN:C	1:G:173:ILE:N	2.77	0.42
1:H:62:TYR:HE2	1:H:93:LYS:HB3	1.83	0.42
1:C:66:TYR:HE1	1:C:83:LEU:HB3	1.84	0.42
1:D:91:ARG:NH2	1:E:167:THR:HG23	2.33	0.42
1:E:17:MSE:HE3	1:E:43:VAL:HG11	2.02	0.42
1:E:34:VAL:HG22	1:E:35:ARG:N	2.34	0.42
1:F:30:LYS:HA	1:F:30:LYS:HD2	1.79	0.42
1:F:121:VAL:HG13	1:F:193:LEU:HD21	2.02	0.42
1:H:135:VAL:CG1	1:H:193:LEU:O	2.67	0.42
1:A:58:PHE:CD1	1:A:98:ARG:HG3	2.55	0.42
1:B:16:ASN:OD1	1:B:93:LYS:HE3	2.20	0.42
1:B:192:VAL:C	1:B:193:LEU:HD22	2.45	0.42
1:C:79:GLN:HG3	1:H:143:VAL:HG11	2.02	0.42
1:D:11:VAL:C	1:D:12:VAL:HG23	2.45	0.42
1:D:44:LYS:HE3	1:D:44:LYS:HB2	1.84	0.42
1:D:84:HIS:ND1	1:D:84:HIS:C	2.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:73:ASP:O	1:F:74:LYS:C	2.62	0.42
1:G:20:SER:OG	1:G:36:SER:HB2	2.19	0.42
1:A:165:LYS:HB2	1:C:151:MSE:CE	2.48	0.42
1:C:12:VAL:O	1:C:116:VAL:HG11	2.20	0.42
1:C:173:ILE:CG2	1:C:174:ASP:N	2.83	0.42
1:F:163:MSE:O	1:F:166:SER:HB3	2.20	0.42
1:A:61:LYS:HE3	1:A:94:LYS:HE3	2.00	0.41
1:G:186:ARG:HG3	1:G:186:ARG:HH11	1.84	0.41
1:H:39:THR:HA	1:H:100:GLN:HE22	1.85	0.41
1:A:58:PHE:CG	1:A:98:ARG:HG3	2.55	0.41
1:A:99:PHE:CE2	1:A:120:VAL:HG13	2.54	0.41
1:C:81:GLY:O	1:C:84:HIS:N	2.53	0.41
1:C:140:VAL:HG22	1:C:188:ILE:HD12	2.01	0.41
1:D:87:ASP:HA	1:D:90:ARG:HG2	2.01	0.41
1:G:183:ARG:HH11	1:G:183:ARG:CG	2.33	0.41
1:H:54:ASN:HD21	1:H:72:LYS:NZ	2.17	0.41
1:A:107:ASP:HB2	1:A:108:ILE:HD12	2.02	0.41
1:B:90:ARG:O	1:E:194:PHE:HZ	2.03	0.41
1:B:137:VAL:CG2	1:B:193:LEU:HD23	2.51	0.41
1:B:155:VAL:HG21	1:B:186:ARG:NH1	2.35	0.41
1:C:55:VAL:O	1:C:56:TYR:CD1	2.74	0.41
1:D:136:HIS:CE1	1:D:169:LEU:CD1	3.03	0.41
1:E:16:ASN:HA	1:E:16:ASN:HD22	1.64	0.41
1:E:193:LEU:HD13	1:E:193:LEU:HA	1.65	0.41
1:G:45:LEU:N	1:G:45:LEU:CD1	2.84	0.41
1:G:84:HIS:ND1	1:G:84:HIS:C	2.78	0.41
1:G:151:MSE:O	1:G:155:VAL:HG23	2.20	0.41
1:H:177:ILE:CG2	1:H:188:ILE:HB	2.51	0.41
1:A:27:LEU:O	1:A:32:PHE:HB2	2.21	0.41
1:A:84:HIS:O	1:A:87:ASP:HB3	2.20	0.41
1:A:173:ILE:HG23	1:A:174:ASP:N	2.35	0.41
1:C:70:GLU:C	1:C:72:LYS:N	2.77	0.41
1:D:151:MSE:HA	1:D:151:MSE:CE	2.49	0.41
1:E:181:GLU:HG2	1:E:186:ARG:O	2.20	0.41
1:F:67:ARG:NH1	1:F:67:ARG:HB2	2.35	0.41
1:G:136:HIS:ND1	1:G:136:HIS:N	2.68	0.41
1:B:17:MSE:HE2	1:B:62:TYR:CE1	2.56	0.41
1:B:45:LEU:HB3	1:B:46:PRO:HD2	2.01	0.41
1:B:173:ILE:O	1:B:177:ILE:HG12	2.20	0.41
1:E:19:ARG:NH2	1:E:144:ASP:HB2	2.35	0.41
1:E:45:LEU:CD1	1:E:45:LEU:N	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:150:LEU:O	1:F:154:PHE:HD2	2.03	0.41
1:H:160:ILE:O	1:H:164:ALA:HB2	2.20	0.41
1:B:140:VAL:O	1:B:142:VAL:HG12	2.20	0.41
1:B:151:MSE:CE	1:B:154:PHE:HB2	2.50	0.41
1:C:185:LYS:N	1:C:185:LYS:HD2	2.36	0.41
1:D:139:ASN:HB3	1:D:189:LEU:HB2	2.01	0.41
1:E:12:VAL:HG13	1:E:37:TYR:O	2.20	0.41
1:H:34:VAL:O	1:H:34:VAL:HG13	2.20	0.41
1:H:159:MSE:CE	1:H:188:ILE:HD12	2.49	0.41
1:A:9:VAL:HG12	1:A:10:ALA:N	2.36	0.41
1:B:16:ASN:HD22	1:B:16:ASN:HA	1.71	0.41
1:B:27:LEU:CD2	1:B:157:THR:HA	2.50	0.41
1:B:61:LYS:O	1:B:65:ILE:CD1	2.57	0.41
1:B:115:ARG:O	1:B:119:LEU:HD13	2.20	0.41
1:C:46:PRO:HB3	1:H:50:PHE:CD2	2.56	0.41
1:C:54:ASN:ND2	1:C:69:LEU:HD11	2.36	0.41
1:E:92:ILE:HB	1:E:93:LYS:H	1.62	0.41
1:G:26:PHE:O	1:G:27:LEU:C	2.63	0.41
1:G:114:GLU:HA	1:G:117:TYR:HB3	2.02	0.41
1:H:18:ASN:C	1:H:18:ASN:ND2	2.78	0.41
1:A:158:ASP:CB	1:A:184:ARG:HH21	2.32	0.41
1:E:62:TYR:CZ	1:E:96:PRO:HD3	2.56	0.41
1:G:42:ARG:HE	1:G:55:VAL:HG11	1.86	0.41
1:A:20:SER:OG	1:A:36:SER:HB2	2.21	0.41
1:A:70:GLU:O	1:A:74:LYS:HB2	2.21	0.41
1:A:165:LYS:CD	1:C:151:MSE:HG2	2.50	0.41
1:B:72:LYS:O	1:B:74:LYS:N	2.51	0.41
1:D:160:ILE:HD13	1:D:160:ILE:HA	1.94	0.41
1:G:89:ASN:C	1:G:91:ARG:N	2.75	0.41
1:A:35:ARG:HG3	1:A:106:PHE:HE1	1.85	0.41
1:A:128:GLU:C	1:A:128:GLU:CD	2.89	0.41
1:A:159:MSE:HB2	1:A:180:PHE:CZ	2.55	0.41
1:B:98:ARG:HB3	1:B:101:ASP:OD2	2.21	0.41
1:D:46:PRO:CG	1:D:82:LEU:HD21	2.50	0.41
1:F:79:GLN:O	1:F:81:GLY:N	2.52	0.41
1:H:86:LEU:HD23	1:H:86:LEU:HA	1.88	0.41
1:C:13:CYS:O	1:C:38:GLY:HA2	2.21	0.40
1:C:25:ASN:ND2	1:C:25:ASN:C	2.77	0.40
1:D:22:GLU:OE2	1:D:150:LEU:HD22	2.20	0.40
1:F:168:ASP:HB3	1:F:172:ASP:OD2	2.22	0.40
1:B:65:ILE:N	1:B:65:ILE:HD12	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:93:LYS:HD3	1:C:97:GLU:HG2	2.02	0.40
1:D:130:VAL:HG23	1:D:131:ASP:N	2.36	0.40
1:D:130:VAL:C	1:D:132:ASN:N	2.77	0.40
1:C:22:GLU:OE1	1:C:22:GLU:HA	2.21	0.40
1:D:11:VAL:C	1:D:12:VAL:CG2	2.94	0.40
1:D:37:TYR:HB3	1:D:97:GLU:O	2.21	0.40
1:E:44:LYS:HE3	1:E:44:LYS:HB2	1.95	0.40
1:E:65:ILE:HG22	1:E:69:LEU:CD2	2.51	0.40
1:E:73:ASP:O	1:E:74:LYS:C	2.64	0.40
1:H:106:PHE:O	1:H:195:TYR:HE2	2.03	0.40
1:H:138:LEU:HA	1:H:189:LEU:O	2.21	0.40
1:B:85:MSE:O	1:B:89:ASN:ND2	2.55	0.40
1:C:67:ARG:NH2	1:D:189:LEU:HD13	2.28	0.40
1:E:63:GLU:O	1:E:66:TYR:HB3	2.21	0.40
1:F:190:HIS:ND1	1:F:191:SER:N	2.69	0.40
1:H:27:LEU:HD23	1:H:157:THR:HG23	2.04	0.40
1:A:17:MSE:HE3	1:A:43:VAL:HG11	2.03	0.40
1:A:114:GLU:O	1:A:117:TYR:HB3	2.22	0.40
1:B:45:LEU:HD23	1:B:82:LEU:HD13	2.00	0.40
1:C:7:LEU:N	1:C:7:LEU:HD23	2.36	0.40
1:D:194:PHE:CD2	1:D:194:PHE:N	2.89	0.40
1:E:13:CYS:O	1:E:38:GLY:HA2	2.22	0.40
1:F:66:TYR:CE1	1:F:83:LEU:HD13	2.56	0.40
1:F:79:GLN:C	1:F:81:GLY:N	2.78	0.40
1:H:111:THR:HG22	1:H:120:VAL:HG21	2.02	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	188/195 (96%)	160 (85%)	23 (12%)	5 (3%)	4 23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	188/195 (96%)	157 (84%)	24 (13%)	7 (4%)	2	17
1	C	188/195 (96%)	146 (78%)	35 (19%)	7 (4%)	2	17
1	D	188/195 (96%)	155 (82%)	22 (12%)	11 (6%)	1	9
1	E	188/195 (96%)	147 (78%)	32 (17%)	9 (5%)	2	13
1	F	188/195 (96%)	150 (80%)	31 (16%)	7 (4%)	2	17
1	G	188/195 (96%)	147 (78%)	33 (18%)	8 (4%)	2	15
1	H	188/195 (96%)	153 (81%)	31 (16%)	4 (2%)	5	27
All	All	1504/1560 (96%)	1215 (81%)	231 (15%)	58 (4%)	2	16

All (58) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	131	ASP
1	C	74	LYS
1	C	90	ARG
1	C	191	SER
1	D	73	ASP
1	D	126	SER
1	E	131	ASP
1	E	135	VAL
1	G	52	LYS
1	H	131	ASP
1	A	19	ARG
1	A	126	SER
1	B	40	GLY
1	B	126	SER
1	B	127	MSE
1	C	82	LEU
1	D	127	MSE
1	E	18	ASN
1	F	58	PHE
1	F	81	GLY
1	F	170	ASP
1	G	170	ASP
1	G	172	ASP
1	H	170	ASP
1	B	58	PHE
1	B	73	ASP
1	C	131	ASP
1	D	82	LEU

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Mol	Chain	Res	Type
1	E	58	PHE
1	F	25	ASN
1	G	14	SER
1	G	90	ARG
1	A	170	ASP
1	B	19	ARG
1	C	170	ASP
1	D	19	ARG
1	D	25	ASN
1	D	48	MSE
1	D	132	ASN
1	E	76	PHE
1	E	144	ASP
1	F	191	SER
1	G	191	SER
1	H	172	ASP
1	A	53	PRO
1	C	76	PHE
1	D	146	ALA
1	E	130	VAL
1	F	59	GLY
1	G	74	LYS
1	D	131	ASP
1	H	58	PHE
1	E	92	ILE
1	F	143	VAL
1	G	59	GLY
1	E	134	PRO
1	A	40	GLY
1	D	46	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	174/167 (104%)	156 (90%)	18 (10%)	7 26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	174/167 (104%)	150 (86%)	24 (14%)	3	16
1	C	174/167 (104%)	155 (89%)	19 (11%)	6	24
1	D	174/167 (104%)	158 (91%)	16 (9%)	8	31
1	E	174/167 (104%)	150 (86%)	24 (14%)	3	16
1	F	174/167 (104%)	159 (91%)	15 (9%)	10	34
1	G	174/167 (104%)	159 (91%)	15 (9%)	10	34
1	H	174/167 (104%)	156 (90%)	18 (10%)	7	26
All	All	1392/1336 (104%)	1243 (89%)	149 (11%)	6	24

All (149) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	ASN
1	A	53	PRO
1	A	58	PHE
1	A	69	LEU
1	A	73	ASP
1	A	92	ILE
1	A	100	GLN
1	A	101	ASP
1	A	127	MSE
1	A	128	GLU
1	A	142	VAL
1	A	145	ASN
1	A	148	ASP
1	A	150	LEU
1	A	167	THR
1	A	170	ASP
1	A	188	ILE
1	A	195	TYR
1	B	7	LEU
1	B	14	SER
1	B	25	ASN
1	B	26	PHE
1	B	33	ASN
1	B	35	ARG
1	B	58	PHE
1	B	69	LEU
1	B	73	ASP
1	B	82	LEU

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Mol	Chain	Res	Type
1	B	84	HIS
1	B	90	ARG
1	B	97	GLU
1	B	100	GLN
1	B	101	ASP
1	B	115	ARG
1	B	127	MSE
1	B	142	VAL
1	B	145	ASN
1	B	148	ASP
1	B	150	LEU
1	B	151	MSE
1	B	172	ASP
1	B	193	LEU
1	C	11	VAL
1	C	16	ASN
1	C	35	ARG
1	C	45	LEU
1	C	58	PHE
1	C	69	LEU
1	C	79	GLN
1	C	97	GLU
1	C	100	GLN
1	C	114	GLU
1	C	127	MSE
1	C	128	GLU
1	C	131	ASP
1	C	135	VAL
1	C	142	VAL
1	C	148	ASP
1	C	151	MSE
1	C	167	THR
1	C	183	ARG
1	D	52	LYS
1	D	53	PRO
1	D	58	PHE
1	D	97	GLU
1	D	100	GLN
1	D	107	ASP
1	D	115	ARG
1	D	127	MSE
1	D	141	ASP

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Mol	Chain	Res	Type
1	D	142	VAL
1	D	145	ASN
1	D	148	ASP
1	D	150	LEU
1	D	151	MSE
1	D	178	GLN
1	D	193	LEU
1	E	14	SER
1	E	18	ASN
1	E	45	LEU
1	E	63	GLU
1	E	67	ARG
1	E	69	LEU
1	E	79	GLN
1	E	82	LEU
1	E	90	ARG
1	E	92	ILE
1	E	97	GLU
1	E	100	GLN
1	E	109	ILE
1	E	110	VAL
1	E	127	MSE
1	E	128	GLU
1	E	131	ASP
1	E	134	PRO
1	E	142	VAL
1	E	145	ASN
1	E	148	ASP
1	E	151	MSE
1	E	167	THR
1	E	184	ARG
1	F	58	PHE
1	F	60	THR
1	F	69	LEU
1	F	70	GLU
1	F	73	ASP
1	F	78	THR
1	F	79	GLN
1	F	82	LEU
1	F	100	GLN
1	F	104	GLU
1	F	105	GLN

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Mol	Chain	Res	Type
1	F	107	ASP
1	F	127	MSE
1	F	148	ASP
1	F	151	MSE
1	G	45	LEU
1	G	58	PHE
1	G	69	LEU
1	G	70	GLU
1	G	73	ASP
1	G	82	LEU
1	G	90	ARG
1	G	100	GLN
1	G	101	ASP
1	G	127	MSE
1	G	147	GLU
1	G	148	ASP
1	G	151	MSE
1	G	173	ILE
1	G	183	ARG
1	H	58	PHE
1	H	73	ASP
1	H	82	LEU
1	H	97	GLU
1	H	100	GLN
1	H	101	ASP
1	H	108	ILE
1	H	111	THR
1	H	115	ARG
1	H	127	MSE
1	H	128	GLU
1	H	142	VAL
1	H	143	VAL
1	H	151	MSE
1	H	170	ASP
1	H	172	ASP
1	H	173	ILE
1	H	193	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (65) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	HIS

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Mol	Chain	Res	Type
1	A	25	ASN
1	A	33	ASN
1	A	100	GLN
1	A	105	GLN
1	A	136	HIS
1	A	145	ASN
1	A	190	HIS
1	B	24	HIS
1	B	25	ASN
1	B	33	ASN
1	B	54	ASN
1	B	100	GLN
1	B	139	ASN
1	B	171	ASN
1	B	190	HIS
1	C	24	HIS
1	C	25	ASN
1	C	33	ASN
1	C	100	GLN
1	C	105	GLN
1	C	132	ASN
1	C	136	HIS
1	C	145	ASN
1	D	25	ASN
1	D	33	ASN
1	D	54	ASN
1	D	100	GLN
1	D	105	GLN
1	D	132	ASN
1	D	136	HIS
1	D	139	ASN
1	E	18	ASN
1	E	24	HIS
1	E	25	ASN
1	E	33	ASN
1	E	54	ASN
1	E	100	GLN
1	E	136	HIS
1	E	139	ASN
1	E	145	ASN
1	E	190	HIS
1	F	24	HIS

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Mol	Chain	Res	Type
1	F	25	ASN
1	F	33	ASN
1	F	100	GLN
1	F	105	GLN
1	F	145	ASN
1	F	161	ASN
1	G	18	ASN
1	G	24	HIS
1	G	25	ASN
1	G	33	ASN
1	G	54	ASN
1	G	100	GLN
1	G	171	ASN
1	H	18	ASN
1	H	24	HIS
1	H	25	ASN
1	H	33	ASN
1	H	54	ASN
1	H	100	GLN
1	H	105	GLN
1	H	136	HIS
1	H	139	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	179/195 (91%)	-1.49	0 100 100	39, 67, 100, 109	0
1	B	179/195 (91%)	-1.47	0 100 100	37, 67, 108, 123	0
1	C	179/195 (91%)	-1.50	0 100 100	42, 71, 96, 111	0
1	D	179/195 (91%)	-1.41	0 100 100	53, 84, 112, 127	0
1	E	179/195 (91%)	-1.50	0 100 100	30, 67, 99, 114	0
1	F	179/195 (91%)	-1.32	0 100 100	63, 96, 136, 140	0
1	G	179/195 (91%)	-1.29	0 100 100	60, 103, 143, 147	0
1	H	179/195 (91%)	-1.48	0 100 100	44, 74, 99, 104	0
All	All	1432/1560 (91%)	-1.43	0 100 100	30, 77, 130, 147	0

There are no RSRZ outliers to report.

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 oligosaccharides 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.