Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2023 – 12:58 AM EDT

PDB ID	:	2H4C
Title	:	Structure of Daboiatoxin (heterodimeric PLA2 venom)
Authors	:	Gopalan, G.; Thwin, M.M.; Gopalakrishnakone, P.; Swaminathan, K.
Deposited on	:	2006-05-24
Resolution	:	2.60 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:

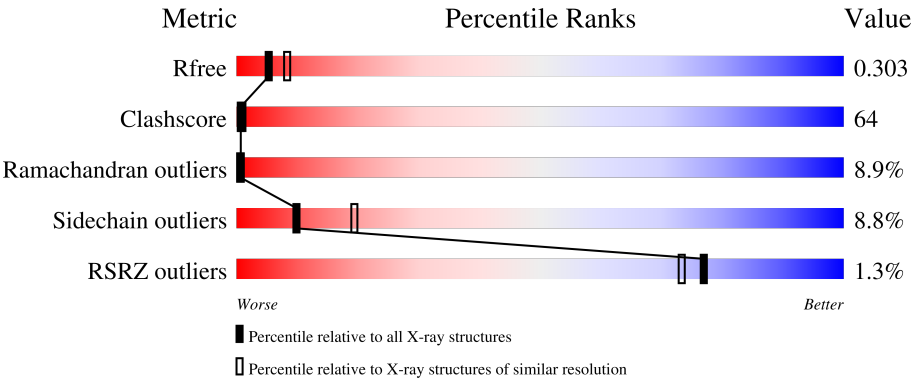
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.60 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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 <=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	122	2% 30% 58% 10% •
1	C	122	2% 23% 61% 16% •
1	E	122	% 28% 58% 11% •
1	G	122	2% 30% 59% 10% •
2	B	122	% 34% 57% 8% •

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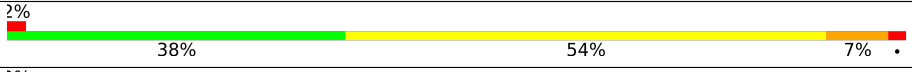
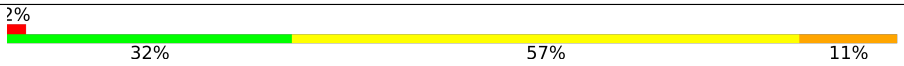
Mol	Chain	Length	Quality of chain
2	D	122	
2	F	122	
2	H	122	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7879 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 Phospholipase A2-III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	122	Total	C	N	O	S	0	0	0
			944	580	156	191	17			
1	C	122	Total	C	N	O	S	0	0	0
			944	580	156	191	17			
1	E	122	Total	C	N	O	S	0	0	0
			944	580	156	191	17			
1	G	122	Total	C	N	O	S	0	0	0
			944	580	156	191	17			

- Molecule 2 is a protein called Phospholipase A2-II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	122	Total	C	N	O	S	0	0	0
			976	614	163	183	16			
2	D	122	Total	C	N	O	S	0	0	0
			976	614	163	183	16			
2	F	122	Total	C	N	O	S	0	0	0
			976	614	163	183	16			
2	H	122	Total	C	N	O	S	0	0	0
			976	614	163	183	16			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	26	Total	O	0	0
			26	26		
3	B	23	Total	O	0	0
			23	23		
3	C	25	Total	O	0	0
			25	25		
3	D	19	Total	O	0	0
			19	19		

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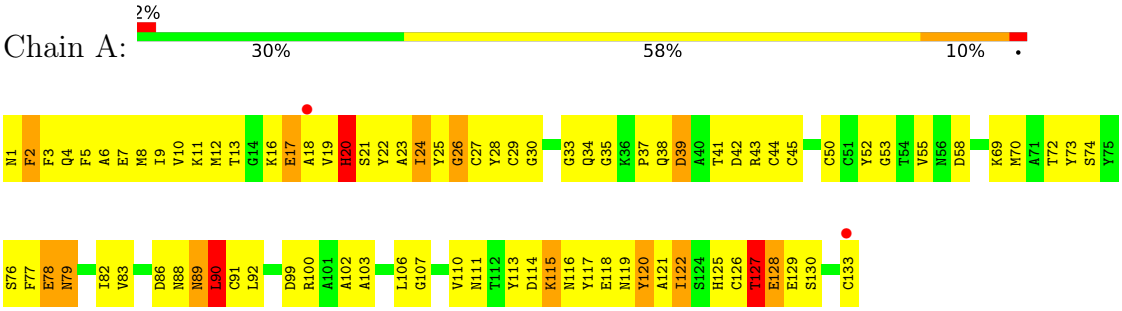
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	31	Total O 31 31	0	0
3	F	25	Total O 25 25	0	0
3	G	23	Total O 23 23	0	0
3	H	27	Total O 27 27	0	0

3 Residue-property plots (i)

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.

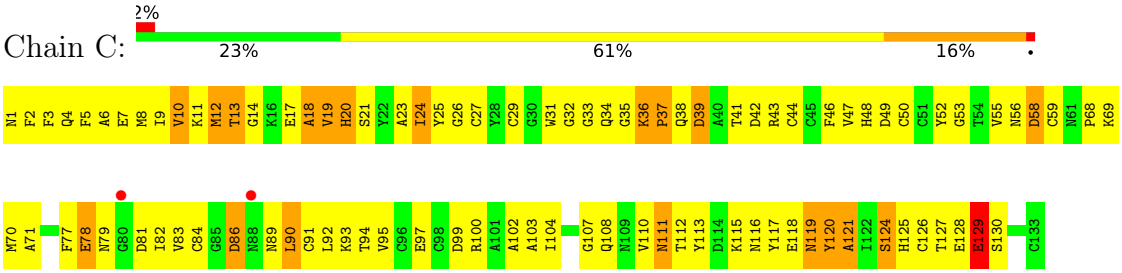
• Molecule 1: Phospholipase A2-III

Chain A:



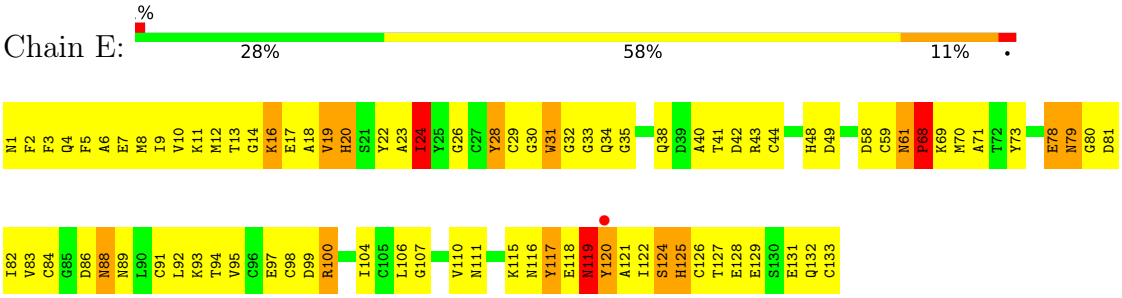
• Molecule 1: Phospholipase A2-III

Chain C:



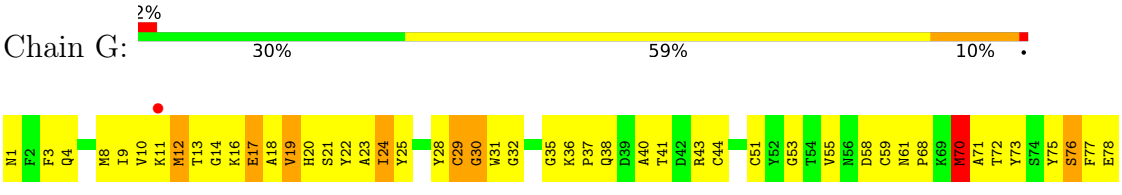
• Molecule 1: Phospholipase A2-III

Chain E:



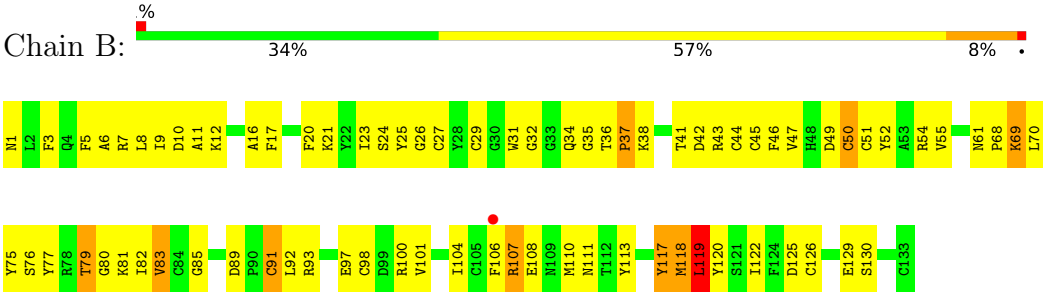
• Molecule 1: Phospholipase A2-III

Chain G:



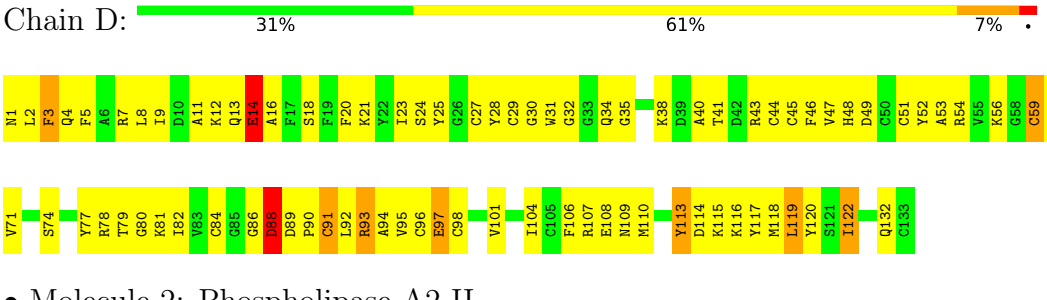
• Molecule 2: Phospholipase A2-II

Chain B:



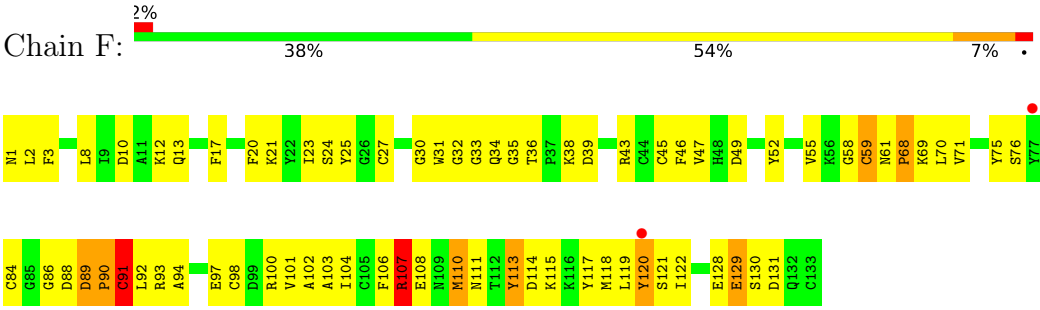
• Molecule 2: Phospholipase A2-II

Chain D:



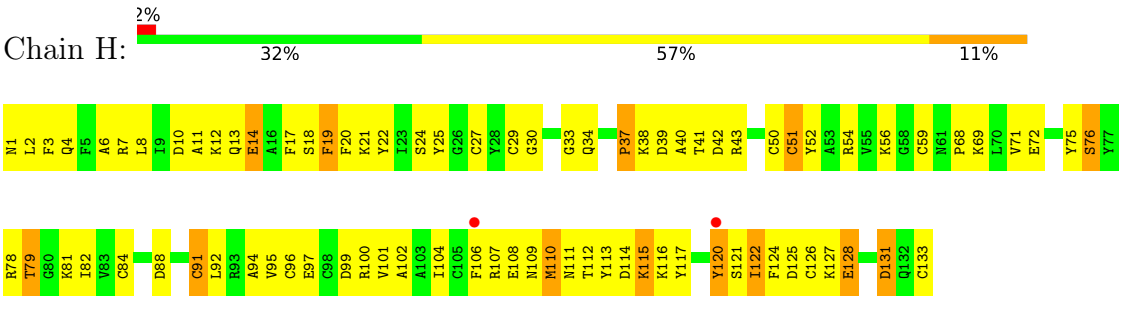
• Molecule 2: Phospholipase A2-II

Chain F:



• Molecule 2: Phospholipase A2-II

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	66.98Å 66.98Å 240.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	7.99 – 2.60 37.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	95.5 (7.99-2.60) 95.6 (37.00-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	7.68 (at 2.61Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.220 , 0.307 0.220 , 0.303	Depositor DCC
R_{free} test set	3262 reflections (9.18%)	wwPDB-VP
Wilson B-factor (Å^2)	37.6	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 35.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l 0.487 for h,-h-k,-l 0.029 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	7879	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.80% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.44	0/964	0.70	0/1302
1	C	0.43	0/964	0.72	0/1302
1	E	0.42	0/964	0.69	0/1302
1	G	0.39	0/964	0.65	0/1302
2	B	0.46	0/999	0.72	0/1341
2	D	0.41	0/999	0.68	0/1341
2	F	0.42	0/999	0.65	0/1341
2	H	0.43	0/999	0.67	1/1341 (0.1%)
All	All	0.43	0/7852	0.69	1/10572 (0.0%)

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	E	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	51	CYS	CA-CB-SG	-5.37	104.33	114.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	28	TYR	Sidechain

5.2 Too-close contacts (i)

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	944	0	844	139	0
1	C	944	0	840	144	2
1	E	944	0	840	133	0
1	G	944	0	840	127	0
2	B	976	0	909	111	0
2	D	976	0	905	109	3
2	F	976	0	907	118	0
2	H	976	0	911	119	3
3	A	26	0	0	6	1
3	B	23	0	0	3	3
3	C	25	0	0	7	1
3	D	19	0	0	12	1
3	E	31	0	0	6	4
3	F	25	0	0	10	1
3	G	23	0	0	6	0
3	H	27	0	0	5	3
All	All	7879	0	6996	926	11

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 64.

All (926) 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:C:36:LYS:HB3	3:C:153:HOH:O	1.40	1.21
2:D:110:MET:HA	3:D:151:HOH:O	1.37	1.21
1:A:133:CYS:HA	3:A:156:HOH:O	1.39	1.18
2:D:93:ARG:NE	3:D:149:HOH:O	1.84	1.09
1:C:10:VAL:HG22	1:C:18:ALA:HB3	1.31	1.07
2:D:93:ARG:HG3	3:D:149:HOH:O	1.53	1.06
2:D:1:ASN:HD22	2:D:3:PHE:HB2	1.20	1.03
2:B:12:LYS:HE2	2:B:107:ARG:HB3	1.39	1.02
2:D:93:ARG:CG	3:D:149:HOH:O	2.07	1.00
1:G:13:THR:HG22	1:G:107:GLY:HA2	1.42	0.99
1:E:84:CYS:HB2	1:E:93:LYS:HE3	1.48	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:59:CYS:HB2	2:D:71:VAL:HG11	1.48	0.95
1:A:34:GLN:HE21	2:B:1:ASN:HD21	1.07	0.95
2:B:12:LYS:HG2	2:B:107:ARG:HG2	1.46	0.94
1:A:10:VAL:HG22	1:A:18:ALA:H	1.32	0.92
1:C:19:VAL:O	1:C:20:HIS:HB2	1.68	0.92
1:E:82:ILE:HB	1:E:100:ARG:HD2	1.50	0.92
1:A:117:TYR:HE2	3:A:154:HOH:O	1.52	0.91
1:G:61:ASN:HD22	1:G:70:MET:HB2	1.35	0.91
1:C:127:THR:HG23	1:C:128:GLU:HG3	1.52	0.91
2:H:122:ILE:HD12	2:H:122:ILE:H	1.32	0.91
1:E:120:TYR:HE1	1:E:125:HIS:CB	1.85	0.90
1:C:129:GLU:HG3	1:C:130:SER:N	1.86	0.89
1:G:11:LYS:NZ	1:G:82:ILE:HG12	1.87	0.88
2:H:13:GLN:O	2:H:14:GLU:HB2	1.74	0.88
2:H:84:CYS:HG	2:H:96:CYS:HG	1.06	0.88
2:F:20:PHE:O	2:F:23:ILE:HG12	1.74	0.87
2:B:12:LYS:HG2	2:B:107:ARG:CG	2.04	0.86
1:A:34:GLN:O	1:A:126:CYS:HB3	1.76	0.85
1:G:9:ILE:HB	1:G:18:ALA:CB	2.07	0.85
1:C:79:ASN:C	1:C:81:ASP:H	1.79	0.85
2:D:1:ASN:ND2	2:D:3:PHE:HB2	1.92	0.84
2:H:13:GLN:HB3	2:H:110:MET:HE1	1.58	0.84
1:A:19:VAL:O	1:A:20:HIS:HB2	1.76	0.84
2:H:79:THR:HA	3:H:160:HOH:O	1.78	0.84
1:A:34:GLN:NE2	2:B:1:ASN:HD21	1.75	0.83
2:B:51:CYS:HG	2:B:98:CYS:HG	1.15	0.83
1:E:13:THR:HG23	1:E:14:GLY:H	1.44	0.83
1:G:61:ASN:ND2	1:G:70:MET:HB2	1.92	0.83
1:A:24:ILE:HG23	1:A:119:ASN:H	1.44	0.83
1:G:36:LYS:NZ	1:G:129:GLU:HB3	1.94	0.82
2:B:24:SER:HB3	2:B:119:LEU:HD13	1.59	0.82
1:C:8:MET:CE	1:C:82:ILE:HG21	2.10	0.82
2:F:23:ILE:O	2:F:30:GLY:HA3	1.78	0.82
2:D:12:LYS:O	2:D:13:GLN:HG3	1.78	0.82
1:C:32:GLY:O	2:D:1:ASN:HB2	1.79	0.81
1:E:9:ILE:O	1:E:13:THR:HG22	1.79	0.81
2:D:93:ARG:CD	3:D:149:HOH:O	2.17	0.81
1:E:49:ASP:HB3	2:F:70:LEU:HD21	1.59	0.81
1:G:11:LYS:HZ2	1:G:82:ILE:HG12	1.45	0.81
1:A:2:PHE:CZ	1:A:69:LYS:HG3	2.16	0.81
1:C:3:PHE:CD1	2:D:122:ILE:HG22	2.16	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:MET:HE2	1:A:100:ARG:HA	1.64	0.80
1:A:1:ASN:OD1	1:A:4:GLN:HG3	1.81	0.80
1:G:9:ILE:HB	1:G:18:ALA:HB2	1.63	0.80
2:H:13:GLN:NE2	2:H:106:PHE:HB3	1.97	0.80
2:D:90:PRO:HA	2:D:93:ARG:HB3	1.64	0.79
1:A:34:GLN:HE21	2:B:1:ASN:ND2	1.79	0.79
1:C:8:MET:HE3	1:C:82:ILE:HG21	1.65	0.78
1:G:12:MET:HG3	1:G:103:ALA:HB1	1.65	0.78
2:H:1:ASN:OD1	2:H:4:GLN:HG3	1.84	0.78
2:B:5:PHE:O	2:B:9:ILE:HG13	1.82	0.78
1:A:8:MET:CE	1:A:100:ARG:HA	2.14	0.78
2:F:58:GLY:O	2:F:59:CYS:HB3	1.82	0.78
2:D:3:PHE:O	2:D:7:ARG:HG3	1.85	0.77
1:E:86:ASP:HB2	1:E:93:LYS:HB2	1.66	0.77
1:E:1:ASN:OD1	1:E:4:GLN:HG3	1.84	0.77
1:E:10:VAL:HG22	1:E:18:ALA:H	1.50	0.77
1:E:24:ILE:HG21	1:E:119:ASN:ND2	2.00	0.77
2:F:91:CYS:SG	3:F:152:HOH:O	2.43	0.76
2:B:27:CYS:HB3	2:B:34:GLN:O	1.86	0.76
2:D:14:GLU:OE1	2:D:18:SER:HB3	1.86	0.76
1:A:27:CYS:HG	1:A:126:CYS:HG	1.32	0.75
1:G:3:PHE:HB3	2:H:122:ILE:HG13	1.68	0.75
1:G:76:SER:OG	1:G:83:VAL:HB	1.87	0.75
1:E:88:ASN:OD1	3:E:159:HOH:O	2.05	0.75
2:B:12:LYS:CE	2:B:107:ARG:HB3	2.17	0.74
1:G:28:TYR:HE2	1:G:37:PRO:HD3	1.52	0.74
1:G:89:ASN:HD22	1:G:92:LEU:H	1.32	0.74
2:D:4:GLN:O	2:D:8:LEU:HG	1.87	0.74
2:F:45:CYS:SG	2:F:106:PHE:HZ	2.10	0.74
2:B:85:GLY:HA3	3:B:149:HOH:O	1.88	0.74
1:G:1:ASN:OD1	1:G:3:PHE:HB2	1.88	0.74
2:F:59:CYS:HB3	3:F:152:HOH:O	1.89	0.73
2:D:59:CYS:HB2	2:D:71:VAL:CG1	2.19	0.72
2:D:101:VAL:HB	3:D:148:HOH:O	1.88	0.72
1:C:48:HIS:HD2	1:C:102:ALA:HB2	1.53	0.72
1:G:13:THR:HG23	3:G:151:HOH:O	1.87	0.72
2:H:8:LEU:HD22	2:H:82:ILE:HD13	1.71	0.72
1:E:23:ALA:O	1:E:24:ILE:HG23	1.90	0.71
2:F:21:LYS:HB2	2:F:113:TYR:OH	1.89	0.71
1:C:125:HIS:CG	1:C:126:CYS:N	2.58	0.71
2:D:93:ARG:HH11	2:D:93:ARG:HB2	1.54	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:91:CYS:SG	2:F:92:LEU:HD23	2.31	0.71
2:B:104:ILE:O	2:B:107:ARG:HG3	1.90	0.71
1:C:129:GLU:CG	1:C:130:SER:N	2.54	0.71
2:H:27:CYS:SG	2:H:38:LYS:HE2	2.30	0.71
1:C:78:GLU:OE1	1:C:83:VAL:HG21	1.90	0.71
2:D:101:VAL:HA	2:D:104:ILE:HD12	1.73	0.70
1:A:8:MET:HE3	1:A:82:ILE:HG21	1.73	0.70
2:D:61:ASN:O	2:D:71:VAL:HG22	1.91	0.70
1:G:58:ASP:HB3	1:G:91:CYS:HB2	1.73	0.70
1:G:77:PHE:CZ	1:G:80:GLY:HA2	2.26	0.70
1:A:23:ALA:O	1:A:30:GLY:HA3	1.91	0.70
1:A:39:ASP:HA	1:A:43:ARG:NH2	2.07	0.70
2:H:4:GLN:NE2	2:H:72:GLU:HG3	2.06	0.70
2:B:97:GLU:OE2	2:B:100:ARG:NE	2.24	0.70
1:E:3:PHE:CD2	2:F:34:GLN:HG2	2.27	0.70
1:G:35:GLY:HA3	1:G:126:CYS:HB3	1.74	0.70
1:A:34:GLN:HB3	2:B:3:PHE:CE1	2.27	0.70
1:G:17:GLU:HG3	1:G:19:VAL:HG23	1.74	0.69
1:A:43:ARG:HG3	1:A:43:ARG:HH11	1.56	0.69
1:A:90:LEU:HD23	1:A:90:LEU:H	1.57	0.69
1:E:129:GLU:O	1:E:129:GLU:HG3	1.93	0.69
2:B:44:CYS:HB2	2:B:106:PHE:CE1	2.27	0.69
2:D:101:VAL:CG1	3:D:148:HOH:O	2.39	0.69
3:E:163:HOH:O	2:F:69:LYS:HD2	1.91	0.69
2:F:71:VAL:CG1	2:F:92:LEU:HD22	2.22	0.69
1:A:89:ASN:CG	1:A:92:LEU:HD13	2.13	0.69
1:E:34:GLN:HB3	2:F:3:PHE:HE1	1.57	0.69
1:E:2:PHE:HB2	2:F:32:GLY:H	1.56	0.69
2:B:91:CYS:SG	2:B:92:LEU:N	2.66	0.69
2:H:17:PHE:HA	2:H:19:PHE:CE1	2.27	0.69
2:D:38:LYS:HB3	2:D:117:TYR:CE2	2.28	0.69
2:D:13:GLN:HG2	2:D:110:MET:SD	2.33	0.68
1:E:82:ILE:HB	1:E:100:ARG:CD	2.23	0.68
1:A:4:GLN:OE1	1:A:72:THR:HA	1.93	0.68
2:B:1:ASN:ND2	2:B:72:GLU:HG3	2.09	0.68
1:G:77:PHE:HA	1:G:81:ASP:O	1.93	0.68
2:H:17:PHE:HA	2:H:19:PHE:HE1	1.59	0.68
1:E:6:ALA:HB1	1:E:19:VAL:CG2	2.24	0.68
1:C:1:ASN:HD21	2:D:34:GLN:NE2	1.92	0.68
2:D:12:LYS:C	2:D:13:GLN:HG3	2.13	0.68
2:D:93:ARG:CZ	3:D:149:HOH:O	2.32	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:12:LYS:HG2	2:B:107:ARG:CB	2.23	0.68
1:A:2:PHE:HZ	1:A:69:LYS:HE3	1.59	0.67
1:G:110:VAL:HA	1:G:113:TYR:HB2	1.75	0.67
2:B:52:TYR:HB3	2:B:68:PRO:HG2	1.76	0.67
1:E:26:GLY:HA3	1:E:42:ASP:OD2	1.93	0.67
2:F:24:SER:O	2:F:119:LEU:N	2.20	0.67
2:H:81:LYS:HD2	2:H:100:ARG:NH2	2.10	0.67
1:E:121:ALA:HB1	2:F:3:PHE:CD2	2.30	0.67
1:E:124:SER:C	1:E:126:CYS:H	1.97	0.67
2:D:27:CYS:SG	2:D:38:LYS:HE2	2.34	0.67
2:B:27:CYS:SG	2:B:38:LYS:HE2	2.34	0.67
1:C:36:LYS:HD2	1:C:129:GLU:CD	2.15	0.67
1:E:34:GLN:HB3	2:F:3:PHE:CE1	2.30	0.67
1:A:34:GLN:HB3	2:B:3:PHE:CD1	2.30	0.66
2:B:38:LYS:HZ2	2:B:125:ASP:HB3	1.58	0.66
1:G:11:LYS:CE	1:G:82:ILE:HG12	2.24	0.66
2:H:71:VAL:HG23	3:H:138:HOH:O	1.94	0.66
2:B:77:TYR:CZ	2:B:80:GLY:HA2	2.30	0.66
2:D:25:TYR:O	2:D:29:CYS:HB2	1.96	0.66
1:G:3:PHE:CD2	2:H:34:GLN:HG2	2.30	0.66
1:G:16:LYS:HE3	3:G:150:HOH:O	1.95	0.66
1:G:36:LYS:HZ3	1:G:129:GLU:HB3	1.60	0.66
2:H:12:LYS:HG2	2:H:107:ARG:HH11	1.61	0.66
1:A:24:ILE:HG12	1:A:120:TYR:H	1.59	0.66
2:B:117:TYR:HA	2:B:120:TYR:CE1	2.31	0.66
1:C:125:HIS:CG	1:C:126:CYS:H	2.12	0.66
2:F:115:LYS:O	2:F:118:MET:HG2	1.95	0.66
1:E:4:GLN:O	1:E:8:MET:HG3	1.95	0.66
1:G:58:ASP:HB3	1:G:91:CYS:CB	2.26	0.65
1:G:9:ILE:HB	1:G:18:ALA:HB1	1.78	0.65
1:A:10:VAL:HG12	1:A:10:VAL:O	1.95	0.65
1:C:129:GLU:O	1:C:130:SER:HB2	1.97	0.65
1:E:78:GLU:O	1:E:81:ASP:HB3	1.96	0.65
1:A:10:VAL:HG22	1:A:18:ALA:N	2.10	0.65
1:C:33:GLY:HA3	2:D:1:ASN:HB3	1.79	0.65
1:E:124:SER:O	1:E:126:CYS:N	2.29	0.65
1:E:120:TYR:CE1	1:E:125:HIS:CB	2.75	0.64
1:G:24:ILE:HA	1:G:30:GLY:HA3	1.78	0.64
1:C:24:ILE:HG21	1:C:119:ASN:HA	1.78	0.64
1:E:13:THR:HG23	1:E:14:GLY:N	2.10	0.64
1:G:89:ASN:ND2	1:G:92:LEU:H	1.94	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:PRO:HA	1:C:42:ASP:OD2	1.96	0.64
2:D:86:GLY:O	2:D:88:ASP:O	2.14	0.64
2:D:101:VAL:HA	2:D:104:ILE:CD1	2.27	0.64
2:F:120:TYR:HD1	2:F:121:SER:H	1.44	0.64
2:H:114:ASP:OD1	2:H:116:LYS:HB2	1.97	0.64
1:E:6:ALA:HB2	2:F:31:TRP:CE3	2.32	0.64
2:F:115:LYS:HG3	2:F:118:MET:HE1	1.80	0.64
1:C:129:GLU:CG	1:C:130:SER:H	2.11	0.64
2:H:29:CYS:SG	2:H:42:ASP:HA	2.38	0.64
2:H:84:CYS:CB	2:H:96:CYS:HG	2.09	0.63
2:D:46:PHE:HE2	3:D:150:HOH:O	1.81	0.63
1:G:36:LYS:HZ1	1:G:129:GLU:HB3	1.62	0.63
1:G:122:ILE:HG12	2:H:7:ARG:NH1	2.13	0.63
1:G:8:MET:HA	1:G:11:LYS:HE2	1.80	0.63
2:F:45:CYS:SG	2:F:106:PHE:CZ	2.91	0.63
2:F:55:VAL:HG22	2:F:94:ALA:HB1	1.79	0.63
2:H:54:ARG:NH2	2:H:133:CYS:HB3	2.13	0.63
1:A:126:CYS:C	1:A:128:GLU:H	2.00	0.63
2:B:20:PHE:O	2:B:23:ILE:HG12	1.97	0.63
1:E:1:ASN:ND2	2:F:34:GLN:HB3	2.13	0.63
1:E:6:ALA:HB1	1:E:19:VAL:HG22	1.79	0.63
1:E:38:GLN:NE2	1:E:38:GLN:N	2.46	0.63
2:B:8:LEU:HD21	2:B:75:TYR:CD2	2.33	0.63
1:E:121:ALA:HB1	2:F:3:PHE:CE2	2.34	0.63
1:E:3:PHE:HZ	2:F:27:CYS:HA	1.63	0.63
1:E:18:ALA:O	1:E:19:VAL:C	2.35	0.63
2:B:45:CYS:SG	2:B:106:PHE:CZ	2.92	0.63
1:G:23:ALA:O	1:G:30:GLY:HA3	1.99	0.63
1:A:10:VAL:HG13	1:A:16:LYS:HA	1.81	0.62
1:C:79:ASN:C	1:C:81:ASP:N	2.49	0.62
1:E:89:ASN:HD22	1:E:92:LEU:H	1.46	0.62
1:G:97:GLU:OE2	1:G:100:ARG:HD3	1.99	0.62
2:D:59:CYS:N	2:D:91:CYS:SG	2.72	0.62
2:F:8:LEU:HD13	2:F:82:ILE:HD13	1.81	0.62
1:C:32:GLY:HA2	2:D:3:PHE:CD2	2.34	0.62
1:E:100:ARG:HH11	1:E:100:ARG:HG2	1.64	0.62
1:G:61:ASN:HD22	1:G:70:MET:CB	2.10	0.62
1:A:2:PHE:N	1:A:2:PHE:CD2	2.64	0.62
2:F:12:LYS:HB3	2:F:107:ARG:CB	2.30	0.62
1:G:58:ASP:HB3	1:G:91:CYS:SG	2.40	0.62
2:B:16:ALA:O	2:B:17:PHE:HB2	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:107:ARG:HG3	2:D:107:ARG:HH11	1.63	0.62
2:F:71:VAL:HG11	2:F:92:LEU:HD22	1.82	0.62
1:C:1:ASN:HB2	2:D:32:GLY:O	2.00	0.62
1:E:7:GLU:O	1:E:11:LYS:HG3	1.99	0.62
2:D:117:TYR:O	2:D:120:TYR:HB2	2.00	0.62
1:E:10:VAL:HG22	1:E:18:ALA:N	2.14	0.62
2:F:91:CYS:SG	2:F:92:LEU:N	2.72	0.62
1:A:28:TYR:O	1:A:45:CYS:HB3	2.00	0.61
1:C:115:LYS:O	1:C:117:TYR:N	2.33	0.61
2:D:93:ARG:HH11	2:D:93:ARG:CB	2.12	0.61
1:E:24:ILE:HG13	1:E:119:ASN:CG	2.20	0.61
2:B:104:ILE:C	2:B:107:ARG:HG3	2.20	0.61
1:C:3:PHE:O	1:C:7:GLU:HG3	1.99	0.61
1:G:77:PHE:CE1	1:G:80:GLY:HA2	2.35	0.61
1:C:1:ASN:ND2	2:D:34:GLN:HE21	1.98	0.61
1:C:58:ASP:HB3	1:C:91:CYS:HB2	1.82	0.61
1:A:24:ILE:HD13	1:A:119:ASN:HA	1.81	0.61
1:G:55:VAL:HG12	1:G:55:VAL:O	1.99	0.61
1:C:86:ASP:HB2	3:C:149:HOH:O	2.00	0.61
2:F:115:LYS:HG3	2:F:118:MET:CE	2.29	0.61
2:H:13:GLN:HB3	2:H:110:MET:CE	2.28	0.61
2:D:90:PRO:O	2:D:93:ARG:N	2.33	0.61
2:F:91:CYS:HB3	3:F:152:HOH:O	2.01	0.61
1:A:113:TYR:HE1	1:A:115:LYS:HA	1.66	0.61
1:C:23:ALA:O	1:C:24:ILE:HG13	2.00	0.61
1:A:16:LYS:O	1:A:17:GLU:HB2	2.01	0.61
2:B:8:LEU:HD21	2:B:75:TYR:CE2	2.36	0.61
1:E:120:TYR:HE1	1:E:125:HIS:HB2	1.63	0.61
1:G:4:GLN:O	1:G:8:MET:HG2	2.01	0.61
1:C:12:MET:O	1:C:12:MET:SD	2.58	0.61
1:C:25:TYR:O	1:C:29:CYS:HB2	2.01	0.61
1:E:28:TYR:CE1	1:E:33:GLY:HA2	2.36	0.61
1:E:38:GLN:HB3	1:E:117:TYR:CE2	2.36	0.61
2:B:122:ILE:HG12	2:B:122:ILE:O	2.01	0.60
1:C:34:GLN:NE2	1:C:127:THR:HB	2.16	0.60
1:A:26:GLY:HA2	1:A:38:GLN:OE1	1.99	0.60
2:F:12:LYS:HB3	2:F:107:ARG:HB2	1.83	0.60
1:A:37:PRO:HB2	1:A:43:ARG:HD3	1.83	0.60
2:F:61:ASN:HB3	2:F:70:LEU:HB2	1.82	0.60
2:D:91:CYS:O	2:D:95:VAL:HG23	2.01	0.60
1:E:120:TYR:HE1	1:E:125:HIS:HB3	1.63	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:TYR:HB2	1:A:86:ASP:OD2	2.00	0.60
2:H:21:LYS:NZ	2:H:110:MET:HE3	2.16	0.60
1:C:13:THR:HG23	1:C:14:GLY:N	2.16	0.60
1:G:36:LYS:HG2	1:G:131:GLU:OE1	2.01	0.60
2:H:38:LYS:HG3	2:H:120:TYR:HE1	1.67	0.60
1:C:23:ALA:C	1:C:24:ILE:HG13	2.22	0.60
2:H:24:SER:HA	2:H:30:GLY:HA3	1.84	0.60
2:B:21:LYS:NZ	2:B:110:MET:SD	2.67	0.60
2:B:45:CYS:SG	2:B:106:PHE:HZ	2.24	0.60
1:C:29:CYS:SG	1:C:42:ASP:HA	2.42	0.60
1:E:120:TYR:CE1	1:E:125:HIS:HB3	2.37	0.60
1:C:4:GLN:O	1:C:8:MET:HG2	2.01	0.60
1:C:5:PHE:CZ	1:C:9:ILE:HD11	2.37	0.60
1:A:21:SER:HB3	1:A:113:TYR:CE2	2.37	0.60
1:E:59:CYS:N	1:E:91:CYS:SG	2.75	0.60
1:G:93:LYS:O	1:G:96:CYS:HB3	2.02	0.60
2:H:21:LYS:NZ	2:H:110:MET:CE	2.65	0.60
1:A:120:TYR:CE2	1:A:125:HIS:HB2	2.36	0.59
1:C:90:LEU:HA	1:C:93:LYS:HE2	1.82	0.59
1:A:122:ILE:HG12	1:A:122:ILE:O	2.03	0.59
1:A:2:PHE:CZ	1:A:69:LYS:HE3	2.37	0.59
1:C:33:GLY:HA3	2:D:1:ASN:CB	2.33	0.59
2:H:6:ALA:HB1	2:H:19:PHE:CD2	2.36	0.59
1:A:2:PHE:CE2	1:A:69:LYS:HG3	2.37	0.59
2:B:24:SER:OG	2:B:119:LEU:HA	2.03	0.59
1:A:25:TYR:HB3	1:A:29:CYS:CB	2.32	0.59
2:F:102:ALA:HB2	3:F:156:HOH:O	2.01	0.59
1:A:115:LYS:HG2	1:A:115:LYS:O	2.03	0.59
2:B:24:SER:CB	2:B:119:LEU:HD13	2.32	0.59
1:C:10:VAL:CG2	1:C:18:ALA:HB3	2.21	0.59
2:F:101:VAL:O	2:F:104:ILE:HB	2.02	0.59
1:G:1:ASN:HB2	2:H:33:GLY:HA3	1.83	0.59
1:A:114:ASP:C	1:A:116:ASN:H	2.06	0.59
2:D:12:LYS:O	2:D:107:ARG:NH1	2.36	0.59
1:C:27:CYS:H	1:C:42:ASP:CG	2.06	0.59
1:C:68:PRO:HD3	3:C:151:HOH:O	2.03	0.59
1:G:12:MET:HG3	1:G:103:ALA:CB	2.31	0.59
1:A:10:VAL:HG13	1:A:16:LYS:C	2.23	0.58
1:C:10:VAL:HG22	1:C:18:ALA:CB	2.22	0.58
3:E:163:HOH:O	2:F:69:LYS:CD	2.48	0.58
2:H:109:ASN:C	2:H:111:ASN:H	2.05	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:ALA:HB2	2:B:31:TRP:CE3	2.38	0.58
1:C:24:ILE:CG2	1:C:119:ASN:HA	2.32	0.58
2:D:54:ARG:HG2	2:D:54:ARG:HH11	1.68	0.58
1:E:3:PHE:HD2	2:F:34:GLN:HG2	1.66	0.58
1:C:115:LYS:O	1:C:118:GLU:HG3	2.03	0.58
2:F:91:CYS:CB	3:F:152:HOH:O	2.52	0.58
2:D:45:CYS:SG	2:D:106:PHE:HZ	2.27	0.58
1:E:12:MET:CE	1:E:12:MET:HA	2.32	0.58
2:F:61:ASN:O	2:F:71:VAL:HG23	2.03	0.58
1:A:10:VAL:CG2	1:A:18:ALA:H	2.12	0.58
1:E:122:ILE:O	1:E:124:SER:C	2.42	0.58
2:F:90:PRO:O	2:F:92:LEU:N	2.36	0.58
2:F:91:CYS:C	2:F:93:ARG:H	2.05	0.58
1:C:26:GLY:O	1:C:120:TYR:HE2	1.86	0.58
1:G:32:GLY:HA2	2:H:3:PHE:CD2	2.39	0.58
2:F:38:LYS:NZ	2:F:120:TYR:CE2	2.72	0.58
1:A:74:SER:N	1:A:86:ASP:OD2	2.29	0.57
1:C:1:ASN:OD1	1:C:3:PHE:HB2	2.04	0.57
1:C:49:ASP:O	2:D:70:LEU:HD21	2.04	0.57
1:G:13:THR:CG2	1:G:107:GLY:HA2	2.26	0.57
2:B:34:GLN:O	2:B:126:CYS:HB3	2.04	0.57
2:D:113:TYR:HB2	3:D:151:HOH:O	2.04	0.57
1:C:12:MET:O	1:C:13:THR:CB	2.52	0.57
2:H:124:PHE:HD1	2:H:127:LYS:HZ1	1.51	0.57
1:G:55:VAL:HG11	1:G:95:VAL:CG2	2.34	0.57
2:H:54:ARG:HH21	2:H:133:CYS:HB3	1.69	0.57
1:A:5:PHE:HB2	1:A:99:ASP:OD2	2.05	0.57
1:E:35:GLY:HA2	1:E:128:GLU:O	2.05	0.57
2:F:46:PHE:HZ	2:F:131:ASP:O	1.87	0.57
2:F:104:ILE:HG23	2:F:107:ARG:NH1	2.19	0.57
2:B:26:GLY:N	2:B:117:TYR:O	2.37	0.57
2:B:35:GLY:HA3	2:B:126:CYS:HA	1.87	0.57
1:C:13:THR:HG23	1:C:14:GLY:H	1.69	0.57
1:E:12:MET:HA	1:E:12:MET:HE2	1.87	0.57
1:E:94:THR:HG22	3:E:157:HOH:O	2.05	0.57
1:A:24:ILE:HG21	1:A:119:ASN:OD1	2.05	0.57
1:A:34:GLN:HG2	1:A:126:CYS:O	2.05	0.57
1:A:58:ASP:HB2	1:A:91:CYS:SG	2.44	0.57
1:E:3:PHE:HB3	2:F:122:ILE:HD11	1.87	0.57
1:C:12:MET:O	1:C:13:THR:HB	2.05	0.57
1:E:2:PHE:HE1	1:E:69:LYS:HB2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:79:ASN:O	1:E:81:ASP:N	2.38	0.57
2:H:54:ARG:O	2:H:56:LYS:HG3	2.05	0.57
1:C:34:GLN:HE21	1:C:127:THR:CA	2.18	0.56
2:F:1:ASN:HA	2:F:69:LYS:O	2.04	0.56
1:G:1:ASN:OD1	1:G:3:PHE:N	2.28	0.56
1:E:2:PHE:HB2	2:F:32:GLY:N	2.21	0.56
1:A:78:GLU:O	1:A:79:ASN:CB	2.53	0.56
1:A:90:LEU:HD23	1:A:90:LEU:N	2.20	0.56
2:F:91:CYS:O	2:F:94:ALA:N	2.38	0.56
1:G:11:LYS:HE3	1:G:82:ILE:HG12	1.86	0.56
2:H:13:GLN:HE22	2:H:106:PHE:HB3	1.69	0.56
2:D:90:PRO:O	2:D:91:CYS:C	2.43	0.56
1:G:24:ILE:HG23	1:G:24:ILE:O	2.05	0.56
1:A:21:SER:HB3	1:A:113:TYR:HE2	1.70	0.56
2:F:100:ARG:NH1	3:F:142:HOH:O	2.38	0.56
1:G:131:GLU:OE2	1:G:131:GLU:HA	2.04	0.56
1:A:90:LEU:H	1:A:90:LEU:CD2	2.18	0.56
1:C:120:TYR:O	1:C:121:ALA:HB3	2.06	0.56
1:A:24:ILE:HG23	1:A:119:ASN:N	2.18	0.56
1:E:127:THR:HG22	1:E:127:THR:O	2.05	0.56
2:H:114:ASP:HB3	2:H:117:TYR:CD2	2.39	0.56
2:B:34:GLN:HG3	2:B:126:CYS:CB	2.36	0.56
2:B:97:GLU:O	2:B:101:VAL:HG23	2.06	0.56
1:E:24:ILE:HG13	1:E:119:ASN:CB	2.35	0.56
2:H:99:ASP:O	2:H:102:ALA:HB3	2.05	0.56
2:H:34:GLN:OE1	2:H:122:ILE:HG23	2.05	0.56
1:A:24:ILE:HG23	1:A:24:ILE:O	2.06	0.55
1:A:126:CYS:C	1:A:128:GLU:N	2.60	0.55
2:B:69:LYS:HE2	2:B:69:LYS:O	2.05	0.55
2:D:122:ILE:HD12	2:D:122:ILE:O	2.07	0.55
2:F:91:CYS:C	2:F:93:ARG:N	2.59	0.55
1:C:35:GLY:H	1:C:130:SER:HA	1.71	0.55
1:G:13:THR:C	1:G:16:LYS:H	2.09	0.55
2:H:121:SER:O	2:H:124:PHE:N	2.39	0.55
1:C:24:ILE:CD1	1:C:119:ASN:OD1	2.54	0.55
1:G:36:LYS:HE2	1:G:129:GLU:H	1.72	0.55
2:H:75:TYR:CD2	2:H:76:SER:N	2.74	0.55
2:B:12:LYS:HG2	2:B:107:ARG:HB3	1.89	0.55
2:B:25:TYR:O	2:B:29:CYS:HB2	2.06	0.55
1:G:16:LYS:HG2	1:G:17:GLU:N	2.21	0.55
1:E:2:PHE:HE1	1:E:69:LYS:CB	2.19	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:MET:CE	1:A:82:ILE:HG21	2.36	0.55
1:A:41:THR:O	1:A:44:CYS:HB2	2.07	0.55
1:C:97:GLU:OE2	1:C:100:ARG:NE	2.39	0.55
2:F:35:GLY:HA2	2:F:128:GLU:O	2.07	0.55
1:C:43:ARG:O	1:C:47:VAL:HG23	2.06	0.55
1:C:82:ILE:HG22	1:C:83:VAL:H	1.71	0.55
1:E:14:GLY:O	1:E:17:GLU:N	2.39	0.55
1:G:8:MET:O	1:G:11:LYS:HG2	2.06	0.55
2:H:127:LYS:O	2:H:128:GLU:O	2.25	0.55
1:A:2:PHE:HD1	2:B:31:TRP:HA	1.72	0.55
1:C:97:GLU:O	1:C:100:ARG:HB3	2.05	0.55
2:D:71:VAL:HB	2:D:92:LEU:CD2	2.37	0.55
2:H:71:VAL:HG21	2:H:92:LEU:HG	1.87	0.55
2:F:12:LYS:HE3	2:F:104:ILE:HG12	1.87	0.55
2:H:92:LEU:HD12	2:H:92:LEU:H	1.71	0.55
1:A:10:VAL:HG13	1:A:17:GLU:N	2.22	0.54
2:F:2:LEU:HG	2:F:69:LYS:HG3	1.89	0.54
2:F:38:LYS:HB3	2:F:117:TYR:CZ	2.42	0.54
1:G:71:ALA:HB1	1:G:92:LEU:HD21	1.88	0.54
1:A:55:VAL:HG13	1:A:91:CYS:SG	2.47	0.54
1:A:117:TYR:CE2	3:A:154:HOH:O	2.38	0.54
1:C:18:ALA:O	1:C:19:VAL:HB	2.08	0.54
1:C:59:CYS:N	1:C:91:CYS:SG	2.80	0.54
1:E:23:ALA:C	1:E:24:ILE:HD13	2.26	0.54
1:E:61:ASN:HB2	1:E:70:MET:HB2	1.89	0.54
1:C:8:MET:O	1:C:12:MET:HB2	2.07	0.54
1:E:13:THR:CG2	1:E:18:ALA:HB2	2.38	0.54
1:A:37:PRO:CB	1:A:43:ARG:HD3	2.37	0.54
1:G:55:VAL:HG11	1:G:95:VAL:HG22	1.88	0.54
1:G:89:ASN:HB3	1:G:92:LEU:HB2	1.89	0.54
1:C:78:GLU:HB2	1:C:83:VAL:CG2	2.36	0.54
1:E:97:GLU:O	1:E:100:ARG:HB3	2.07	0.54
2:B:38:LYS:NZ	2:B:125:ASP:HB3	2.21	0.54
2:D:118:MET:O	2:D:119:LEU:C	2.46	0.54
1:G:1:ASN:CB	2:H:33:GLY:HA3	2.38	0.54
2:B:89:ASP:HB3	2:B:92:LEU:HD12	1.88	0.54
1:C:12:MET:O	1:C:13:THR:HG22	2.06	0.54
1:E:82:ILE:CB	1:E:100:ARG:HD2	2.31	0.54
1:G:75:TYR:CD2	1:G:76:SER:N	2.75	0.54
1:G:76:SER:HB3	3:G:137:HOH:O	2.07	0.54
1:G:114:ASP:OD2	1:G:116:ASN:ND2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:PHE:CD2	2:B:34:GLN:HG2	2.43	0.54
1:A:39:ASP:O	1:A:43:ARG:HG2	2.08	0.54
1:C:129:GLU:HG3	1:C:130:SER:H	1.63	0.54
1:E:69:LYS:HD3	2:F:49:ASP:CG	2.29	0.54
1:A:114:ASP:OD2	1:A:116:ASN:HB2	2.08	0.54
1:E:16:LYS:HG3	1:E:17:GLU:HG3	1.90	0.54
1:A:43:ARG:HG3	1:A:43:ARG:NH1	2.23	0.53
1:A:78:GLU:OE2	1:A:83:VAL:HG21	2.08	0.53
1:C:34:GLN:NE2	1:C:127:THR:CB	2.71	0.53
2:D:23:ILE:O	2:D:30:GLY:HA3	2.07	0.53
1:C:8:MET:HE1	1:C:82:ILE:HG21	1.89	0.53
1:C:104:ILE:HG23	1:C:108:GLN:HE21	1.73	0.53
2:D:94:ALA:HA	2:D:97:GLU:HB2	1.90	0.53
1:A:34:GLN:HA	1:A:130:SER:OG	2.08	0.53
2:F:25:TYR:HA	2:F:118:MET:HA	1.88	0.53
1:G:90:LEU:O	1:G:90:LEU:HD23	2.07	0.53
2:B:12:LYS:CG	2:B:107:ARG:HG2	2.30	0.53
1:G:131:GLU:HA	1:G:132:GLN:NE2	2.22	0.53
2:H:25:TYR:CE2	2:H:117:TYR:HB2	2.43	0.53
2:B:11:ALA:HA	3:B:145:HOH:O	2.08	0.53
1:C:12:MET:HG3	1:C:103:ALA:HB1	1.91	0.53
1:G:116:ASN:OD1	1:G:116:ASN:C	2.46	0.53
2:H:79:THR:HG22	2:H:79:THR:O	2.08	0.53
1:A:50:CYS:SG	1:A:133:CYS:SG	3.02	0.53
2:B:37:PRO:HG2	2:B:43:ARG:HG3	1.91	0.53
1:C:17:GLU:O	1:C:18:ALA:O	2.26	0.53
1:G:36:LYS:HE2	1:G:129:GLU:N	2.24	0.53
2:H:34:GLN:O	2:H:34:GLN:HG3	2.08	0.53
1:C:125:HIS:O	1:C:126:CYS:HB2	2.09	0.53
2:H:51:CYS:O	2:H:54:ARG:N	2.39	0.53
2:H:122:ILE:H	2:H:122:ILE:CD1	2.10	0.53
1:C:86:ASP:OD1	1:C:92:LEU:HB2	2.08	0.53
1:C:111:ASN:ND2	1:C:112:THR:HG23	2.24	0.53
1:G:71:ALA:HB1	1:G:92:LEU:CD2	2.39	0.53
1:A:122:ILE:O	1:A:127:THR:N	2.42	0.53
1:G:29:CYS:O	1:G:30:GLY:O	2.27	0.52
1:G:124:SER:HA	1:G:127:THR:HG23	1.91	0.52
1:A:126:CYS:O	1:A:128:GLU:N	2.43	0.52
2:D:107:ARG:HG3	2:D:107:ARG:NH1	2.22	0.52
2:H:82:ILE:HB	2:H:100:ARG:HD2	1.91	0.52
1:A:25:TYR:HB3	1:A:29:CYS:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:TYR:O	1:A:26:GLY:C	2.47	0.52
1:G:32:GLY:O	2:H:1:ASN:HB2	2.09	0.52
2:F:106:PHE:C	2:F:108:GLU:H	2.13	0.52
2:F:8:LEU:HD23	2:F:8:LEU:N	2.24	0.52
2:H:40:ALA:HB3	2:H:112:THR:OG1	2.10	0.52
1:C:19:VAL:O	1:C:19:VAL:HG22	2.09	0.52
2:F:120:TYR:CD1	2:F:121:SER:N	2.74	0.52
1:E:6:ALA:HB1	1:E:19:VAL:HG21	1.92	0.52
1:C:34:GLN:O	1:C:126:CYS:HB3	2.09	0.52
1:C:41:THR:O	1:C:44:CYS:HB2	2.10	0.52
2:H:56:LYS:O	2:H:91:CYS:SG	2.64	0.52
1:A:22:TYR:CE1	1:A:106:LEU:HD22	2.45	0.51
1:A:24:ILE:O	1:A:119:ASN:N	2.42	0.51
2:B:37:PRO:HG2	2:B:43:ARG:CG	2.40	0.51
1:C:1:ASN:OD1	1:C:4:GLN:HG3	2.10	0.51
1:C:37:PRO:HB3	1:C:43:ARG:HA	1.92	0.51
2:D:41:THR:O	2:D:44:CYS:HB2	2.11	0.51
1:C:34:GLN:HE21	1:C:127:THR:HA	1.75	0.51
2:H:13:GLN:OE1	2:H:110:MET:CE	2.58	0.51
2:H:114:ASP:HB3	2:H:117:TYR:CE2	2.45	0.51
2:D:7:ARG:NH1	2:D:7:ARG:HB3	2.25	0.51
2:D:41:THR:HG23	2:D:106:PHE:HE1	1.76	0.51
1:C:55:VAL:HG13	1:C:94:THR:OG1	2.10	0.51
2:D:104:ILE:O	2:D:108:GLU:HG2	2.11	0.51
1:E:24:ILE:HG21	1:E:119:ASN:HD21	1.74	0.51
1:G:10:VAL:HG23	1:G:18:ALA:CB	2.40	0.51
2:H:121:SER:C	2:H:124:PHE:N	2.64	0.51
1:C:34:GLN:NE2	1:C:127:THR:HA	2.25	0.51
1:C:104:ILE:CG2	1:C:108:GLN:HE21	2.22	0.51
1:E:73:TYR:OH	1:E:99:ASP:OD2	2.28	0.51
2:F:71:VAL:HG13	2:F:92:LEU:HD22	1.93	0.51
1:G:40:ALA:HB2	1:G:43:ARG:NH2	2.26	0.51
2:H:114:ASP:C	2:H:116:LYS:H	2.14	0.51
2:H:124:PHE:HD1	2:H:127:LYS:NZ	2.08	0.51
1:A:107:GLY:O	1:A:110:VAL:HG22	2.11	0.51
2:B:17:PHE:HB3	2:B:20:PHE:CE1	2.46	0.51
2:F:94:ALA:O	2:F:98:CYS:SG	2.68	0.51
1:G:36:LYS:HE2	1:G:128:GLU:HB3	1.93	0.51
2:H:107:ARG:HG3	3:H:152:HOH:O	2.10	0.51
1:A:50:CYS:SG	1:A:133:CYS:CB	2.99	0.51
2:F:91:CYS:O	2:F:93:ARG:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:PHE:HB2	1:C:99:ASP:OD2	2.11	0.51
2:D:24:SER:HB3	2:D:119:LEU:HD23	1.93	0.51
2:F:104:ILE:O	2:F:108:GLU:HB2	2.11	0.51
1:G:128:GLU:HB2	3:G:141:HOH:O	2.10	0.51
2:F:1:ASN:OD1	2:F:3:PHE:HB2	2.11	0.50
2:F:38:LYS:HZ3	2:F:120:TYR:HE2	1.57	0.50
1:A:2:PHE:HB2	2:B:31:TRP:HA	1.93	0.50
2:B:34:GLN:HG3	2:B:126:CYS:HB3	1.93	0.50
2:B:129:GLU:CD	2:B:129:GLU:H	2.15	0.50
1:C:31:TRP:HA	2:D:2:LEU:HB2	1.93	0.50
1:E:120:TYR:HE1	1:E:125:HIS:CG	2.28	0.50
1:E:120:TYR:CG	1:E:120:TYR:O	2.63	0.50
2:H:91:CYS:O	2:H:94:ALA:N	2.40	0.50
2:B:104:ILE:CA	2:B:107:ARG:HG3	2.41	0.50
2:F:128:GLU:O	2:F:129:GLU:C	2.50	0.50
1:G:75:TYR:O	1:G:76:SER:HB3	2.12	0.50
2:B:119:LEU:N	2:B:119:LEU:HD22	2.26	0.50
1:C:127:THR:OG1	1:C:128:GLU:N	2.44	0.50
1:E:10:VAL:HG13	1:E:14:GLY:O	2.10	0.50
2:H:17:PHE:O	2:H:20:PHE:HB2	2.12	0.50
2:D:7:ARG:HB3	2:D:7:ARG:HH11	1.75	0.50
2:B:8:LEU:HD22	2:B:82:ILE:HD13	1.94	0.50
1:E:49:ASP:OD1	2:F:69:LYS:HD3	2.11	0.50
1:E:91:CYS:HB2	3:E:150:HOH:O	2.12	0.50
2:D:56:LYS:O	2:D:91:CYS:SG	2.69	0.50
2:H:34:GLN:NE2	2:H:126:CYS:O	2.43	0.50
2:H:39:ASP:O	2:H:43:ARG:HB2	2.11	0.50
1:G:23:ALA:C	1:G:30:GLY:HA3	2.32	0.50
2:H:4:GLN:HE22	2:H:72:GLU:HG3	1.73	0.50
1:G:9:ILE:O	1:G:12:MET:HB2	2.12	0.50
1:A:8:MET:HE3	1:A:82:ILE:HD13	1.93	0.49
1:A:122:ILE:HD12	2:B:3:PHE:HB3	1.94	0.49
2:B:104:ILE:O	2:B:107:ARG:CG	2.59	0.49
2:D:8:LEU:O	2:D:11:ALA:HB3	2.12	0.49
1:G:41:THR:HG21	1:G:113:TYR:HD2	1.77	0.49
2:H:13:GLN:HB3	2:H:110:MET:SD	2.51	0.49
2:H:18:SER:O	2:H:21:LYS:HG2	2.12	0.49
1:A:117:TYR:HE1	1:A:120:TYR:HH	1.57	0.49
2:B:104:ILE:HA	2:B:107:ARG:HG3	1.94	0.49
2:D:43:ARG:O	2:D:44:CYS:C	2.50	0.49
2:H:21:LYS:CE	2:H:110:MET:HE3	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:GLU:HB2	1:C:83:VAL:HG23	1.95	0.49
2:D:114:ASP:C	2:D:114:ASP:OD2	2.51	0.49
2:F:10:ASP:OD2	2:F:17:PHE:N	2.45	0.49
2:H:50:CYS:O	2:H:51:CYS:C	2.50	0.49
2:F:61:ASN:OD1	2:F:70:LEU:HD23	2.12	0.49
1:A:3:PHE:CD2	2:B:32:GLY:HA2	2.48	0.49
1:A:24:ILE:CD1	1:A:119:ASN:HA	2.42	0.49
2:D:118:MET:CE	2:D:119:LEU:HG	2.43	0.49
1:A:25:TYR:HB3	1:A:29:CYS:SG	2.52	0.49
2:B:21:LYS:HB2	2:B:113:TYR:OH	2.13	0.49
1:C:10:VAL:HG12	1:C:11:LYS:N	2.26	0.49
1:C:52:TYR:O	1:C:55:VAL:HG23	2.12	0.49
2:D:13:GLN:O	2:D:14:GLU:C	2.51	0.49
1:G:9:ILE:HD12	1:G:18:ALA:HB1	1.94	0.49
2:H:115:LYS:O	2:H:115:LYS:HG2	2.12	0.49
1:C:37:PRO:HD2	3:C:153:HOH:O	2.13	0.49
1:G:44:CYS:SG	1:G:106:LEU:N	2.86	0.49
1:A:76:SER:OG	1:A:78:GLU:HG2	2.13	0.49
2:B:11:ALA:HB1	2:B:77:TYR:CE1	2.48	0.49
2:B:111:ASN:ND2	2:B:111:ASN:N	2.61	0.49
2:D:71:VAL:HB	2:D:92:LEU:HD21	1.95	0.49
1:G:16:LYS:HE2	1:G:21:SER:OG	2.13	0.49
1:G:122:ILE:HG23	2:H:3:PHE:CG	2.48	0.49
1:E:107:GLY:O	1:E:110:VAL:HG13	2.13	0.48
1:G:11:LYS:HD2	1:G:77:PHE:CD2	2.48	0.48
1:G:31:TRP:HA	2:H:2:LEU:CD1	2.43	0.48
1:G:97:GLU:OE2	1:G:97:GLU:HA	2.13	0.48
2:H:92:LEU:HD12	2:H:92:LEU:N	2.28	0.48
1:C:12:MET:HG2	1:C:82:ILE:HD11	1.95	0.48
1:C:25:TYR:HE2	1:C:41:THR:HB	1.78	0.48
2:D:84:CYS:SG	2:D:96:CYS:O	2.70	0.48
1:E:23:ALA:CB	1:E:24:ILE:HD13	2.43	0.48
1:E:40:ALA:HA	1:E:43:ARG:HD2	1.95	0.48
1:G:132:GLN:HG2	3:G:149:HOH:O	2.12	0.48
2:H:34:GLN:HG3	2:H:126:CYS:O	2.14	0.48
1:A:29:CYS:HA	1:A:45:CYS:HB3	1.95	0.48
1:E:1:ASN:N	1:E:71:ALA:O	2.37	0.48
1:C:84:CYS:HB3	3:C:149:HOH:O	2.14	0.48
1:C:113:TYR:OH	1:C:118:GLU:OE2	2.32	0.48
2:D:21:LYS:HB2	2:D:113:TYR:OH	2.13	0.48
1:E:71:ALA:HB1	1:E:92:LEU:HD23	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:81:LYS:HG2	2:H:82:ILE:N	2.29	0.48
2:D:41:THR:HG23	2:D:106:PHE:CE1	2.48	0.48
1:A:24:ILE:O	1:A:118:GLU:HA	2.14	0.48
1:A:27:CYS:CB	1:A:126:CYS:SG	3.01	0.48
1:G:14:GLY:HA3	3:G:147:HOH:O	2.13	0.48
2:H:21:LYS:HZ1	2:H:110:MET:HE3	1.77	0.48
2:B:89:ASP:CB	2:B:92:LEU:HD12	2.43	0.48
1:C:24:ILE:HD12	1:C:119:ASN:OD1	2.13	0.48
2:D:12:LYS:HB3	2:D:107:ARG:HB2	1.94	0.48
2:D:48:HIS:O	2:D:51:CYS:HB3	2.13	0.48
2:D:59:CYS:CB	2:D:71:VAL:HG11	2.34	0.48
2:H:19:PHE:H	2:H:19:PHE:HD1	1.62	0.48
2:D:20:PHE:O	2:D:23:ILE:HG12	2.13	0.48
1:E:24:ILE:HB	1:E:119:ASN:HA	1.95	0.48
1:A:2:PHE:CD1	2:B:31:TRP:HA	2.47	0.48
1:C:1:ASN:ND2	2:D:34:GLN:NE2	2.57	0.48
1:C:37:PRO:HB3	1:C:42:ASP:O	2.14	0.48
1:C:37:PRO:HB3	1:C:42:ASP:C	2.34	0.48
1:C:37:PRO:HB3	1:C:43:ARG:CA	2.44	0.48
1:E:13:THR:HG21	1:E:18:ALA:HB2	1.96	0.48
2:F:129:GLU:OE1	2:F:129:GLU:HA	2.14	0.48
1:G:10:VAL:CG2	1:G:18:ALA:H	2.27	0.48
1:A:88:ASN:O	1:A:89:ASN:C	2.50	0.47
2:D:77:TYR:HD1	2:D:82:ILE:CG1	2.27	0.47
2:D:16:ALA:C	2:D:18:SER:H	2.16	0.47
2:B:1:ASN:HD21	2:B:72:GLU:HG3	1.78	0.47
2:B:61:ASN:O	2:B:71:VAL:HB	2.14	0.47
1:C:110:VAL:HA	1:C:113:TYR:HB2	1.96	0.47
2:D:47:VAL:HG22	3:D:150:HOH:O	2.13	0.47
2:D:101:VAL:CB	3:D:148:HOH:O	2.51	0.47
1:E:3:PHE:CZ	2:F:32:GLY:HA2	2.49	0.47
1:E:38:GLN:NE2	1:E:38:GLN:H	2.11	0.47
2:F:1:ASN:HA	2:F:69:LYS:C	2.34	0.47
2:H:37:PRO:HA	2:H:42:ASP:OD2	2.13	0.47
2:B:1:ASN:OD1	2:B:3:PHE:HB2	2.14	0.47
2:B:12:LYS:HB2	2:B:107:ARG:HE	1.80	0.47
1:C:53:GLY:HA2	2:D:61:ASN:ND2	2.29	0.47
1:E:86:ASP:CB	1:E:93:LYS:HB2	2.40	0.47
2:F:120:TYR:HD1	2:F:121:SER:N	2.11	0.47
2:D:21:LYS:HB2	2:D:113:TYR:CZ	2.50	0.47
1:G:31:TRP:HA	2:H:2:LEU:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:38:LYS:HB3	2:B:117:TYR:CE1	2.50	0.47
2:B:42:ASP:O	2:B:45:CYS:HB2	2.15	0.47
1:C:95:VAL:C	1:C:97:GLU:N	2.68	0.47
2:D:52:TYR:CD1	2:D:68:PRO:HB3	2.49	0.47
2:B:77:TYR:OH	2:B:80:GLY:HA2	2.14	0.47
2:F:36:THR:HA	2:F:131:ASP:OD2	2.15	0.47
2:F:106:PHE:C	2:F:108:GLU:N	2.68	0.47
2:F:129:GLU:HA	3:F:143:HOH:O	2.14	0.47
2:H:21:LYS:HZ3	2:H:110:MET:HE2	1.80	0.47
2:H:117:TYR:HD1	2:H:120:TYR:OH	1.96	0.47
2:B:34:GLN:HG3	2:B:126:CYS:HB2	1.97	0.47
1:E:9:ILE:HG22	1:E:18:ALA:CB	2.44	0.47
1:E:131:GLU:HG2	1:E:132:GLN:N	2.30	0.47
2:H:104:ILE:O	2:H:108:GLU:HG3	2.15	0.47
1:A:10:VAL:HG13	1:A:16:LYS:CA	2.45	0.47
2:B:37:PRO:CG	2:B:43:ARG:HG3	2.44	0.47
2:B:104:ILE:HG23	2:B:107:ARG:HD2	1.96	0.47
1:E:48:HIS:CD2	1:E:98:CYS:HB3	2.49	0.47
2:F:128:GLU:HB2	3:F:157:HOH:O	2.14	0.47
2:H:81:LYS:HG2	2:H:82:ILE:H	1.79	0.47
1:A:27:CYS:SG	1:A:38:GLN:HG3	2.55	0.47
1:C:2:PHE:CD1	2:D:31:TRP:HA	2.50	0.47
2:H:8:LEU:HD22	2:H:82:ILE:CD1	2.44	0.47
1:C:19:VAL:O	1:C:19:VAL:HG13	2.15	0.46
1:E:28:TYR:CD1	1:E:33:GLY:HA2	2.51	0.46
1:E:124:SER:C	1:E:126:CYS:N	2.66	0.46
2:F:58:GLY:O	2:F:59:CYS:CB	2.56	0.46
2:D:114:ASP:O	2:D:116:LYS:N	2.49	0.46
1:E:58:ASP:O	1:E:59:CYS:C	2.53	0.46
1:C:12:MET:CG	1:C:103:ALA:HB1	2.46	0.46
1:C:79:ASN:O	1:C:81:ASP:N	2.40	0.46
1:G:122:ILE:HG12	2:H:7:ARG:HH12	1.78	0.46
1:C:24:ILE:HD13	1:C:119:ASN:OD1	2.15	0.46
1:E:31:TRP:HE1	2:F:23:ILE:HD13	1.81	0.46
1:E:100:ARG:HG2	1:E:100:ARG:NH1	2.31	0.46
2:H:59:CYS:O	2:H:68:PRO:HD3	2.14	0.46
2:H:109:ASN:C	2:H:111:ASN:N	2.69	0.46
1:C:120:TYR:O	1:C:121:ALA:CB	2.62	0.46
2:F:76:SER:HB2	2:F:83:VAL:HB	1.97	0.46
2:F:106:PHE:O	2:F:108:GLU:N	2.48	0.46
1:C:48:HIS:CD2	1:C:102:ALA:HB2	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:69:LYS:HD3	2:F:49:ASP:OD1	2.15	0.46
1:A:91:CYS:HB2	3:A:149:HOH:O	2.16	0.46
1:C:12:MET:HG3	1:C:103:ALA:CB	2.46	0.46
1:C:107:GLY:O	1:C:110:VAL:HG22	2.15	0.46
2:D:54:ARG:HG2	2:D:54:ARG:NH1	2.29	0.46
2:H:10:ASP:O	2:H:12:LYS:N	2.49	0.46
2:H:109:ASN:O	2:H:111:ASN:N	2.49	0.46
1:A:33:GLY:HA3	2:B:69:LYS:CE	2.45	0.46
1:A:130:SER:OG	2:B:72:GLU:CD	2.54	0.46
1:E:116:ASN:C	1:E:118:GLU:N	2.69	0.46
2:F:52:TYR:CE2	2:F:68:PRO:HB3	2.51	0.46
1:G:131:GLU:HA	1:G:132:GLN:HE21	1.81	0.46
1:C:34:GLN:NE2	1:C:127:THR:CA	2.79	0.46
1:C:97:GLU:OE1	1:C:100:ARG:NH2	2.49	0.46
2:H:2:LEU:HG	2:H:69:LYS:HG3	1.98	0.46
1:A:11:LYS:HD2	1:A:77:PHE:CD2	2.51	0.45
1:E:59:CYS:O	1:E:68:PRO:HD3	2.16	0.45
2:F:101:VAL:O	2:F:104:ILE:N	2.49	0.45
1:G:19:VAL:O	1:G:21:SER:N	2.48	0.45
1:A:114:ASP:C	1:A:116:ASN:N	2.68	0.45
2:B:104:ILE:O	2:B:108:GLU:OE1	2.34	0.45
1:E:44:CYS:SG	1:E:106:LEU:HD23	2.55	0.45
2:B:25:TYR:HB3	2:B:29:CYS:HB2	1.98	0.45
1:C:37:PRO:HG3	1:C:46:PHE:HB2	1.98	0.45
2:D:93:ARG:CG	2:D:93:ARG:HH11	2.29	0.45
1:E:33:GLY:O	1:E:34:GLN:HB2	2.17	0.45
2:F:70:LEU:N	2:F:70:LEU:HD22	2.31	0.45
2:D:95:VAL:C	2:D:97:GLU:N	2.67	0.45
2:F:107:ARG:O	2:F:107:ARG:HG2	2.17	0.45
1:G:124:SER:CA	1:G:127:THR:HG23	2.47	0.45
2:H:13:GLN:HE21	2:H:107:ARG:N	2.15	0.45
1:A:24:ILE:CG2	1:A:119:ASN:HA	2.46	0.45
2:B:104:ILE:HA	2:B:107:ARG:CG	2.46	0.45
1:C:12:MET:O	1:C:13:THR:CG2	2.64	0.45
1:C:47:VAL:HG12	3:C:154:HOH:O	2.16	0.45
1:C:97:GLU:O	1:C:100:ARG:N	2.46	0.45
2:H:22:TYR:CE1	2:H:113:TYR:HE2	2.34	0.45
2:H:125:ASP:HB2	3:H:134:HOH:O	2.15	0.45
1:A:10:VAL:O	1:A:10:VAL:CG1	2.63	0.45
1:A:88:ASN:O	1:A:90:LEU:N	2.50	0.45
2:H:71:VAL:HG11	2:H:95:VAL:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:PHE:O	1:A:3:PHE:C	2.55	0.45
2:F:13:GLN:OE1	2:F:110:MET:SD	2.75	0.45
2:F:36:THR:HG23	2:F:128:GLU:HB3	1.97	0.45
2:F:45:CYS:HB3	3:F:145:HOH:O	2.16	0.45
2:F:59:CYS:CB	3:F:152:HOH:O	2.54	0.45
1:A:2:PHE:CB	2:B:31:TRP:HA	2.46	0.45
1:C:37:PRO:HG2	1:C:43:ARG:HG3	1.99	0.45
2:D:118:MET:HE1	2:D:119:LEU:HG	1.99	0.45
1:G:90:LEU:HD23	1:G:90:LEU:C	2.37	0.45
1:A:34:GLN:OE1	1:A:127:THR:HA	2.16	0.45
1:C:38:GLN:HG3	1:C:120:TYR:OH	2.17	0.45
2:F:89:ASP:OD2	2:F:90:PRO:HD2	2.17	0.45
1:G:11:LYS:HZ1	1:G:82:ILE:HG23	1.82	0.45
2:D:90:PRO:O	2:D:92:LEU:N	2.50	0.44
1:E:19:VAL:O	1:E:20:HIS:C	2.56	0.44
1:E:120:TYR:CE1	1:E:125:HIS:CG	3.05	0.44
2:H:124:PHE:C	2:H:126:CYS:H	2.21	0.44
1:E:88:ASN:N	1:E:88:ASN:HD22	2.14	0.44
2:F:129:GLU:OE1	2:F:129:GLU:CA	2.65	0.44
2:B:76:SER:O	2:B:83:VAL:HG13	2.17	0.44
1:C:8:MET:HE3	1:C:82:ILE:HD13	1.99	0.44
2:F:52:TYR:CD2	2:F:68:PRO:HB3	2.51	0.44
1:C:12:MET:CB	1:C:103:ALA:HB1	2.46	0.44
1:E:32:GLY:O	2:F:1:ASN:HB2	2.17	0.44
2:F:129:GLU:O	2:F:130:SER:C	2.54	0.44
1:G:10:VAL:O	1:G:14:GLY:HA2	2.17	0.44
1:G:61:ASN:ND2	1:G:70:MET:SD	2.90	0.44
2:H:21:LYS:HZ1	2:H:110:MET:CE	2.29	0.44
1:A:50:CYS:O	1:A:53:GLY:N	2.50	0.44
1:G:11:LYS:HD2	1:G:77:PHE:CE2	2.52	0.44
2:H:34:GLN:HE22	2:H:122:ILE:HG22	1.83	0.44
1:A:121:ALA:O	1:A:122:ILE:HB	2.17	0.44
1:C:55:VAL:HG12	1:C:91:CYS:SG	2.58	0.44
1:C:127:THR:O	1:C:128:GLU:HB2	2.17	0.44
1:E:5:PHE:O	1:E:9:ILE:HG13	2.17	0.44
2:H:41:THR:HG22	2:H:42:ASP:N	2.32	0.44
1:A:8:MET:HE1	1:A:100:ARG:HA	1.93	0.44
1:E:8:MET:SD	1:E:99:ASP:HB3	2.58	0.44
2:F:21:LYS:HB2	2:F:113:TYR:HH	1.82	0.44
1:G:20:HIS:C	1:G:22:TYR:N	2.71	0.44
1:A:1:ASN:HB2	2:B:32:GLY:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:GLU:O	1:A:79:ASN:HB3	2.18	0.44
2:B:111:ASN:N	2:B:111:ASN:HD22	2.14	0.44
1:E:81:ASP:OD2	1:E:83:VAL:HG22	2.17	0.44
2:F:46:PHE:CZ	2:F:131:ASP:O	2.71	0.44
1:A:24:ILE:HG21	1:A:119:ASN:HA	1.98	0.44
2:B:7:ARG:HD3	2:B:7:ARG:HA	1.81	0.44
2:B:41:THR:O	2:B:106:PHE:HE1	2.00	0.44
1:C:18:ALA:O	1:C:19:VAL:CB	2.66	0.44
2:F:55:VAL:HG22	2:F:94:ALA:CB	2.47	0.44
2:H:13:GLN:OE1	2:H:110:MET:HE3	2.18	0.44
1:A:13:THR:HG21	3:A:139:HOH:O	2.18	0.43
1:A:99:ASP:O	1:A:102:ALA:HB3	2.18	0.43
2:B:34:GLN:C	2:B:126:CYS:HB3	2.38	0.43
1:E:3:PHE:HB3	2:F:122:ILE:CD1	2.48	0.43
1:G:132:GLN:O	1:G:133:CYS:OXT	2.35	0.43
1:A:6:ALA:O	1:A:10:VAL:HG23	2.18	0.43
2:D:108:GLU:C	2:D:110:MET:H	2.21	0.43
1:G:40:ALA:HB2	1:G:43:ARG:HH22	1.84	0.43
1:G:75:TYR:HA	1:G:84:CYS:HA	2.00	0.43
2:H:25:TYR:CZ	2:H:117:TYR:HD2	2.36	0.43
1:C:56:ASN:O	1:C:58:ASP:CB	2.65	0.43
2:B:52:TYR:HA	2:B:55:VAL:HG23	2.00	0.43
2:D:3:PHE:O	2:D:7:ARG:CG	2.61	0.43
1:E:2:PHE:O	1:E:3:PHE:C	2.57	0.43
1:C:6:ALA:HB2	2:D:31:TRP:CE3	2.54	0.43
1:C:77:PHE:O	1:C:78:GLU:O	2.36	0.43
2:D:14:GLU:HB2	2:D:16:ALA:H	1.58	0.43
2:D:132:GLN:HG3	2:D:132:GLN:O	2.18	0.43
1:E:18:ALA:O	1:E:19:VAL:O	2.37	0.43
2:F:75:TYR:O	2:F:76:SER:OG	2.33	0.43
1:C:48:HIS:HE1	1:C:52:TYR:CZ	2.36	0.43
1:A:34:GLN:OE1	1:A:122:ILE:HD11	2.18	0.43
1:G:79:ASN:CG	1:G:79:ASN:O	2.57	0.43
1:E:115:LYS:O	1:E:118:GLU:HG3	2.19	0.43
1:G:8:MET:O	1:G:12:MET:HG2	2.19	0.43
1:G:10:VAL:HG23	1:G:18:ALA:HB2	2.01	0.43
2:H:10:ASP:OD1	2:H:18:SER:N	2.51	0.43
2:H:97:GLU:O	2:H:101:VAL:HG23	2.19	0.43
2:D:8:LEU:HB3	2:D:82:ILE:HD13	2.01	0.43
1:G:11:LYS:HE3	1:G:82:ILE:CD1	2.49	0.43
1:G:58:ASP:O	1:G:59:CYS:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:ILE:C	1:A:11:LYS:H	2.21	0.43
2:D:5:PHE:O	2:D:9:ILE:HG13	2.19	0.43
1:E:3:PHE:CE2	2:F:32:GLY:HA2	2.54	0.43
2:B:46:PHE:CE2	2:B:50:CYS:SG	3.12	0.42
2:B:54:ARG:NH1	3:B:152:HOH:O	2.51	0.42
2:B:79:THR:HG22	2:B:79:THR:O	2.19	0.42
2:D:51:CYS:C	2:D:98:CYS:SG	2.98	0.42
2:D:84:CYS:SG	2:D:96:CYS:C	2.97	0.42
1:E:22:TYR:HE1	1:E:41:THR:HG21	1.84	0.42
2:F:43:ARG:O	2:F:47:VAL:HG23	2.19	0.42
1:G:28:TYR:CE2	1:G:37:PRO:HD3	2.42	0.42
2:H:122:ILE:O	2:H:126:CYS:O	2.37	0.42
1:A:6:ALA:HB1	1:A:19:VAL:CG2	2.49	0.42
1:C:115:LYS:C	1:C:117:TYR:H	2.21	0.42
1:E:84:CYS:CB	1:E:93:LYS:HE3	2.35	0.42
2:F:90:PRO:O	2:F:93:ARG:N	2.49	0.42
1:G:12:MET:C	1:G:14:GLY:N	2.71	0.42
1:G:12:MET:O	1:G:13:THR:C	2.57	0.42
1:G:75:TYR:CG	1:G:76:SER:N	2.86	0.42
2:H:84:CYS:HB3	2:H:96:CYS:SG	2.60	0.42
1:A:28:TYR:CD1	1:A:33:GLY:HA2	2.54	0.42
2:B:6:ALA:O	2:B:10:ASP:OD1	2.37	0.42
1:C:79:ASN:HD22	1:C:79:ASN:HA	1.71	0.42
1:G:12:MET:CE	1:G:12:MET:HA	2.48	0.42
2:B:122:ILE:O	2:B:122:ILE:CG1	2.67	0.42
1:E:3:PHE:CE2	2:F:34:GLN:HG2	2.54	0.42
1:E:104:ILE:HD11	3:E:134:HOH:O	2.19	0.42
2:F:100:ARG:O	2:F:103:ALA:HB3	2.18	0.42
2:H:34:GLN:CD	2:H:122:ILE:HG23	2.40	0.42
2:B:35:GLY:HA3	2:B:126:CYS:CA	2.49	0.42
2:D:40:ALA:HB1	2:D:109:ASN:CG	2.40	0.42
1:E:78:GLU:O	1:E:79:ASN:C	2.58	0.42
2:H:92:LEU:H	2:H:92:LEU:CD1	2.33	0.42
1:A:13:THR:HG23	1:A:110:VAL:HG11	2.01	0.42
1:E:91:CYS:O	1:E:94:THR:HB	2.19	0.42
2:F:36:THR:HG22	2:F:131:ASP:OD2	2.20	0.42
1:G:51:CYS:C	1:G:53:GLY:H	2.23	0.42
2:H:12:LYS:CG	2:H:107:ARG:HH11	2.30	0.42
1:A:35:GLY:H	1:A:130:SER:HA	1.85	0.42
1:E:16:LYS:O	1:E:17:GLU:HG3	2.19	0.42
1:G:24:ILE:CA	1:G:30:GLY:HA3	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:129:GLU:HG2	1:G:130:SER:N	2.34	0.42
2:H:120:TYR:HB3	3:H:134:HOH:O	2.19	0.42
1:A:24:ILE:HG12	1:A:119:ASN:CA	2.49	0.42
1:C:47:VAL:CG1	3:C:154:HOH:O	2.67	0.42
1:C:70:MET:O	1:C:71:ALA:C	2.57	0.42
1:E:23:ALA:HB3	1:E:24:ILE:HD13	2.00	0.42
2:H:115:LYS:O	2:H:115:LYS:CG	2.68	0.42
2:D:28:TYR:OH	2:D:35:GLY:O	2.29	0.42
2:D:52:TYR:O	2:D:54:ARG:N	2.52	0.42
2:F:114:ASP:OD2	2:F:114:ASP:C	2.58	0.42
1:G:4:GLN:OE1	1:G:73:TYR:CD2	2.72	0.42
1:G:93:LYS:O	1:G:96:CYS:N	2.53	0.42
1:G:122:ILE:HG12	2:H:7:ARG:CZ	2.50	0.42
1:A:69:LYS:HB3	3:A:141:HOH:O	2.18	0.42
1:C:53:GLY:HA2	2:D:61:ASN:HD21	1.85	0.42
1:C:118:GLU:O	1:C:119:ASN:C	2.58	0.42
1:A:3:PHE:HE1	2:B:120:TYR:O	2.03	0.41
1:A:24:ILE:CG1	1:A:119:ASN:HA	2.50	0.41
2:F:39:ASP:OD2	2:F:117:TYR:CD2	2.73	0.41
1:G:3:PHE:CE2	2:H:34:GLN:HG2	2.55	0.41
2:H:19:PHE:N	2:H:19:PHE:CD1	2.88	0.41
2:H:84:CYS:HB3	2:H:96:CYS:HG	1.84	0.41
1:A:38:GLN:OE1	1:A:117:TYR:CD1	2.72	0.41
1:A:114:ASP:O	1:A:116:ASN:N	2.53	0.41
2:B:44:CYS:HB2	2:B:106:PHE:CZ	2.54	0.41
1:E:34:GLN:HG2	1:E:35:GLY:N	2.35	0.41
1:A:38:GLN:O	1:A:39:ASP:HB3	2.20	0.41
2:B:17:PHE:CD2	2:B:20:PHE:CZ	3.08	0.41
1:C:39:ASP:OD1	1:C:41:THR:HB	2.20	0.41
1:C:121:ALA:C	1:C:124:SER:H	2.22	0.41
1:E:61:ASN:O	1:E:68:PRO:C	2.59	0.41
1:E:70:MET:HE1	2:F:33:GLY:HA2	2.02	0.41
2:H:71:VAL:CG2	2:H:92:LEU:HG	2.51	0.41
2:H:117:TYR:HD1	2:H:120:TYR:HH	1.61	0.41
2:B:47:VAL:O	2:B:51:CYS:HB2	2.21	0.41
1:E:1:ASN:N	1:E:4:GLN:OE1	2.53	0.41
1:E:97:GLU:OE2	1:E:100:ARG:HD3	2.21	0.41
2:H:13:GLN:O	2:H:14:GLU:CB	2.55	0.41
1:A:55:VAL:CG1	1:A:91:CYS:SG	3.09	0.41
2:B:49:ASP:C	2:B:51:CYS:H	2.23	0.41
2:F:83:VAL:O	2:F:84:CYS:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:ILE:HA	1:A:103:ALA:HB1	2.01	0.41
1:C:89:ASN:HB3	1:C:92:LEU:HD12	2.01	0.41
1:C:97:GLU:OE2	1:C:100:ARG:CZ	2.68	0.41
1:E:2:PHE:HB2	2:F:32:GLY:O	2.21	0.41
1:E:2:PHE:CE1	1:E:69:LYS:HB2	2.52	0.41
1:A:50:CYS:SG	1:A:133:CYS:HB2	2.61	0.41
1:C:13:THR:CG2	1:C:14:GLY:N	2.83	0.41
2:F:23:ILE:HD13	2:F:23:ILE:HA	1.93	0.41
1:G:4:GLN:NE2	1:G:73:TYR:O	2.38	0.41
2:H:76:SER:O	2:H:78:ARG:HG3	2.21	0.41
2:H:121:SER:C	2:H:124:PHE:H	2.24	0.41
2:B:37:PRO:CB	2:B:43:ARG:HG3	2.51	0.41
2:B:43:ARG:O	2:B:46:PHE:N	2.50	0.41
2:B:118:MET:O	2:B:119:LEU:C	2.57	0.41
1:C:5:PHE:CE1	1:C:9:ILE:HD11	2.55	0.41
1:E:95:VAL:HG12	1:E:95:VAL:O	2.21	0.41
1:E:116:ASN:C	1:E:118:GLU:H	2.24	0.41
1:E:118:GLU:O	1:E:120:TYR:N	2.54	0.41
1:G:51:CYS:C	1:G:53:GLY:N	2.74	0.41
2:H:2:LEU:HD12	2:H:69:LYS:HE3	2.02	0.41
1:A:106:LEU:O	1:A:110:VAL:HG13	2.20	0.41
2:D:78:ARG:O	2:D:81:LYS:N	2.49	0.41
1:E:1:ASN:HD21	2:F:34:GLN:HB3	1.83	0.41
1:E:6:ALA:CB	1:E:19:VAL:HG22	2.49	0.41
1:E:43:ARG:O	1:E:44:CYS:C	2.58	0.41
2:F:21:LYS:HD2	2:F:113:TYR:CE2	2.56	0.41
1:G:132:GLN:C	1:G:133:CYS:OXT	2.59	0.41
2:H:34:GLN:HE21	2:H:127:LYS:HA	1.86	0.41
1:C:121:ALA:C	1:C:124:SER:N	2.73	0.41
2:D:13:GLN:CG	2:D:110:MET:SD	3.08	0.41
1:E:33:GLY:O	2:F:1:ASN:HB3	2.21	0.41
1:A:25:TYR:CD1	1:A:26:GLY:N	2.89	0.40
2:D:78:ARG:O	2:D:80:GLY:N	2.55	0.40
1:E:117:TYR:HA	1:E:120:TYR:HD2	1.86	0.40
1:G:11:LYS:HE3	1:G:82:ILE:CG1	2.51	0.40
1:A:3:PHE:HD2	2:B:34:GLN:HG2	1.84	0.40
1:A:113:TYR:C	1:A:113:TYR:CD1	2.94	0.40
2:B:70:LEU:N	2:B:70:LEU:HD12	2.36	0.40
2:B:10:ASP:OD2	2:B:17:PHE:N	2.44	0.40
2:B:71:VAL:HG22	2:B:92:LEU:HD21	2.02	0.40
1:C:69:LYS:HD3	2:D:49:ASP:OD1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:16:ALA:C	2:D:18:SER:N	2.75	0.40
2:F:38:LYS:HA	2:F:38:LYS:HD3	1.91	0.40
1:G:35:GLY:O	1:G:130:SER:HA	2.22	0.40
1:G:61:ASN:HA	1:G:68:PRO:HD3	1.90	0.40
1:A:121:ALA:O	1:A:122:ILE:CB	2.70	0.40
1:C:125:HIS:CE1	1:C:126:CYS:H	2.34	0.40
2:D:24:SER:O	2:D:119:LEU:N	2.54	0.40
1:E:30:GLY:O	1:E:32:GLY:N	2.54	0.40
1:A:3:PHE:CG	2:B:32:GLY:HA2	2.57	0.40
2:F:81:LYS:O	2:F:83:VAL:HG23	2.21	0.40
1:G:16:LYS:NZ	1:G:21:SER:OG	2.50	0.40
1:G:25:TYR:HE2	1:G:114:ASP:O	2.05	0.40
1:G:38:GLN:HE21	1:G:38:GLN:N	2.20	0.40

All (11) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:159:HOH:O	3:C:158:HOH:O[3_664]	0.22	1.98
2:D:86:GLY:CA	3:B:153:HOH:O[2_665]	0.60	1.60
2:H:88:ASP:OD2	3:E:161:HOH:O[3_764]	1.05	1.15
2:D:86:GLY:N	3:B:153:HOH:O[2_665]	1.31	0.89
2:H:88:ASP:CG	3:E:161:HOH:O[3_764]	1.44	0.76
2:H:88:ASP:OD1	3:E:161:HOH:O[3_764]	1.73	0.47
2:D:86:GLY:C	3:B:153:HOH:O[2_665]	1.87	0.33
1:C:43:ARG:NH2	3:H:156:HOH:O[3_665]	1.88	0.32
3:E:161:HOH:O	3:H:145:HOH:O[2_645]	1.90	0.30
3:D:152:HOH:O	3:F:146:HOH:O[2_654]	2.07	0.13
1:C:108:GLN:OE1	3:H:160:HOH:O[3_665]	2.10	0.10

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	120/122 (98%)	89 (74%)	21 (18%)	10 (8%)	1 1
1	C	120/122 (98%)	77 (64%)	28 (23%)	15 (12%)	0 0
1	E	120/122 (98%)	87 (72%)	21 (18%)	12 (10%)	0 0
1	G	120/122 (98%)	88 (73%)	21 (18%)	11 (9%)	1 0
2	B	120/122 (98%)	88 (73%)	24 (20%)	8 (7%)	1 1
2	D	120/122 (98%)	88 (73%)	23 (19%)	9 (8%)	1 1
2	F	120/122 (98%)	87 (72%)	24 (20%)	9 (8%)	1 1
2	H	120/122 (98%)	88 (73%)	21 (18%)	11 (9%)	1 0
All	All	960/976 (98%)	692 (72%)	183 (19%)	85 (9%)	1 0

All (85) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	17	GLU
1	A	20	HIS
1	A	122	ILE
2	B	107	ARG
1	C	13	THR
1	C	18	ALA
1	C	19	VAL
1	C	20	HIS
1	C	78	GLU
1	C	116	ASN
1	C	121	ALA
2	D	79	THR
2	D	88	ASP
1	E	16	LYS
1	E	19	VAL
1	E	20	HIS
1	E	119	ASN
1	E	125	HIS
2	F	91	CYS
2	F	113	TYR
1	G	29	CYS
2	H	14	GLU
2	H	128	GLU
1	A	24	ILE
2	B	37	PRO
2	B	79	THR
2	B	130	SER

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Mol	Chain	Res	Type
1	C	10	VAL
1	C	58	ASP
1	C	86	ASP
1	C	119	ASN
2	D	113	TYR
2	D	115	LYS
1	E	24	ILE
1	E	31	TRP
1	E	79	ASN
1	E	80	GLY
1	E	124	SER
2	F	59	CYS
2	F	90	PRO
1	G	24	ILE
1	G	30	GLY
1	G	84	CYS
1	G	124	SER
1	G	128	GLU
2	H	11	ALA
2	H	76	SER
2	H	79	THR
2	H	115	LYS
2	H	122	ILE
2	H	131	ASP
1	A	26	GLY
1	A	90	LEU
2	B	50	CYS
2	B	119	LEU
1	C	129	GLU
2	D	14	GLU
2	D	53	ALA
2	D	119	LEU
2	F	107	ARG
2	F	129	GLU
1	G	12	MET
1	G	70	MET
1	G	121	ALA
2	H	110	MET
1	A	89	ASN
1	A	127	THR
2	D	59	CYS
2	D	91	CYS

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Mol	Chain	Res	Type
1	E	29	CYS
1	E	68	PRO
2	F	68	PRO
2	F	86	GLY
1	A	39	ASP
1	A	115	LYS
2	B	117	TYR
1	C	37	PRO
1	G	76	SER
1	G	78	GLU
2	H	52	TYR
1	C	124	SER
2	F	110	MET
2	B	36	THR
1	C	24	ILE
2	H	37	PRO

5.3.2 Protein sidechains (i)

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	103/103 (100%)	88 (85%)	15 (15%)	3 5
1	C	103/103 (100%)	94 (91%)	9 (9%)	10 20
1	E	103/103 (100%)	92 (89%)	11 (11%)	6 12
1	G	103/103 (100%)	93 (90%)	10 (10%)	8 15
2	B	105/105 (100%)	96 (91%)	9 (9%)	10 20
2	D	105/105 (100%)	97 (92%)	8 (8%)	13 26
2	F	105/105 (100%)	98 (93%)	7 (7%)	16 33
2	H	105/105 (100%)	101 (96%)	4 (4%)	33 59
All	All	832/832 (100%)	759 (91%)	73 (9%)	10 19

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	PHE
1	A	7	GLU
1	A	12	MET
1	A	20	HIS
1	A	42	ASP
1	A	52	TYR
1	A	70	MET
1	A	78	GLU
1	A	79	ASN
1	A	90	LEU
1	A	111	ASN
1	A	120	TYR
1	A	127	THR
1	A	128	GLU
1	A	129	GLU
2	B	69	LYS
2	B	71	VAL
2	B	74	SER
2	B	81	LYS
2	B	83	VAL
2	B	91	CYS
2	B	93	ARG
2	B	118	MET
2	B	119	LEU
1	C	12	MET
1	C	21	SER
1	C	36	LYS
1	C	39	ASP
1	C	50	CYS
1	C	90	LEU
1	C	111	ASN
1	C	120	TYR
1	C	129	GLU
2	D	3	PHE
2	D	14	GLU
2	D	74	SER
2	D	88	ASP
2	D	89	ASP
2	D	93	ARG
2	D	97	GLU
2	D	122	ILE
1	E	24	ILE
1	E	61	ASN

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Mol	Chain	Res	Type
1	E	68	PRO
1	E	78	GLU
1	E	88	ASN
1	E	100	ARG
1	E	111	ASN
1	E	117	TYR
1	E	119	ASN
1	E	120	TYR
1	E	133	CYS
2	F	88	ASP
2	F	89	ASP
2	F	91	CYS
2	F	97	GLU
2	F	107	ARG
2	F	111	ASN
2	F	120	TYR
1	G	17	GLU
1	G	19	VAL
1	G	70	MET
1	G	72	THR
1	G	86	ASP
1	G	112	THR
1	G	115	LYS
1	G	116	ASN
1	G	120	TYR
1	G	132	GLN
2	H	19	PHE
2	H	91	CYS
2	H	120	TYR
2	H	131	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	79	ASN
1	A	132	GLN
2	B	13	GLN
2	B	111	ASN
1	C	34	GLN
1	C	48	HIS
1	C	79	ASN

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Mol	Chain	Res	Type
1	C	108	GLN
2	D	1	ASN
2	D	13	GLN
2	D	34	GLN
2	D	61	ASN
2	D	111	ASN
1	E	38	GLN
1	E	88	ASN
1	E	89	ASN
1	E	119	ASN
2	F	111	ASN
1	G	38	GLN
1	G	61	ASN
1	G	89	ASN
1	G	132	GLN
2	H	109	ASN
2	H	111	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

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	122/122 (100%)	0.07	2 (1%) 72 68	21, 36, 49, 62	2 (1%)
1	C	122/122 (100%)	0.06	2 (1%) 72 68	17, 39, 55, 62	2 (1%)
1	E	122/122 (100%)	-0.07	1 (0%) 86 84	14, 35, 54, 63	2 (1%)
1	G	122/122 (100%)	0.14	3 (2%) 57 51	27, 38, 54, 60	2 (1%)
2	B	122/122 (100%)	-0.01	1 (0%) 86 84	23, 35, 54, 58	2 (1%)
2	D	122/122 (100%)	-0.13	0 100 100	15, 33, 45, 52	2 (1%)
2	F	122/122 (100%)	0.03	2 (1%) 72 68	11, 35, 54, 64	1 (0%)
2	H	122/122 (100%)	0.00	2 (1%) 72 68	20, 33, 50, 56	1 (0%)
All	All	976/976 (100%)	0.01	13 (1%) 77 73	11, 35, 53, 64	14 (1%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	106	PHE	3.7
1	E	120	TYR	3.7
1	G	129	GLU	3.5
2	H	120	TYR	3.1
1	G	120	TYR	3.1
2	F	77	TYR	2.5
1	G	11	LYS	2.3
2	H	106	PHE	2.3
1	A	133	CYS	2.2
1	A	18	ALA	2.2
2	F	120	TYR	2.1
1	C	80	GLY	2.1
1	C	88	ASN	2.1

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 monosaccharides 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.