Full wwPDB X-ray Structure Validation Report (i)

Aug 15, 2023 – 12:56 AM EDT

PDB ID	:	1R5I
Title	:	Crystal structure of the MAM-MHC complex
Authors	:	Zhao, Y.; Li, Z.; Drozd, S.J.; Guo, Y.; Mourad, W.; Li, H.
Deposited on	:	2003-10-10
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 (i) 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 (i)) were used in the production of this report:

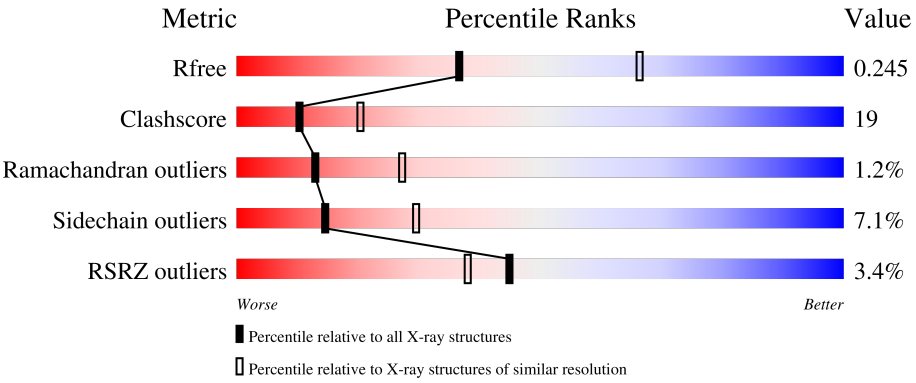
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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	181	2% 67% 30%
1	E	181	2% 67% 28%
2	B	190	6% 63% 33%
2	F	190	6% 61% 34% 5%
3	C	13	38% 62%

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Mol	Chain	Length	Quality of chain
3	G	13	38% 54% 8%
4	D	216	2% 62% 31% 5%
4	H	216	3% 64% 29% 6%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 10014 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	181	Total	C	N	O	S	Se	0	0	0
			1491	966	242	278	2	3			
1	E	181	Total	C	N	O	S	Se	0	0	0
			1491	966	242	278	2	3			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	MSE	MET	modified residue	UNP P01903
A	36	MSE	MET	modified residue	UNP P01903
A	73	MSE	MET	modified residue	UNP P01903
E	23	MSE	MET	modified residue	UNP P01903
E	36	MSE	MET	modified residue	UNP P01903
E	73	MSE	MET	modified residue	UNP P01903

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	190	Total	C	N	O	S	0	0	0
			1557	979	279	293	6			
2	F	190	Total	C	N	O	S	0	0	0
			1557	979	279	293	6			

- Molecule 3 is a protein called Hemagglutinin peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	0	0	0
			106	69	18	19			
3	G	13	Total	C	N	O	0	0	0
			102	66	17	19			

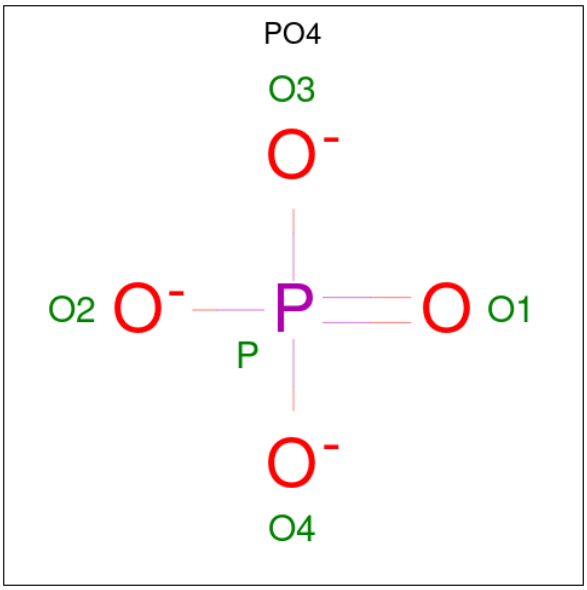
- Molecule 4 is a protein called superantigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	214	Total	C	N	O	S	0	0	0
			1792	1157	302	328	5			
4	H	214	Total	C	N	O	S	0	0	0
			1792	1157	302	328	5			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	LEU	-	cloning artifact	UNP Q48898
D	-1	GLY	-	cloning artifact	UNP Q48898
D	0	SER	-	cloning artifact	UNP Q48898
H	-2	LEU	-	cloning artifact	UNP Q48898
H	-1	GLY	-	cloning artifact	UNP Q48898
H	0	SER	-	cloning artifact	UNP Q48898

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		
5	E	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		

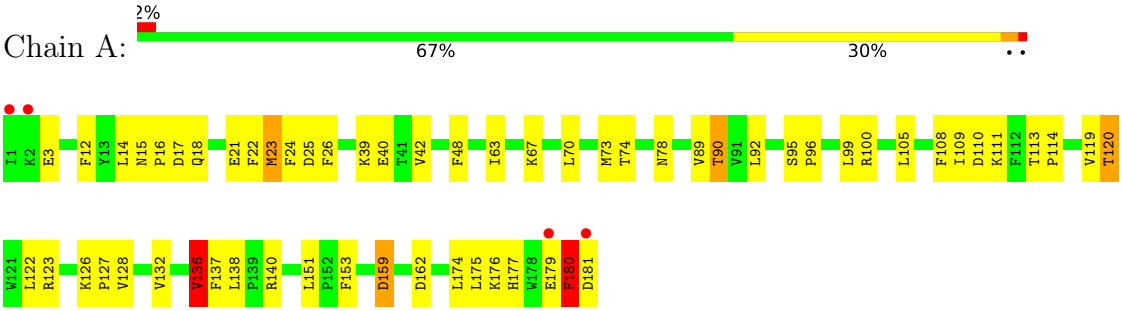
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	23	Total O 23 23	0	0
6	B	18	Total O 18 18	0	0
6	D	17	Total O 17 17	0	0
6	E	23	Total O 23 23	0	0
6	F	12	Total O 12 12	0	0
6	H	13	Total O 13 13	0	0

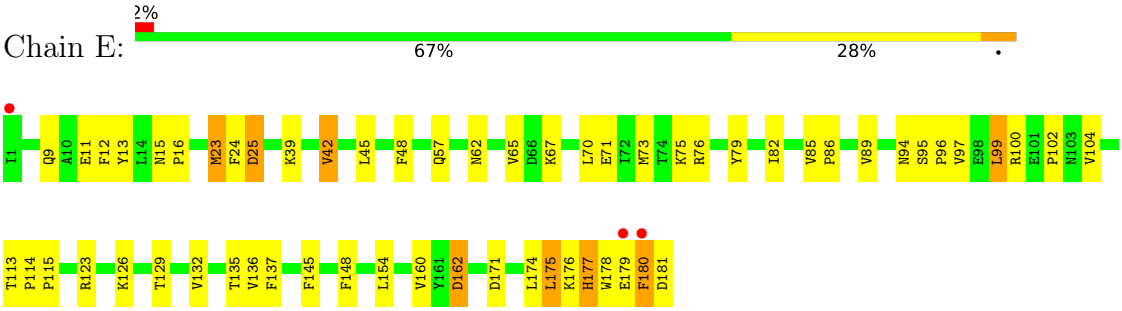
3 Residue-property plots (i)

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.

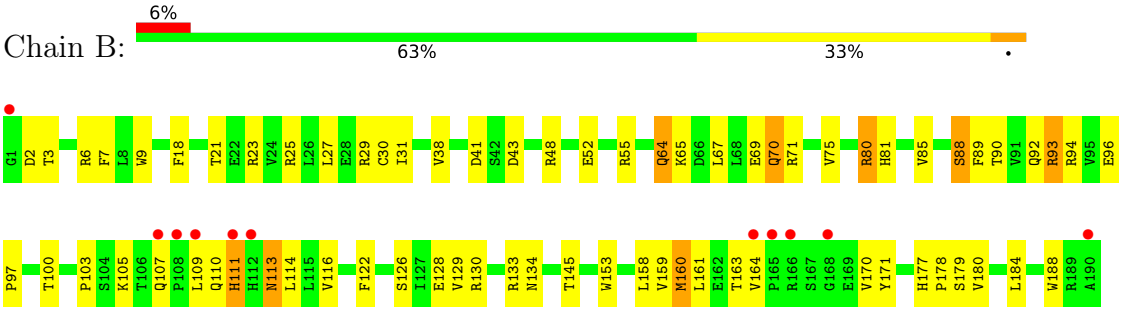
• Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



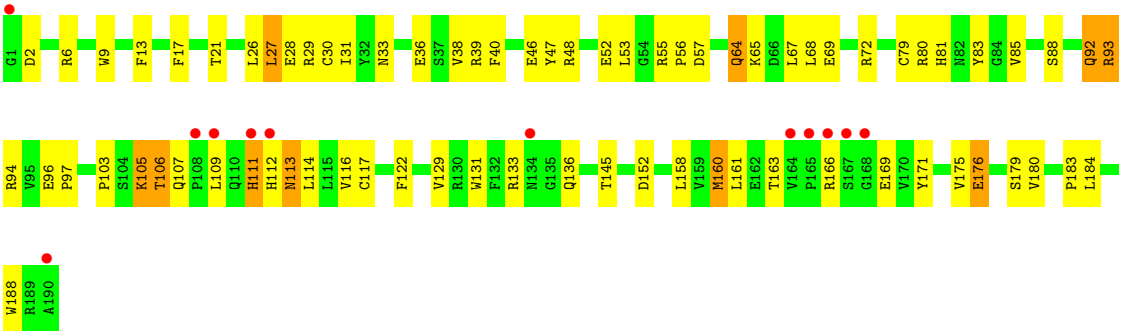
• Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



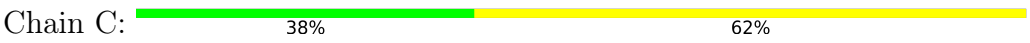
• Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain



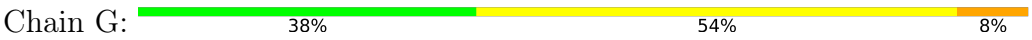
• Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain

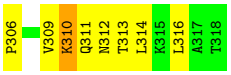


• Molecule 3: Hemagglutinin peptide

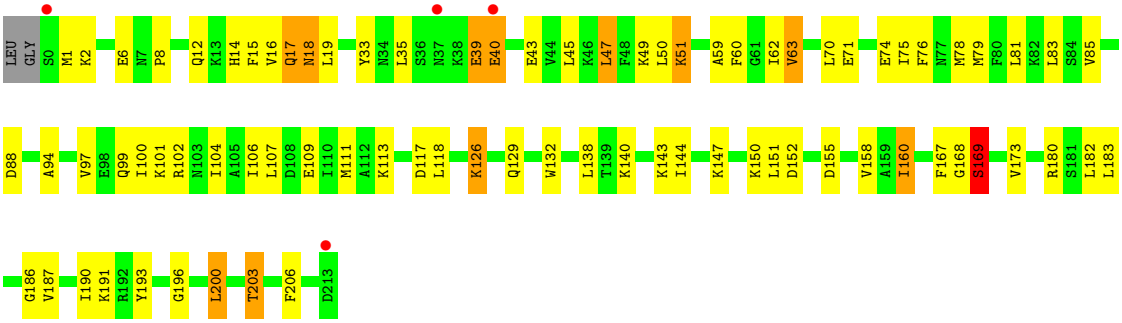


• Molecule 3: Hemagglutinin peptide

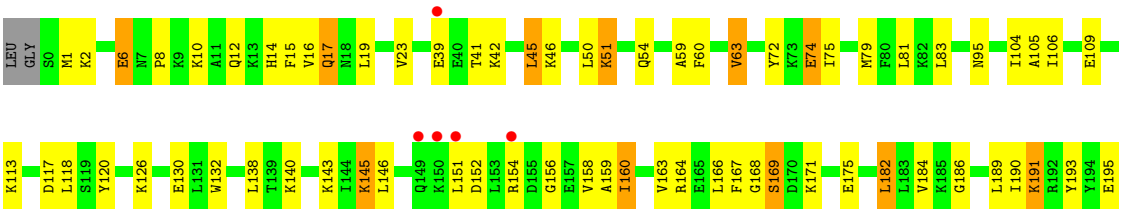


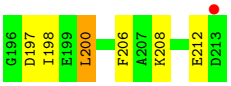


• Molecule 4: superantigen



• Molecule 4: superantigen




G196
D197
I198
E199
L200
F206
A207
K208
E212
D213

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	138.29Å 178.81Å 179.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.23 – 2.60 42.23 – 2.49	Depositor EDS
% Data completeness (in resolution range)	95.3 (42.23-2.60) 92.2 (42.23-2.49)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	1.17 (at 2.48Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.238 , 0.246 0.237 , 0.245	Depositor DCC
R_{free} test set	5067 reflections (7.09%)	wwPDB-VP
Wilson B-factor (Å^2)	43.4	Xtriage
Anisotropy	0.608	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 37.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.076 for -h,-l,-k	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	10014	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.80% 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

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.48	0/1533	0.69	0/2083
1	E	0.48	0/1533	0.70	0/2083
2	B	0.43	0/1597	0.66	0/2168
2	F	0.43	0/1597	0.65	0/2168
3	C	0.48	0/107	0.74	0/141
3	G	0.49	0/103	0.87	0/137
4	D	0.46	0/1822	0.61	0/2439
4	H	0.48	0/1822	0.61	0/2439
All	All	0.46	0/10114	0.66	0/13658

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1491	0	1434	49	0
1	E	1491	0	1434	53	0
2	B	1557	0	1488	62	0
2	F	1557	0	1488	74	0
3	C	106	0	119	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	102	0	108	14	0
4	D	1792	0	1836	76	0
4	H	1792	0	1836	75	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
5	E	5	0	0	0	0
5	H	5	0	0	0	0
6	A	23	0	0	1	0
6	B	18	0	0	0	0
6	D	17	0	0	0	0
6	E	23	0	0	1	0
6	F	12	0	0	0	0
6	H	13	0	0	0	0
All	All	10014	0	9743	368	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 19.

All (368) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:18:ASN:H	4:D:18:ASN:HD22	1.09	0.99
4:D:160:ILE:HD12	4:D:160:ILE:H	1.34	0.90
2:B:114:LEU:HD12	2:B:160:MET:HB3	1.56	0.87
1:E:99:LEU:HD13	1:E:100:ARG:HG2	1.59	0.83
4:H:160:ILE:H	4:H:160:ILE:HD12	1.45	0.81
2:F:55:ARG:HH21	2:F:55:ARG:HG3	1.44	0.81
1:A:90:THR:HG23	1:A:108:PHE:HB2	1.63	0.79
2:B:97:PRO:HB3	2:B:122:PHE:HB3	1.63	0.79
2:B:107:GLN:NE2	2:B:109:LEU:HD11	1.98	0.79
4:H:143:LYS:HA	4:H:190:ILE:HD12	1.65	0.78
2:F:114:LEU:H	2:F:114:LEU:HD23	1.47	0.78
4:D:17:GLN:H	4:D:17:GLN:NE2	1.82	0.78
2:F:105:LYS:HE2	2:F:112:HIS:HA	1.66	0.78
2:F:97:PRO:HB3	2:F:122:PHE:HB3	1.63	0.78
4:H:1:MET:CE	4:H:132:TRP:HB3	2.14	0.77
4:H:39:GLU:HG3	4:H:42:LYS:HZ2	1.48	0.77
1:A:99:LEU:HD23	1:A:100:ARG:N	1.98	0.77
4:H:51:LYS:HG3	4:H:104:ILE:HG23	1.67	0.77
2:F:92:GLN:HE21	2:F:92:GLN:HA	1.50	0.77
4:D:18:ASN:H	4:D:18:ASN:ND2	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:SER:HB2	1:A:96:PRO:HD2	1.68	0.76
4:H:164:ARG:HG3	4:H:164:ARG:HH11	1.51	0.74
1:E:75:LYS:HE2	1:E:79:TYR:OH	1.87	0.74
1:E:16:PRO:HD2	2:F:6:ARG:HD3	1.69	0.74
2:F:133:ARG:HG3	2:F:171:TYR:CE1	2.23	0.74
2:F:2:ASP:CG	2:F:6:ARG:HH12	1.90	0.73
1:A:70:LEU:HD23	2:B:9:TRP:HB2	1.71	0.73
4:D:6:GLU:CD	4:D:6:GLU:H	1.91	0.73
1:A:39:LYS:O	1:A:39:LYS:HD3	1.88	0.73
4:D:45:LEU:HD11	4:D:49:LYS:HE3	1.72	0.72
4:D:160:ILE:HD12	4:D:160:ILE:N	2.03	0.72
2:B:21:THR:O	2:B:80:ARG:NH1	2.23	0.71
1:E:23:MSE:HG2	1:E:24:PHE:N	2.06	0.71
2:B:52:GLU:OE2	2:B:55:ARG:HD2	1.91	0.71
2:B:81:HIS:HD2	3:C:309:VAL:HG12	1.55	0.71
4:D:18:ASN:HD22	4:D:18:ASN:N	1.80	0.71
2:F:93:ARG:HG2	2:F:93:ARG:HH21	1.55	0.71
4:D:1:MET:HE2	4:D:132:TRP:HB3	1.71	0.70
2:B:133:ARG:HG3	2:B:171:TYR:CE1	2.27	0.70
4:H:1:MET:HE1	4:H:132:TRP:HB3	1.72	0.70
4:D:1:MET:CE	4:D:132:TRP:HB3	2.21	0.70
4:D:160:ILE:H	4:D:160:ILE:CD1	2.05	0.69
4:D:106:ILE:HA	4:D:109:GLU:HG3	1.73	0.69
4:H:59:ALA:HA	4:H:79:MET:HE1	1.74	0.69
2:F:55:ARG:HG3	2:F:55:ARG:NH2	2.08	0.69
4:H:6:GLU:CD	4:H:6:GLU:H	1.94	0.69
4:D:1:MET:CE	4:D:129:GLN:HA	2.24	0.68
2:F:93:ARG:O	2:F:94:ARG:HD3	1.93	0.68
1:A:16:PRO:HD2	2:B:6:ARG:HD3	1.76	0.68
4:H:16:VAL:HG21	4:H:81:LEU:HD11	1.76	0.68
4:H:39:GLU:HG3	4:H:42:LYS:NZ	2.08	0.68
2:B:161:LEU:HG	2:B:163:THR:HG23	1.75	0.67
2:F:29:ARG:HD2	2:F:36:GLU:OE2	1.95	0.67
4:D:143:LYS:HA	4:D:190:ILE:HD12	1.75	0.66
2:B:88:SER:O	2:B:92:GLN:HB2	1.96	0.66
1:E:70:LEU:HD13	2:F:9:TRP:HB2	1.76	0.66
2:F:106:THR:HB	2:F:113:ASN:ND2	2.10	0.65
4:D:33:TYR:CD1	4:D:49:LYS:HE2	2.31	0.65
4:H:146:LEU:HD22	4:H:151:LEU:HD21	1.77	0.65
4:D:43:GLU:O	4:D:47:LEU:HD23	1.97	0.65
4:D:97:VAL:O	4:D:101:LYS:HG2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:17:GLN:H	4:H:17:GLN:NE2	1.95	0.65
4:H:60:PHE:HA	4:H:63:VAL:HG13	1.79	0.64
4:H:159:ALA:O	4:H:163:VAL:HG23	1.98	0.64
1:E:13:TYR:CE2	1:E:67:LYS:HG3	2.33	0.64
4:D:85:VAL:O	4:D:88:ASP:HB2	1.98	0.64
1:E:162:ASP:OD2	1:E:177:HIS:HD2	1.81	0.63
2:F:64:GLN:HB3	2:F:67:LEU:HB3	1.79	0.63
4:D:60:PHE:HA	4:D:63:VAL:CG1	2.28	0.63
4:D:62:ILE:HD12	4:D:79:MET:CE	2.28	0.63
2:B:64:GLN:HE21	2:B:64:GLN:N	1.96	0.63
4:D:51:LYS:HE3	4:D:111:MET:HE1	1.81	0.63
1:A:179:GLU:C	1:A:181:ASP:H	2.02	0.62
1:A:132:VAL:HG12	1:A:151:LEU:HD13	1.81	0.62
4:D:1:MET:HE3	4:D:129:GLN:HA	1.80	0.62
4:D:51:LYS:HG3	4:D:104:ILE:HG23	1.82	0.62
2:F:114:LEU:HD12	2:F:160:MET:HB3	1.80	0.62
2:B:114:LEU:HD23	2:B:114:LEU:H	1.63	0.62
2:F:103:PRO:HD3	2:F:188:TRP:CH2	2.33	0.62
1:E:62:ASN:HA	3:G:313:THR:CG2	2.29	0.62
4:H:138:LEU:HD22	4:H:167:PHE:CE2	2.34	0.62
2:B:21:THR:HB	2:B:80:ARG:HD3	1.82	0.61
2:B:64:GLN:HG2	4:D:15:PHE:CE2	2.35	0.61
4:D:16:VAL:HG21	4:D:81:LEU:HD11	1.81	0.61
2:F:161:LEU:HG	2:F:163:THR:HG23	1.82	0.61
4:H:138:LEU:HD22	4:H:167:PHE:HE2	1.65	0.61
1:A:23:MSE:HG2	1:A:24:PHE:N	2.15	0.61
4:H:1:MET:HE1	4:H:132:TRP:CB	2.31	0.60
2:F:107:GLN:HB3	2:F:109:LEU:CD2	2.30	0.60
4:D:126:LYS:HD2	4:D:126:LYS:C	2.22	0.60
1:E:179:GLU:O	1:E:181:ASP:N	2.33	0.60
2:F:105:LYS:HG3	2:F:111:HIS:O	2.01	0.60
4:D:62:ILE:HD12	4:D:79:MET:HE2	1.84	0.59
1:A:89:VAL:O	1:A:176:LYS:HE3	2.02	0.59
1:A:15:ASN:ND2	1:A:70:LEU:HD12	2.18	0.59
3:C:317:ALA:O	3:C:318:THR:HG22	2.01	0.59
1:A:23:MSE:HE3	1:A:25:ASP:HB2	1.85	0.59
1:E:62:ASN:HA	3:G:313:THR:HG22	1.82	0.59
2:B:114:LEU:HD12	2:B:160:MET:CB	2.32	0.59
2:F:88:SER:O	2:F:92:GLN:HB2	2.03	0.58
2:B:85:VAL:HG13	3:C:306:PRO:HB2	1.84	0.58
2:F:107:GLN:HB3	2:F:109:LEU:HD23	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:VAL:HG13	1:A:137:PHE:N	2.19	0.58
2:F:68:LEU:O	2:F:72:ARG:HG3	2.04	0.58
4:H:208:LYS:O	4:H:212:GLU:HB2	2.03	0.58
1:E:25:ASP:C	1:E:25:ASP:OD2	2.42	0.57
4:H:41:THR:HG21	4:H:95:ASN:HD22	1.69	0.57
4:H:105:ALA:O	4:H:109:GLU:HG3	2.04	0.57
4:H:1:MET:HE2	4:H:132:TRP:CE3	2.40	0.57
1:E:65:VAL:HB	3:G:313:THR:CG2	2.34	0.57
1:E:129:THR:O	1:E:132:VAL:HG22	2.05	0.57
1:A:179:GLU:O	1:A:179:GLU:HG2	2.04	0.56
4:D:15:PHE:HA	4:D:17:GLN:HE22	1.70	0.56
1:A:92:LEU:HD11	1:A:108:PHE:CZ	2.40	0.56
1:A:110:ASP:OD1	1:A:111:LYS:N	2.34	0.56
3:G:312:ASN:ND2	4:H:12:GLN:HG2	2.20	0.56
1:E:9:GLN:HG3	1:E:24:PHE:CE1	2.41	0.56
2:F:64:GLN:CG	4:H:15:PHE:CE2	2.89	0.56
4:D:35:LEU:HB3	4:D:94:ALA:CB	2.36	0.55
1:A:122:LEU:HB2	1:A:162:ASP:OD2	2.07	0.55
4:D:186:GLY:O	4:D:190:ILE:HG12	2.05	0.55
1:A:99:LEU:HD23	1:A:100:ARG:H	1.69	0.55
1:E:39:LYS:HE3	1:E:57:GLN:NE2	2.21	0.55
1:E:123:ARG:HE	1:E:126:LYS:NZ	2.04	0.55
2:F:180:VAL:HG11	2:F:184:LEU:HD13	1.87	0.55
4:H:191:LYS:HE2	4:H:195:GLU:HG3	1.89	0.55
2:F:106:THR:O	2:F:107:GLN:HG3	2.07	0.54
2:F:21:THR:O	2:F:80:ARG:NH1	2.40	0.54
2:F:28:GLU:C	2:F:29:ARG:HG2	2.26	0.54
2:B:31:ILE:N	2:B:31:ILE:HD12	2.22	0.54
1:E:73:MSE:HG2	3:G:316:LEU:CD1	2.37	0.54
4:H:164:ARG:HH11	4:H:164:ARG:CG	2.20	0.54
1:A:39:LYS:O	1:A:39:LYS:CD	2.54	0.54
4:H:14:HIS:N	4:H:74:GLU:OE1	2.38	0.54
4:H:191:LYS:HE3	4:H:191:LYS:HA	1.90	0.54
1:A:73:MSE:HG3	2:B:9:TRP:CZ3	2.43	0.54
4:D:200:LEU:O	4:D:203:THR:HB	2.08	0.54
1:E:62:ASN:O	3:G:313:THR:HG21	2.08	0.54
4:H:197:ASP:HB3	4:H:200:LEU:HD13	1.90	0.54
2:F:81:HIS:HD2	3:G:309:VAL:HG22	1.73	0.53
1:E:45:LEU:HD12	1:E:48:PHE:CZ	2.42	0.53
4:D:59:ALA:HA	4:D:79:MET:CE	2.38	0.53
1:E:162:ASP:OD2	1:E:177:HIS:CD2	2.62	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:180:PHE:HB3	6:E:213:HOH:O	2.08	0.53
2:F:31:ILE:HD12	2:F:31:ILE:N	2.23	0.53
1:A:17:ASP:CG	2:B:6:ARG:HH21	2.12	0.53
4:H:75:ILE:CD1	4:H:118:LEU:HA	2.38	0.53
1:A:92:LEU:HD11	1:A:108:PHE:HZ	1.74	0.53
2:B:116:VAL:HG22	2:B:160:MET:HG2	1.91	0.53
4:H:15:PHE:HA	4:H:17:GLN:HE22	1.73	0.53
1:E:39:LYS:HE3	1:E:57:GLN:HE21	1.74	0.52
2:F:9:TRP:CH2	2:F:30:CYS:HB3	2.43	0.52
2:F:13:PHE:CE2	2:F:28:GLU:HG3	2.45	0.52
2:F:64:GLN:HG2	4:H:15:PHE:CE2	2.44	0.52
2:B:70:GLN:HE22	2:B:71:ARG:HH11	1.58	0.52
4:H:113:LYS:NZ	4:H:117:ASP:OD1	2.43	0.52
1:A:122:LEU:HD23	1:A:127:PRO:HA	1.92	0.52
4:D:75:ILE:HD11	4:D:118:LEU:HA	1.92	0.52
2:F:116:VAL:HG22	2:F:160:MET:HG2	1.92	0.52
3:C:315:LYS:HD3	3:C:316:LEU:O	2.10	0.52
4:D:75:ILE:CD1	4:D:118:LEU:HA	2.40	0.52
2:F:96:GLU:HA	2:F:179:SER:OG	2.10	0.52
4:H:186:GLY:O	4:H:190:ILE:HG12	2.10	0.52
1:E:95:SER:HB2	1:E:96:PRO:HD2	1.91	0.51
4:D:1:MET:HE1	4:D:129:GLN:HA	1.91	0.51
4:D:39:GLU:CD	4:D:39:GLU:H	2.13	0.51
2:F:94:ARG:HG3	2:F:94:ARG:HH11	1.75	0.51
1:A:70:LEU:HD23	2:B:9:TRP:CB	2.39	0.51
2:B:164:VAL:HG13	2:B:164:VAL:O	2.10	0.51
4:D:18:ASN:ND2	4:D:18:ASN:N	2.51	0.51
1:E:135:THR:HG23	1:E:148:PHE:HB2	1.92	0.51
4:H:152:ASP:O	4:H:158:VAL:HG21	2.10	0.51
1:E:39:LYS:NZ	4:H:109:GLU:OE2	2.44	0.51
2:B:97:PRO:CB	2:B:122:PHE:HB3	2.38	0.51
4:D:70:LEU:HB3	4:D:71:GLU:OE2	2.10	0.51
4:D:16:VAL:HG22	4:D:19:LEU:HD12	1.93	0.51
4:D:60:PHE:HA	4:D:63:VAL:HG12	1.92	0.51
2:F:166:ARG:HG2	2:F:169:GLU:CD	2.31	0.51
1:E:123:ARG:O	1:E:126:LYS:HG2	2.11	0.51
2:B:81:HIS:HD2	3:C:309:VAL:CG1	2.24	0.50
4:D:173:VAL:HG13	4:D:180:ARG:HG3	1.92	0.50
2:F:180:VAL:HG11	2:F:184:LEU:CD1	2.42	0.50
2:B:70:GLN:NE2	2:B:71:ARG:HH11	2.10	0.50
2:F:92:GLN:HA	2:F:92:GLN:NE2	2.22	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:97:PRO:CB	2:F:122:PHE:HB3	2.38	0.50
2:F:145:THR:HG23	2:F:158:LEU:HB2	1.94	0.50
4:D:144:ILE:HD13	4:H:46:LYS:HD3	1.94	0.50
4:H:156:GLY:O	4:H:160:ILE:HD11	2.12	0.50
2:B:110:GLN:HB3	2:B:113:ASN:OD1	2.12	0.50
1:A:179:GLU:O	1:A:180:PHE:CG	2.65	0.50
4:D:76:PHE:O	4:D:79:MET:HB2	2.12	0.50
1:E:65:VAL:HB	3:G:313:THR:HG23	1.92	0.50
1:E:13:TYR:CZ	1:E:67:LYS:HG3	2.47	0.49
2:B:105:LYS:HG2	2:B:111:HIS:O	2.12	0.49
4:D:107:LEU:O	4:D:111:MET:HG3	2.12	0.49
4:D:151:LEU:HB2	4:D:191:LYS:HD3	1.94	0.49
1:E:23:MSE:HE1	1:E:137:PHE:O	2.12	0.49
1:E:82:ILE:HB	2:F:33:ASN:OD1	2.12	0.49
2:B:96:GLU:HA	2:B:179:SER:OG	2.13	0.49
4:H:59:ALA:HA	4:H:79:MET:CE	2.43	0.49
4:H:154:ARG:HG3	4:H:154:ARG:HH11	1.78	0.49
2:F:2:ASP:CG	2:F:6:ARG:NH1	2.64	0.48
2:B:134:ASN:ND2	2:B:170:VAL:HG12	2.28	0.48
4:D:150:LYS:HE2	4:D:152:ASP:HB2	1.95	0.48
1:E:89:VAL:HG23	1:E:174:LEU:HD23	1.96	0.48
4:H:145:LYS:HD3	4:H:166:LEU:HD22	1.96	0.48
2:F:55:ARG:HB2	2:F:56:PRO:HD3	1.94	0.48
2:B:177:HIS:CD2	2:B:178:PRO:HD2	2.48	0.48
4:H:41:THR:CG2	4:H:95:ASN:HD22	2.26	0.48
1:A:26:PHE:CE2	2:B:90:THR:HB	2.49	0.48
1:A:111:LYS:HG2	1:A:140:ARG:CZ	2.43	0.48
2:F:55:ARG:NH2	2:F:55:ARG:CG	2.75	0.48
1:A:120:THR:HG23	6:A:192:HOH:O	2.14	0.47
2:B:65:LYS:O	2:B:69:GLU:HG3	2.14	0.47
4:D:1:MET:HE1	4:D:132:TRP:HB3	1.96	0.47
2:F:129:VAL:HG22	2:F:175:VAL:HG22	1.97	0.47
4:D:16:VAL:HG21	4:D:81:LEU:CD1	2.44	0.47
4:H:16:VAL:HG22	4:H:16:VAL:O	2.14	0.47
1:E:12:PHE:CD1	1:E:12:PHE:C	2.87	0.47
1:E:178:TRP:CH2	1:E:180:PHE:HB2	2.49	0.47
2:F:106:THR:HG22	2:F:107:GLN:HG3	1.96	0.47
1:E:76:ARG:HG2	2:F:53:LEU:HD22	1.97	0.47
4:H:16:VAL:CG2	4:H:19:LEU:HD12	2.45	0.47
1:A:67:LYS:NZ	4:D:88:ASP:OD1	2.48	0.46
1:A:105:LEU:HG	1:A:153:PHE:CE1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:186:GLY:O	4:H:189:LEU:HB2	2.16	0.46
2:B:9:TRP:CH2	2:B:30:CYS:HB3	2.50	0.46
2:B:64:GLN:HB3	2:B:67:LEU:HB3	1.97	0.46
2:B:161:LEU:HG	2:B:163:THR:CG2	2.43	0.46
4:D:196:GLY:HA2	4:H:54:GLN:HG3	1.97	0.46
2:F:93:ARG:HG2	2:F:93:ARG:NH2	2.25	0.46
4:D:100:ILE:O	4:D:104:ILE:HG13	2.16	0.46
2:F:106:THR:OG1	2:F:114:LEU:HD22	2.15	0.46
2:F:109:LEU:HD23	2:F:109:LEU:N	2.31	0.46
4:H:163:VAL:HG21	4:H:184:VAL:HG22	1.97	0.46
2:B:94:ARG:NH1	2:B:94:ARG:HG3	2.30	0.46
2:B:170:VAL:HG13	2:B:170:VAL:O	2.15	0.46
4:D:182:LEU:HG	4:D:206:PHE:CE1	2.51	0.46
2:F:40:PHE:HB2	2:F:47:TYR:CE1	2.50	0.46
2:F:105:LYS:CG	2:F:111:HIS:O	2.64	0.46
1:A:14:LEU:HD12	2:B:7:PHE:O	2.16	0.46
1:A:123:ARG:HD3	1:A:159:ASP:OD1	2.16	0.46
2:B:21:THR:HB	2:B:80:ARG:CD	2.46	0.46
4:H:186:GLY:HA2	4:H:189:LEU:HD12	1.97	0.46
2:B:94:ARG:HG3	2:B:94:ARG:HH11	1.81	0.45
2:F:114:LEU:HD23	2:F:114:LEU:N	2.24	0.45
2:B:103:PRO:HD3	2:B:188:TRP:CH2	2.51	0.45
2:F:117:CYS:HB2	2:F:131:TRP:CZ2	2.51	0.45
2:B:107:GLN:HB3	2:B:109:LEU:HG	1.99	0.45
2:B:107:GLN:C	2:B:109:LEU:H	2.20	0.45
1:A:174:LEU:HD23	1:A:175:LEU:N	2.31	0.45
4:D:39:GLU:OE2	4:D:40:GLU:N	2.50	0.45
2:F:94:ARG:HG3	2:F:94:ARG:NH1	2.32	0.45
1:A:179:GLU:C	1:A:181:ASP:N	2.70	0.45
2:F:85:VAL:HG13	3:G:306:PRO:HB2	1.98	0.45
2:F:131:TRP:CD1	2:F:161:LEU:HB2	2.52	0.45
4:D:14:HIS:HD2	4:D:78:MET:SD	2.40	0.45
2:F:26:LEU:HD13	2:F:79:CYS:SG	2.57	0.45
4:H:164:ARG:CG	4:H:164:ARG:NH1	2.80	0.45
4:H:39:GLU:CG	4:H:42:LYS:HZ2	2.22	0.44
4:H:45:LEU:HD22	4:H:45:LEU:O	2.17	0.44
4:H:171:LYS:HE3	4:H:175:GLU:OE1	2.17	0.44
1:E:11:GLU:OE1	1:E:62:ASN:HB3	2.18	0.44
4:H:41:THR:OG1	4:H:95:ASN:ND2	2.50	0.44
1:A:22:PHE:HB2	1:A:63:ILE:CD1	2.48	0.44
1:E:62:ASN:HA	3:G:313:THR:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:57:ASP:CG	3:G:316:LEU:HD22	2.38	0.44
1:A:123:ARG:HD2	1:A:126:LYS:HZ1	1.83	0.44
3:C:312:ASN:HB3	4:D:12:GLN:CD	2.38	0.44
4:H:126:LYS:HD2	4:H:126:LYS:C	2.37	0.44
4:H:140:LYS:O	4:H:143:LYS:HB3	2.18	0.44
4:H:190:ILE:O	4:H:193:TYR:HB3	2.18	0.44
1:A:15:ASN:HD22	1:A:70:LEU:HD12	1.83	0.43
1:A:179:GLU:O	1:A:179:GLU:CG	2.66	0.43
1:E:94:ASN:HB2	1:E:104:VAL:HB	1.98	0.43
1:E:97:VAL:HG11	1:E:180:PHE:CG	2.53	0.43
4:H:2:LYS:O	4:H:2:LYS:HG3	2.17	0.43
1:A:3:GLU:HA	2:B:18:PHE:CD2	2.53	0.43
2:B:64:GLN:N	2:B:64:GLN:NE2	2.65	0.43
2:B:177:HIS:CG	2:B:178:PRO:HD2	2.53	0.43
4:H:106:ILE:HA	4:H:109:GLU:HG3	2.00	0.43
4:H:167:PHE:O	4:H:169:SER:N	2.51	0.43
1:A:14:LEU:HD11	2:B:6:ARG:HB3	2.00	0.43
4:D:51:LYS:HA	4:D:51:LYS:HD3	1.74	0.43
1:E:160:VAL:HG13	1:E:160:VAL:O	2.19	0.43
1:A:21:GLU:OE2	1:A:136:VAL:HG22	2.19	0.43
2:B:48:ARG:HD3	2:B:48:ARG:HA	1.87	0.43
2:B:25:ARG:NH1	2:B:41:ASP:OD2	2.51	0.43
2:B:128:GLU:OE1	2:B:130:ARG:NH2	2.51	0.43
2:B:93:ARG:NH1	2:B:153:TRP:O	2.52	0.43
4:H:198:ILE:H	4:H:198:ILE:HG12	1.61	0.43
2:B:85:VAL:HG13	3:C:306:PRO:CB	2.47	0.43
2:B:145:THR:HG23	2:B:158:LEU:HB2	2.00	0.43
1:E:115:PRO:HD3	1:E:145:PHE:CE1	2.53	0.43
4:D:2:LYS:HE3	4:D:2:LYS:HA	2.01	0.43
4:D:59:ALA:HA	4:D:79:MET:HE3	2.01	0.43
4:D:167:PHE:O	4:D:169:SER:N	2.52	0.43
4:H:143:LYS:CA	4:H:190:ILE:HD12	2.43	0.43
4:D:113:LYS:NZ	4:D:117:ASP:OD2	2.51	0.43
4:D:138:LEU:HD13	4:D:167:PHE:CD2	2.53	0.43
1:E:154:LEU:HD12	1:E:154:LEU:HA	1.93	0.43
4:H:182:LEU:HD12	4:H:182:LEU:HA	1.80	0.42
1:A:12:PHE:CD1	1:A:12:PHE:C	2.92	0.42
4:D:140:LYS:O	4:D:143:LYS:HB3	2.19	0.42
1:A:17:ASP:O	1:A:18:GLN:HB2	2.19	0.42
1:E:42:VAL:O	1:E:42:VAL:HG22	2.20	0.42
4:H:1:MET:HE2	4:H:132:TRP:HE3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:THR:HG23	2:B:7:PHE:CD1	2.55	0.42
4:D:152:ASP:O	4:D:158:VAL:HG21	2.19	0.42
2:F:17:PHE:CZ	2:F:83:TYR:HB2	2.54	0.42
1:A:109:ILE:HD11	1:A:119:VAL:HG21	2.01	0.42
2:F:52:GLU:CD	2:F:55:ARG:HH22	2.21	0.42
4:D:193:TYR:CE1	4:H:54:GLN:NE2	2.88	0.42
4:H:126:LYS:HE3	4:H:130:GLU:OE1	2.20	0.42
4:H:151:LEU:HB2	4:H:191:LYS:HD2	2.02	0.42
2:B:109:LEU:C	2:B:109:LEU:HD12	2.39	0.42
1:E:113:THR:OG1	1:E:114:PRO:HA	2.20	0.42
4:H:10:LYS:HD2	4:H:120:TYR:OH	2.20	0.42
1:A:113:THR:OG1	1:A:114:PRO:HA	2.20	0.42
4:D:47:LEU:H	4:D:47:LEU:CD2	2.33	0.42
4:D:144:ILE:O	4:D:147:LYS:HB2	2.18	0.42
1:E:70:LEU:HD13	2:F:9:TRP:CB	2.47	0.42
1:E:135:THR:CG2	1:E:148:PHE:HB2	2.49	0.42
1:E:162:ASP:HA	1:E:176:LYS:O	2.19	0.42
4:H:75:ILE:HD11	4:H:118:LEU:HA	2.02	0.42
1:A:73:MSE:HG2	3:C:316:LEU:CD1	2.50	0.42
2:F:176:GLU:HG3	2:F:183:PRO:HB3	2.02	0.42
4:H:16:VAL:HG21	4:H:81:LEU:CD1	2.48	0.42
3:C:310:LYS:NZ	4:D:12:GLN:OE1	2.53	0.41
4:D:51:LYS:CG	4:D:104:ILE:HG23	2.49	0.41
4:D:59:ALA:HA	4:D:79:MET:HE1	2.01	0.41
4:H:6:GLU:O	4:H:8:PRO:HD3	2.20	0.41
2:F:152:ASP:OD2	2:F:152:ASP:C	2.59	0.41
1:E:160:VAL:HG21	1:E:177:HIS:CE1	2.55	0.41
1:E:162:ASP:HB2	1:E:175:LEU:CD2	2.51	0.41
2:F:107:GLN:C	2:F:109:LEU:H	2.24	0.41
1:E:99:LEU:CD1	1:E:100:ARG:HG2	2.40	0.41
2:F:38:VAL:HG12	2:F:39:ARG:N	2.36	0.41
2:F:64:GLN:HG3	4:H:15:PHE:CE2	2.54	0.41
2:F:65:LYS:HE3	2:F:69:GLU:OE1	2.21	0.41
2:B:180:VAL:HG21	2:B:184:LEU:CD1	2.51	0.41
4:D:6:GLU:O	4:D:8:PRO:HD3	2.21	0.41
3:G:310:LYS:HG2	3:G:311:GLN:O	2.21	0.41
2:B:129:VAL:HB	2:B:159:VAL:HG21	2.02	0.41
4:D:182:LEU:HD12	4:D:182:LEU:HA	1.83	0.41
2:F:46:GLU:OE2	2:F:48:ARG:NH2	2.46	0.41
4:D:14:HIS:CD2	4:D:78:MET:SD	3.14	0.41
1:E:65:VAL:HB	3:G:313:THR:HG21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:27:LEU:HD13	2:F:27:LEU:HA	1.95	0.41
4:H:132:TRP:CH2	4:H:206:PHE:HA	2.56	0.41
1:A:48:PHE:CD1	2:B:89:PHE:CD2	3.09	0.41
4:D:155:ASP:OD1	4:D:155:ASP:C	2.59	0.41
2:F:107:GLN:HB3	2:F:109:LEU:HD21	2.01	0.41
3:G:311:GLN:HA	3:G:311:GLN:OE1	2.21	0.41
4:H:39:GLU:HA	4:H:42:LYS:HG3	2.03	0.41
4:H:41:THR:HG21	4:H:95:ASN:HA	2.03	0.41
2:B:2:ASP:CG	2:B:6:ARG:NH1	2.75	0.40
2:F:13:PHE:CD2	2:F:28:GLU:HG3	2.56	0.40
2:F:114:LEU:H	2:F:114:LEU:CD2	2.24	0.40
4:D:99:GLN:NE2	4:D:102:ARG:HD2	2.36	0.40
1:E:85:VAL:HA	1:E:86:PRO:HD2	1.93	0.40
4:D:47:LEU:CD2	4:D:47:LEU:N	2.84	0.40
2:B:52:GLU:OE1	2:B:55:ARG:CZ	2.70	0.40
1:E:15:ASN:ND2	1:E:70:LEU:HD23	2.37	0.40
1:E:89:VAL:CG2	1:E:174:LEU:HD23	2.52	0.40
4:H:191:LYS:HE3	4:H:191:LYS:CA	2.51	0.40
1:A:108:PHE:CD1	1:A:108:PHE:N	2.89	0.40
4:D:39:GLU:CD	4:D:39:GLU:N	2.75	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	179/181 (99%)	167 (93%)	10 (6%)	2 (1%)	14	30
1	E	179/181 (99%)	166 (93%)	11 (6%)	2 (1%)	14	30
2	B	188/190 (99%)	174 (93%)	12 (6%)	2 (1%)	14	30
2	F	188/190 (99%)	174 (93%)	12 (6%)	2 (1%)	14	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	11/13 (85%)	11 (100%)	0	0	100	100
3	G	11/13 (85%)	11 (100%)	0	0	100	100
4	D	212/216 (98%)	203 (96%)	6 (3%)	3 (1%)	11	22
4	H	212/216 (98%)	202 (95%)	7 (3%)	3 (1%)	11	22
All	All	1180/1200 (98%)	1108 (94%)	58 (5%)	14 (1%)	13	27

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	111	HIS
4	D	169	SER
1	E	180	PHE
2	F	111	HIS
4	H	169	SER
2	B	113	ASN
2	F	113	ASN
4	H	200	LEU
1	A	180	PHE
4	D	200	LEU
4	H	168	GLY
4	D	168	GLY
1	E	136	VAL
1	A	136	VAL

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	166/163 (102%)	154 (93%)	12 (7%)	14	29
1	E	166/163 (102%)	156 (94%)	10 (6%)	19	39
2	B	171/171 (100%)	156 (91%)	15 (9%)	10	19
2	F	171/171 (100%)	162 (95%)	9 (5%)	22	45
3	C	12/12 (100%)	12 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	G	11/12 (92%)	9 (82%)	2 (18%)	1 2
4	D	197/198 (100%)	181 (92%)	16 (8%)	11 23
4	H	197/198 (100%)	183 (93%)	14 (7%)	14 29
All	All	1091/1088 (100%)	1013 (93%)	78 (7%)	14 29

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	MSE
1	A	40	GLU
1	A	42	VAL
1	A	78	ASN
1	A	90	THR
1	A	120	THR
1	A	128	VAL
1	A	136	VAL
1	A	138	LEU
1	A	159	ASP
1	A	177	HIS
1	A	180	PHE
2	B	3	THR
2	B	23	ARG
2	B	27	LEU
2	B	29	ARG
2	B	38	VAL
2	B	43	ASP
2	B	64	GLN
2	B	70	GLN
2	B	75	VAL
2	B	80	ARG
2	B	88	SER
2	B	93	ARG
2	B	100	THR
2	B	126	SER
2	B	160	MET
4	D	17	GLN
4	D	18	ASN
4	D	39	GLU
4	D	40	GLU
4	D	47	LEU
4	D	50	LEU

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Mol	Chain	Res	Type
4	D	51	LYS
4	D	63	VAL
4	D	74	GLU
4	D	83	LEU
4	D	126	LYS
4	D	160	ILE
4	D	169	SER
4	D	183	LEU
4	D	187	VAL
4	D	203	THR
1	E	23	MSE
1	E	25	ASP
1	E	42	VAL
1	E	71	GLU
1	E	99	LEU
1	E	102	PRO
1	E	162	ASP
1	E	171	ASP
1	E	175	LEU
1	E	177	HIS
2	F	27	LEU
2	F	64	GLN
2	F	92	GLN
2	F	93	ARG
2	F	105	LYS
2	F	106	THR
2	F	136	GLN
2	F	160	MET
2	F	176	GLU
3	G	310	LYS
3	G	314	LEU
4	H	6	GLU
4	H	17	GLN
4	H	23	VAL
4	H	45	LEU
4	H	50	LEU
4	H	51	LYS
4	H	63	VAL
4	H	72	TYR
4	H	74	GLU
4	H	83	LEU
4	H	145	LYS

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Mol	Chain	Res	Type
4	H	160	ILE
4	H	182	LEU
4	H	191	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	78	ASN
2	B	19	ASN
2	B	64	GLN
2	B	70	GLN
2	B	81	HIS
2	B	107	GLN
2	B	134	ASN
4	D	17	GLN
4	D	18	ASN
4	D	53	ASN
4	D	64	ASN
4	D	90	GLN
4	D	99	GLN
4	D	103	ASN
1	E	57	GLN
1	E	143	HIS
1	E	149	HIS
1	E	177	HIS
2	F	19	ASN
2	F	81	HIS
2	F	92	GLN
2	F	107	GLN
2	F	110	GLN
2	F	113	ASN
2	F	156	GLN
2	F	174	GLN
4	H	17	GLN
4	H	34	ASN
4	H	95	ASN
4	H	161	ASN
4	H	172	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	PO4	H	214	-	4,4,4	1.57	0	6,6,6	0.41	0
5	PO4	E	204	-	4,4,4	1.54	0	6,6,6	0.42	0
5	PO4	D	214	-	4,4,4	1.64	0	6,6,6	0.46	0
5	PO4	C	202	-	4,4,4	1.51	0	6,6,6	0.44	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	178/181 (98%)	-0.23	4 (2%) 62 56	26, 39, 59, 89	0
1	E	178/181 (98%)	-0.27	3 (1%) 70 66	25, 38, 59, 93	0
2	B	190/190 (100%)	-0.11	11 (5%) 23 17	28, 43, 82, 108	0
2	F	190/190 (100%)	0.02	12 (6%) 20 15	29, 45, 83, 106	0
3	C	13/13 (100%)	0.11	0 100 100	32, 40, 52, 60	0
3	G	13/13 (100%)	-0.09	0 100 100	35, 40, 50, 58	0
4	D	214/216 (99%)	-0.21	4 (1%) 66 62	30, 45, 65, 85	0
4	H	214/216 (99%)	-0.06	6 (2%) 53 46	27, 46, 68, 86	0
All	All	1190/1200 (99%)	-0.14	40 (3%) 45 38	25, 43, 71, 108	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	1	GLY	6.9
2	B	109	LEU	6.5
2	B	111	HIS	5.1
2	F	165	PRO	4.9
2	B	1	GLY	4.8
4	D	213	ASP	4.3
1	E	1	ILE	4.2
2	F	109	LEU	4.1
1	E	180	PHE	3.9
4	H	150	LYS	3.8
4	H	213	ASP	3.8
2	F	111	HIS	3.3
2	B	112	HIS	3.0
2	F	112	HIS	3.0
2	B	190	ALA	3.0
2	F	166	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
4	D	40	GLU	2.9
2	F	190	ALA	2.8
4	H	154	ARG	2.7
2	B	165	PRO	2.7
4	D	0	SER	2.7
1	A	1	ILE	2.6
2	B	168	GLY	2.6
4	H	39	GLU	2.6
2	F	108	PRO	2.5
2	B	107	GLN	2.5
2	F	167	SER	2.5
2	B	108	PRO	2.4
2	B	166	ARG	2.4
2	F	168	GLY	2.3
2	F	164	VAL	2.3
4	D	37	ASN	2.2
1	A	2	LYS	2.2
1	A	179	GLU	2.2
1	A	181	ASP	2.1
1	E	179	GLU	2.1
2	B	164	VAL	2.1
2	F	134	ASN	2.1
4	H	151	LEU	2.0
4	H	149	GLN	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	PO4	C	202	5/5	0.88	0.23	103,103,104,104	0
5	PO4	E	204	5/5	0.90	0.19	104,106,106,106	0
5	PO4	H	214	5/5	0.90	0.28	87,88,89,89	0
5	PO4	D	214	5/5	0.94	0.23	85,85,86,86	0

6.5 Other polymers (i)

There are no such residues in this entry.