



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:22 PM UTC

PDB ID : 1XCT / pdb_00001xct
Title : Complex HCV core-Fab 19D9D6-Protein L mutant (D55A, L57H, Y64W) in space group P21212
Authors : Menez, R.; Housden, N.G.; Harrison, S.; Jolivet-Reynaud, C.; Gore, M.G.; Stura, E.A.
Deposited on : 2004-09-03
Resolution : 3.05 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

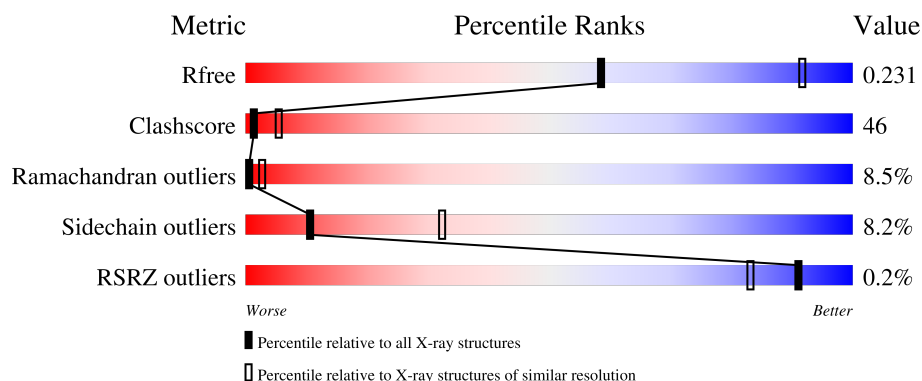
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	P	44	2% 16% 23% 23% 7% 32%
1	Q	44	23% 23% . . 50%
2	A	220	42% 50% 7%
2	C	220	36% 50% 13% .
3	B	218	41% 45% 13%

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Mol	Chain	Length	Quality of chain
3	D	218	34%54%11%
4	L	80	34%44%9%12%
4	M	80	28%45%14%11%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8552 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 Capsid protein C.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	P	30	Total	C	N	O	0	0	0
			225	141	48	36			
1	Q	22	Total	C	N	O	0	0	0
			155	98	32	25			

- Molecule 2 is a protein called Monoclonal antibody 19D9D6 Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	220	Total	C	N	O	S	0	0	0
			1708	1063	291	346	8			
2	C	220	Total	C	N	O	S	0	0	0
			1708	1063	291	346	8			

- Molecule 3 is a protein called Monoclonal antibody 19D9D6 Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	218	Total	C	N	O	S	0	0	0
			1660	1058	270	325	7			
3	D	218	Total	C	N	O	S	0	0	0
			1654	1052	270	325	7			

- Molecule 4 is a protein called Protein L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	70	Total	C	N	O	S	0	0	0
			547	346	90	110	1			
4	M	71	Total	C	N	O	S	0	0	0
			556	352	92	111	1			

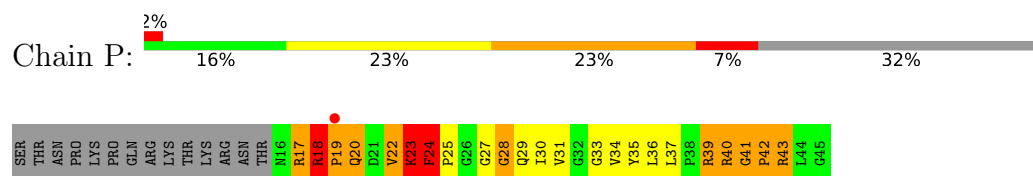
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	P	15	Total 15	O 15	0	0
5	Q	10	Total 10	O 10	0	0
5	A	91	Total 91	O 91	0	0
5	B	83	Total 83	O 83	0	0
5	L	21	Total 21	O 21	0	0
5	C	46	Total 46	O 46	0	0
5	D	57	Total 57	O 57	0	0
5	M	16	Total 16	O 16	0	0

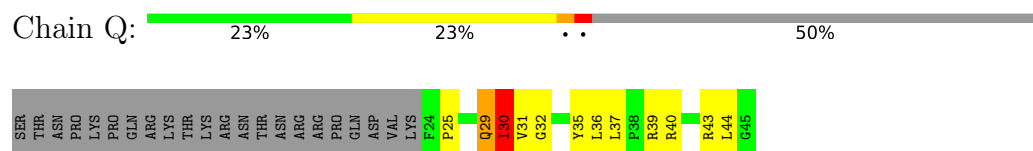
3 Residue-property plots [i](#)

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: Capsid protein C



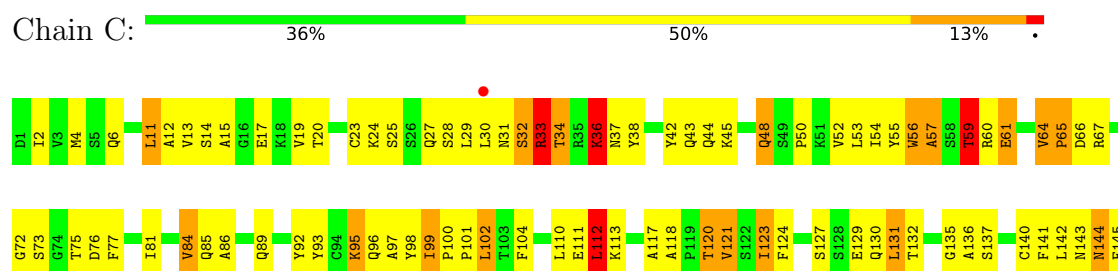
- Molecule 1: Capsid protein C

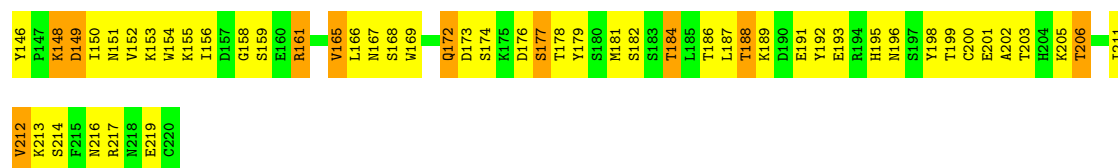


- Molecule 2: Monoclonal antibody 19D9D6 Light chain



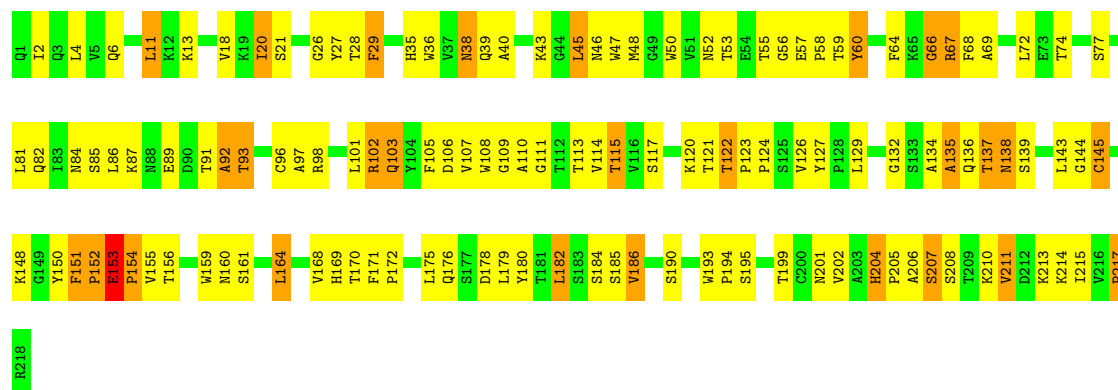
- Molecule 2: Monoclonal antibody 19D9D6 Light chain





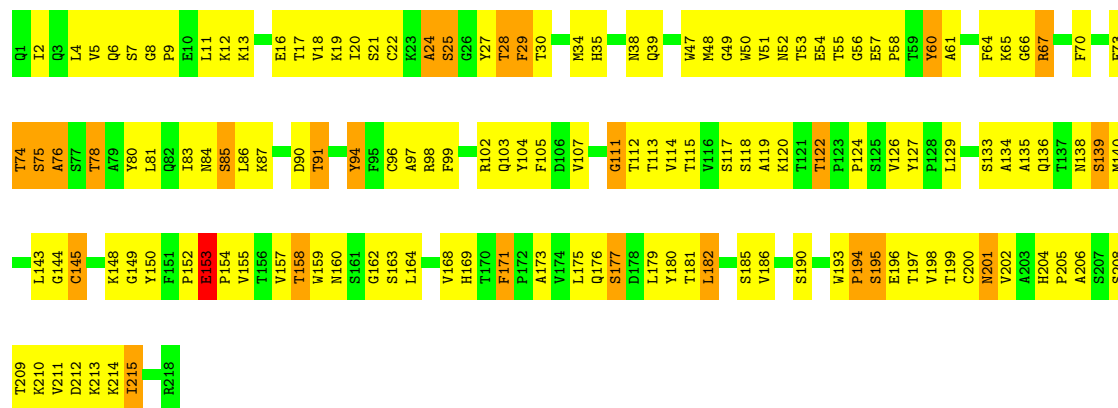
• Molecule 3: Monoclonal antibody 19D9D6 Heavy chain

Chain B: 41% 45% 13%



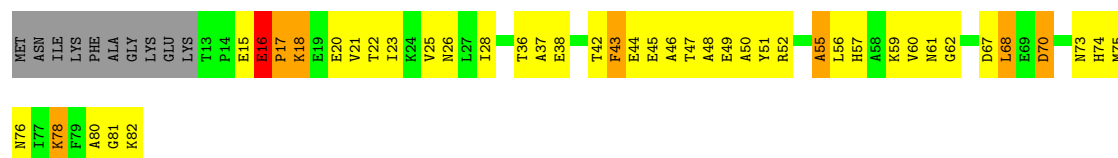
• Molecule 3: Monoclonal antibody 19D9D6 Heavy chain

Chain D: 34% 54% 11%

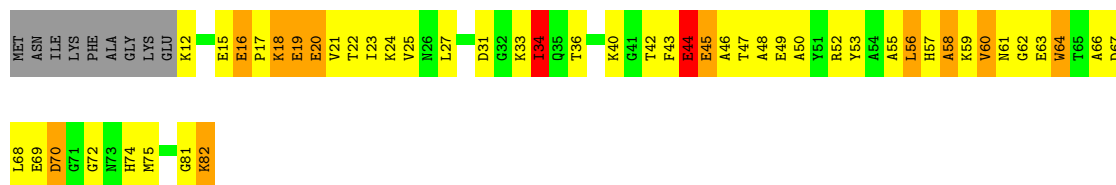


• Molecule 4: Protein L

Chain L: 34% 44% 9% 12%



• Molecule 4: Protein L



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	129.50Å 222.48Å 43.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.05 20.00 – 3.05	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-3.05) 89.0 (20.00-3.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 3.04Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.193 , 0.329 0.205 , 0.231	Depositor DCC
R_{free} test set	1161 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	54.2	Xtriage
Anisotropy	0.244	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 57.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8552	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	P	0.76	0/230	1.54	8/307 (2.6%)
1	Q	0.43	0/158	0.94	1/211 (0.5%)
2	A	0.48	0/1745	0.97	7/2366 (0.3%)
2	C	0.43	0/1745	0.94	8/2366 (0.3%)
3	B	0.51	0/1707	1.05	14/2335 (0.6%)
3	D	0.44	0/1700	0.91	3/2326 (0.1%)
4	L	0.48	0/558	1.07	5/751 (0.7%)
4	M	0.50	0/567	0.96	2/762 (0.3%)
All	All	0.48	0/8410	1.00	48/11424 (0.4%)

There are no bond length outliers.

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	41	GLY	CA-C-N	8.95	131.03	119.84
1	P	41	GLY	C-N-CA	8.95	131.03	119.84
2	C	34	THR	N-CA-C	-7.74	104.36	113.88
2	C	121	VAL	N-CA-C	7.65	119.13	108.12
4	L	16	GLU	CA-C-N	7.13	127.17	119.90
4	L	16	GLU	C-N-CA	7.13	127.17	119.90
3	D	148	LYS	N-CA-C	7.09	121.23	109.46
3	B	154	PRO	N-CA-C	6.86	121.26	110.50
3	B	204	HIS	CA-C-N	6.80	128.34	119.84
3	B	204	HIS	C-N-CA	6.80	128.34	119.84
3	B	103	GLN	N-CA-C	6.72	120.92	111.92
1	P	24	PHE	N-CA-C	6.33	123.80	109.81
3	B	148	LYS	N-CA-C	6.29	118.11	108.42
3	B	52	ASN	N-CA-C	-6.28	100.36	109.59
2	A	212	VAL	N-CA-C	6.27	117.77	107.24
1	P	18	ARG	N-CA-C	6.24	123.61	109.81
4	L	17	PRO	N-CA-C	6.17	120.90	111.15
3	D	153	GLU	N-CA-C	6.11	123.32	109.81
2	C	212	VAL	N-CA-C	6.00	118.00	108.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	102	ARG	N-CA-C	-5.92	105.82	113.16
3	B	153	GLU	N-CA-C	5.87	122.78	109.81
1	P	24	PHE	CA-C-N	-5.85	112.53	119.84
1	P	24	PHE	C-N-CA	-5.85	112.53	119.84
1	P	22	VAL	N-CA-C	5.80	121.42	109.34
3	B	207	SER	N-CA-C	-5.69	106.42	113.19
3	B	127	TYR	CA-C-N	5.61	126.47	120.13
3	B	127	TYR	C-N-CA	5.61	126.47	120.13
3	B	69	ALA	N-CA-C	5.60	117.55	108.26
2	C	102	LEU	N-CA-C	-5.58	102.22	110.48
4	L	70	ASP	N-CA-C	-5.53	106.12	112.86
2	A	34	THR	N-CA-C	-5.49	105.84	112.54
1	Q	30	ILE	N-CA-C	5.46	116.03	108.23
2	C	188	THR	N-CA-C	-5.37	103.31	110.55
2	A	143	ASN	N-CA-C	5.32	118.41	109.95
2	A	105	GLY	N-CA-C	-5.31	104.05	112.66
4	L	55	ALA	N-CA-C	-5.29	105.20	110.97
2	A	167	ASN	N-CA-C	5.28	118.09	109.59
4	M	64	TRP	N-CA-C	5.24	117.94	109.40
2	A	211	ILE	N-CA-C	-5.23	102.83	109.58
3	D	197	THR	N-CA-C	5.21	117.58	108.52
3	B	56	GLY	N-CA-C	-5.20	107.34	114.67
2	C	120	THR	N-CA-C	-5.19	100.79	109.24
2	C	143	ASN	N-CA-C	5.09	118.05	109.95
3	B	101	LEU	N-CA-C	-5.08	107.04	113.18
2	C	112	LEU	N-CA-C	5.07	117.85	109.85
4	M	63	GLU	N-CA-C	-5.05	103.73	110.55
2	A	66	ASP	N-CA-C	-5.05	107.19	113.19
1	P	19	PRO	N-CA-C	5.04	122.86	112.47

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	P	225	0	228	33	0
1	Q	155	0	161	15	0
2	A	1708	0	1658	124	0
2	C	1708	0	1658	190	0
3	B	1660	0	1615	133	0
3	D	1654	0	1608	171	0
4	L	547	0	522	54	0
4	M	556	0	535	70	0
5	A	91	0	0	4	0
5	B	83	0	0	4	0
5	C	46	0	0	2	0
5	D	57	0	0	2	0
5	L	21	0	0	2	0
5	M	16	0	0	2	0
5	P	15	0	0	0	0
5	Q	10	0	0	0	0
All	All	8552	0	7985	737	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 46.

All (737) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:196:ASN:HD21	2:A:218:ASN:HB3	1.19	1.03
4:M:19:GLU:HG2	4:M:40:LYS:HD2	1.42	1.02
3:D:157:VAL:HG12	3:D:158:THR:H	1.25	1.01
2:A:6:GLN:HG2	2:A:23:CYS:SG	2.07	0.94
2:C:19:VAL:HG12	2:C:81:ILE:HB	1.48	0.93
3:B:151:PHE:HB3	3:B:152:PRO:HD3	1.53	0.90
2:A:199:THR:HB	2:A:214:SER:HB2	1.52	0.89
2:A:3:VAL:H	2:A:26:SER:HB2	1.37	0.89
2:C:60:ARG:HG3	2:C:64:VAL:HB	1.55	0.88
1:Q:32:GLY:H	3:D:103:GLN:HE22	1.18	0.88
3:B:58:PRO:HB2	3:B:60:TYR:HE1	1.36	0.88
2:A:150:ILE:HD13	2:A:151:ASN:N	1.89	0.87
1:P:29:GLN:HE22	3:B:53:THR:H	1.19	0.87
2:A:18:LYS:HG3	2:A:82:SER:HA	1.57	0.87
4:M:62:GLY:HA3	4:M:81:GLY:H	1.39	0.86
2:A:150:ILE:HD13	2:A:151:ASN:H	1.40	0.85
2:A:119:PRO:HG2	2:A:211:ILE:HD12	1.57	0.85
3:B:121:THR:HG23	3:B:152:PRO:HG2	1.57	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:129:LEU:HB2	3:B:144:GLY:HA3	1.59	0.84
1:P:29:GLN:NE2	3:B:53:THR:H	1.76	0.84
2:C:60:ARG:NH2	2:C:66:ASP:HA	1.93	0.84
3:D:91:THR:HG23	3:D:115:THR:HA	1.59	0.83
3:D:157:VAL:HG12	3:D:158:THR:N	1.94	0.82
2:A:196:ASN:ND2	2:A:218:ASN:HB3	1.92	0.82
1:P:23:LYS:O	1:P:24:PHE:HB3	1.79	0.82
2:C:201:GLU:HG2	2:C:212:VAL:HG12	1.60	0.82
3:B:93:THR:HA	3:B:113:THR:HA	1.62	0.81
3:D:13:LYS:H	3:D:13:LYS:HD2	1.45	0.80
3:B:66:GLY:O	3:B:67:ARG:HB2	1.79	0.80
2:C:121:VAL:HG22	2:C:142:LEU:HA	1.65	0.79
2:A:43:GLN:HB2	2:A:53:LEU:HD11	1.65	0.78
4:L:15:GLU:HG3	4:L:16:GLU:H	1.48	0.77
2:C:37:ASN:HB2	2:C:57:ALA:HB2	1.66	0.77
2:A:3:VAL:H	2:A:26:SER:CB	1.99	0.76
4:M:82:LYS:NZ	4:M:82:LYS:HB3	2.00	0.76
4:L:56:LEU:HD23	4:L:56:LEU:O	1.86	0.76
3:D:6:GLN:HA	3:D:22:CYS:HA	1.67	0.76
2:A:112:LEU:HB3	2:A:172:GLN:HE22	1.51	0.76
3:D:9:PRO:HG3	3:D:205:PRO:HB2	1.68	0.75
3:D:13:LYS:HA	3:D:117:SER:O	1.86	0.75
1:P:24:PHE:CG	1:P:25:PRO:HD3	2.22	0.74
3:D:55:THR:HG22	3:D:57:GLU:HB2	1.67	0.74
3:B:202:VAL:CG1	3:B:211:VAL:HG22	2.16	0.74
2:C:169:TRP:CE2	2:C:181:MET:HG3	2.22	0.74
2:C:13:VAL:HG21	2:C:84:VAL:HG21	1.70	0.73
2:A:113:LYS:HA	2:A:146:TYR:OH	1.88	0.73
4:M:48:ALA:O	4:M:52:ARG:HG2	1.88	0.73
4:M:62:GLY:HA3	4:M:81:GLY:N	2.03	0.73
4:M:55:ALA:C	4:M:57:HIS:H	1.96	0.72
2:C:123:ILE:HG12	2:C:200:CYS:SG	2.30	0.72
2:C:100:PRO:HB2	2:C:101:PRO:HD3	1.72	0.72
4:M:19:GLU:HG2	4:M:40:LYS:CD	2.19	0.72
3:B:27:TYR:CZ	3:B:98:ARG:HD2	2.25	0.71
2:A:65:PRO:HB3	2:A:67:ARG:HG3	1.73	0.71
2:C:36:LYS:HE2	2:C:36:LYS:HA	1.71	0.71
2:C:99:ILE:HG13	2:C:101:PRO:HD2	1.72	0.71
2:C:137:SER:OG	2:C:186:THR:HG22	1.90	0.71
4:M:52:ARG:HD2	5:M:88:HOH:O	1.90	0.71
3:D:4:LEU:HD23	3:D:24:ALA:HA	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:19:PRO:O	1:P:20:GLN:HB3	1.91	0.70
1:P:27:GLY:HA2	1:P:30:ILE:HD11	1.72	0.70
2:C:176:ASP:O	2:C:177:SER:HB2	1.89	0.70
3:D:182:LEU:C	3:D:182:LEU:HD12	2.16	0.70
2:A:188:THR:OG1	2:A:191:GLU:HG3	1.91	0.70
2:A:142:LEU:HD23	2:A:142:LEU:N	2.07	0.70
2:A:196:ASN:HD21	2:A:218:ASN:CB	2.00	0.70
2:C:182:SER:HB2	3:D:171:PHE:CD2	2.27	0.70
3:B:161:SER:N	3:B:201:ASN:HD21	1.89	0.70
4:M:53:TYR:O	4:M:57:HIS:HB3	1.91	0.70
4:L:48:ALA:HB1	4:L:52:ARG:HH21	1.55	0.69
2:C:67:ARG:HH11	2:C:85:GLN:HG3	1.55	0.69
3:B:151:PHE:HB3	3:B:152:PRO:CD	2.22	0.69
4:M:22:THR:HG22	4:M:40:LYS:CD	2.22	0.69
3:B:161:SER:H	3:B:201:ASN:HD21	1.39	0.69
3:D:30:THR:HG23	3:D:54:GLU:HG3	1.72	0.69
3:D:157:VAL:CG1	3:D:158:THR:H	2.03	0.69
1:Q:29:GLN:HG2	3:D:52:ASN:HD22	1.57	0.69
3:B:4:LEU:HD23	3:B:107:VAL:HG22	1.75	0.69
3:D:74:THR:C	3:D:76:ALA:H	2.01	0.69
2:C:151:ASN:HB3	2:C:203:THR:HB	1.74	0.68
3:D:215:ILE:N	3:D:215:ILE:HD12	2.08	0.68
4:M:20:GLU:HG2	4:M:42:THR:HA	1.75	0.68
2:C:97:ALA:HB1	3:D:103:GLN:HE21	1.57	0.68
2:C:60:ARG:CG	2:C:64:VAL:HB	2.23	0.68
1:P:33:GLY:HA2	1:P:36:LEU:HD13	1.76	0.68
2:A:172:GLN:NE2	2:A:177:SER:HB3	2.08	0.68
1:Q:31:VAL:HG21	3:D:35:HIS:HE1	1.57	0.68
2:A:199:THR:CB	2:A:214:SER:HB2	2.24	0.68
1:Q:32:GLY:N	3:D:103:GLN:HE22	1.92	0.67
2:C:55:TYR:HE1	2:C:61:GLU:HB3	1.58	0.67
3:D:143:LEU:HD22	3:D:215:ILE:HG21	1.76	0.67
3:D:171:PHE:N	3:D:171:PHE:CD1	2.62	0.67
1:P:22:VAL:O	1:P:23:LYS:HG2	1.95	0.67
2:A:121:VAL:O	2:A:213:LYS:HE2	1.93	0.67
3:D:171:PHE:HD1	3:D:171:PHE:H	1.40	0.67
4:L:25:VAL:HG22	4:L:75:MET:HB3	1.76	0.67
3:B:151:PHE:O	3:B:153:GLU:N	2.28	0.67
3:D:87:LYS:HG2	3:D:90:ASP:OD2	1.94	0.67
4:L:70:ASP:HB3	4:L:74:HIS:H	1.59	0.67
3:B:6:GLN:HE22	3:B:111:GLY:HA2	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:6:GLN:HG3	2:A:105:GLY:HA3	1.77	0.67
3:D:60:TYR:N	3:D:60:TYR:CD2	2.63	0.66
4:M:68:LEU:HD22	4:M:72:GLY:HA2	1.77	0.66
1:P:24:PHE:CD2	1:P:25:PRO:HD3	2.29	0.66
2:C:199:THR:HG22	2:C:214:SER:CB	2.26	0.66
4:M:82:LYS:HB3	4:M:82:LYS:HZ3	1.60	0.66
3:B:202:VAL:HG13	3:B:211:VAL:HG22	1.77	0.66
3:B:152:PRO:O	3:B:154:PRO:HD2	1.96	0.66
3:B:143:LEU:HB2	3:B:186:VAL:HG23	1.78	0.66
4:M:60:VAL:N	4:M:82:LYS:HE2	2.10	0.66
3:D:74:THR:HG22	3:D:75:SER:H	1.61	0.65
3:B:91:THR:HG23	3:B:115:THR:HA	1.78	0.65
3:D:153:GLU:OE1	3:D:173:ALA:HB3	1.97	0.65
4:M:22:THR:HG22	4:M:40:LYS:HD3	1.79	0.65
2:C:199:THR:CB	2:C:214:SER:HB3	2.26	0.65
3:B:126:VAL:HG21	3:B:202:VAL:HG11	1.78	0.65
2:C:153:LYS:HE3	2:C:155:LYS:HE3	1.76	0.65
3:D:160:ASN:HB3	3:D:163:SER:HB2	1.79	0.65
2:A:24:LYS:HA	2:A:75:THR:O	1.96	0.65
2:A:33:ARG:HA	2:A:33:ARG:NE	2.11	0.65
2:C:148:LYS:HB3	2:C:179:TYR:CD1	2.32	0.65
2:C:186:THR:HG21	3:D:176:GLN:HE22	1.62	0.65
1:Q:31:VAL:HG23	3:D:99:PHE:CZ	2.33	0.64
3:B:124:PRO:HB3	3:B:150:TYR:HB3	1.78	0.64
2:A:33:ARG:HA	2:A:33:ARG:HE	1.62	0.64
2:C:37:ASN:HD22	2:C:57:ALA:HB2	1.63	0.64
3:B:151:PHE:O	3:B:152:PRO:C	2.41	0.64
4:L:67:ASP:OD1	4:L:78:LYS:HE3	1.96	0.64
4:L:68:LEU:H	4:L:68:LEU:HD22	1.62	0.64
2:C:165:VAL:HA	2:C:184:THR:O	1.99	0.63
4:M:52:ARG:O	4:M:56:LEU:HD13	1.98	0.63
4:M:17:PRO:O	4:M:18:LYS:HB3	1.98	0.63
3:B:6:GLN:NE2	3:B:111:GLY:H	1.96	0.63
2:C:127:SER:OG	3:D:127:TYR:HB3	1.99	0.63
3:B:59:THR:C	3:B:60:TYR:HD1	2.07	0.63
1:P:18:ARG:HD3	1:P:19:PRO:HD3	1.80	0.63
2:A:116:ASP:OD1	2:A:205:LYS:HE2	1.99	0.63
3:B:38:ASN:HD21	3:B:46:ASN:HB3	1.64	0.63
1:P:18:ARG:CD	1:P:19:PRO:HD3	2.28	0.63
2:A:155:LYS:HA	2:A:159:SER:O	1.99	0.63
2:C:19:VAL:CG1	2:C:81:ILE:HB	2.26	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:175:LEU:HD23	3:B:176:GLN:N	2.14	0.62
3:D:24:ALA:O	3:D:25:SER:HB2	1.99	0.62
3:B:168:VAL:HG22	3:B:186:VAL:HG12	1.80	0.62
2:C:36:LYS:HG3	2:C:56:TRP:HB2	1.80	0.62
2:C:186:THR:HG21	3:D:176:GLN:NE2	2.14	0.62
2:A:24:LYS:C	2:A:24:LYS:HD3	2.25	0.62
3:D:51:VAL:HG23	3:D:57:GLU:O	1.99	0.62
3:D:65:LYS:HD2	3:D:66:GLY:H	1.64	0.62
3:B:122:THR:HG21	3:B:179:LEU:HD21	1.80	0.62
3:B:182:LEU:O	3:B:182:LEU:HD23	2.00	0.62
2:C:13:VAL:HG11	2:C:19:VAL:HG23	1.81	0.62
2:A:54:ILE:HG23	2:A:59:THR:O	2.00	0.61
2:C:11:LEU:HD23	4:M:36:THR:O	2.00	0.61
4:M:47:THR:O	4:M:50:ALA:HB3	2.00	0.61
4:L:17:PRO:HB2	5:L:91:HOH:O	2.00	0.61
2:A:206:THR:O	2:A:207:SER:HB2	2.00	0.61
2:C:150:ILE:HG23	2:C:181:MET:HE3	1.81	0.61
3:D:168:VAL:HG22	3:D:186:VAL:HG23	1.82	0.61
4:L:15:GLU:HG3	4:L:16:GLU:N	2.16	0.61
3:D:201:ASN:HB3	3:D:212:ASP:OD2	2.00	0.61
4:M:18:LYS:O	4:M:19:GLU:HB2	2.00	0.61
3:D:30:THR:HA	3:D:53:THR:CB	2.31	0.61
2:C:67:ARG:HG2	2:C:67:ARG:HH21	1.63	0.61
3:B:155:VAL:HG23	3:B:155:VAL:O	2.01	0.61
1:P:17:ARG:O	3:B:57:GLU:CD	2.44	0.60
4:M:21:VAL:O	4:M:40:LYS:HA	2.00	0.60
2:A:199:THR:HB	2:A:214:SER:CB	2.29	0.60
2:C:150:ILE:HG12	2:C:151:ASN:N	2.15	0.60
4:M:23:ILE:HD13	4:M:46:ALA:HB1	1.83	0.60
3:D:60:TYR:N	3:D:60:TYR:HD2	1.98	0.60
2:A:187:LEU:HB2	2:A:191:GLU:OE2	2.01	0.60
2:C:169:TRP:CZ2	2:C:181:MET:HE2	2.36	0.60
4:M:59:LYS:O	4:M:60:VAL:HB	2.00	0.60
2:C:182:SER:HB2	3:D:171:PHE:CE2	2.37	0.60
2:A:141:PHE:CE1	3:B:185:SER:HB3	2.37	0.60
4:L:28:ILE:HD12	4:L:28:ILE:N	2.16	0.60
2:C:100:PRO:HB2	2:C:101:PRO:CD	2.32	0.60
2:A:87:GLU:HB3	5:A:243:HOH:O	2.02	0.59
3:B:151:PHE:CB	3:B:152:PRO:HD3	2.28	0.59
2:C:42:TYR:HE1	2:C:95:LYS:HB2	1.66	0.59
2:A:10:SER:OG	4:L:38:GLU:HB2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:119:PRO:HG2	2:A:211:ILE:CD1	2.31	0.59
4:L:51:TYR:CD2	4:M:43:PHE:HZ	2.21	0.59
2:C:148:LYS:HB3	2:C:179:TYR:CE1	2.37	0.59
2:C:55:TYR:CE1	2:C:61:GLU:HB3	2.37	0.59
4:M:22:THR:C	4:M:23:ILE:HD12	2.27	0.59
2:C:14:SER:O	2:C:17:GLU:HB2	2.03	0.59
2:C:201:GLU:HG2	2:C:212:VAL:CG1	2.32	0.59
3:D:144:GLY:O	3:D:159:TRP:HH2	1.86	0.59
4:M:68:LEU:HD21	4:M:75:MET:HE2	1.83	0.59
3:D:13:LYS:HD2	3:D:13:LYS:N	2.18	0.59
3:B:129:LEU:HB2	3:B:144:GLY:CA	2.32	0.59
2:C:199:THR:HA	2:C:214:SER:HB3	1.83	0.59
3:D:38:ASN:HB3	3:D:94:TYR:CD1	2.38	0.59
1:Q:25:PRO:HD2	3:D:54:GLU:OE1	2.02	0.58
3:B:86:LEU:C	3:B:87:LYS:HD2	2.27	0.58
1:P:27:GLY:HA3	1:P:43:ARG:HH11	1.68	0.58
2:C:60:ARG:HD2	2:C:65:PRO:O	2.03	0.58
2:A:65:PRO:CB	2:A:67:ARG:HG3	2.33	0.58
2:C:97:ALA:CB	3:D:103:GLN:HB3	2.33	0.58
2:A:12:ALA:HB3	4:L:36:THR:HB	1.84	0.58
2:A:137:SER:HA	2:A:185:LEU:O	2.04	0.58
3:B:20:ILE:HD12	3:B:21:SER:N	2.19	0.58
4:L:16:GLU:OE2	4:L:17:PRO:HD2	2.03	0.58
4:L:22:THR:C	4:L:23:ILE:HD12	2.28	0.58
2:C:130:GLN:HG2	2:C:135:GLY:O	2.03	0.58
4:M:23:ILE:HG22	4:M:25:VAL:HG23	1.84	0.58
2:A:95:LYS:NZ	2:A:95:LYS:HB3	2.19	0.58
3:B:115:THR:HB	5:B:248:HOH:O	2.04	0.58
3:B:153:GLU:HG2	3:B:180:TYR:CE1	2.39	0.58
2:C:123:ILE:HD13	2:C:124:PHE:H	1.69	0.58
3:D:58:PRO:HB2	3:D:60:TYR:CE2	2.39	0.58
3:D:126:VAL:CG2	3:D:211:VAL:HG11	2.34	0.58
4:M:34:ILE:HG12	4:M:34:ILE:O	2.04	0.58
2:C:95:LYS:HE3	2:C:102:LEU:HD13	1.86	0.57
3:D:4:LEU:HD21	3:D:34:MET:HE1	1.86	0.57
3:D:160:ASN:CB	3:D:163:SER:HB2	2.34	0.57
4:M:19:GLU:O	4:M:20:GLU:HB2	2.03	0.57
4:M:55:ALA:O	4:M:57:HIS:N	2.36	0.57
2:C:56:TRP:O	2:C:57:ALA:HB3	2.02	0.57
2:C:169:TRP:NE1	2:C:181:MET:HG3	2.19	0.57
4:M:55:ALA:C	4:M:57:HIS:N	2.63	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:38:ASN:ND2	3:B:46:ASN:HB3	2.19	0.57
2:C:14:SER:HB2	2:C:17:GLU:OE2	2.04	0.57
3:D:193:TRP:HA	3:D:194:PRO:C	2.28	0.57
4:M:42:THR:OG1	4:M:45:GLU:HG3	2.04	0.57
2:A:69:THR:O	2:A:79:LEU:HD12	2.05	0.57
3:D:9:PRO:CG	3:D:205:PRO:HB2	2.34	0.57
2:A:187:LEU:HD11	2:A:192:TYR:HB2	1.87	0.57
3:B:182:LEU:HD23	3:B:182:LEU:C	2.30	0.57
4:L:23:ILE:HD12	4:L:23:ILE:N	2.20	0.57
2:C:43:GLN:HB2	2:C:53:LEU:HD11	1.86	0.57
2:C:199:THR:CA	2:C:214:SER:HB3	2.35	0.57
2:C:24:LYS:HG3	2:C:76:ASP:OD2	2.04	0.57
3:D:48:MET:HA	3:D:64:PHE:CE1	2.39	0.57
3:D:12:LYS:HG3	3:D:18:VAL:HB	1.87	0.57
3:B:4:LEU:CD2	3:B:107:VAL:HG22	2.34	0.57
1:P:19:PRO:O	1:P:20:GLN:CB	2.53	0.56
2:C:4:MET:HE3	2:C:23:CYS:SG	2.45	0.56
2:C:121:VAL:CG2	2:C:142:LEU:HD22	2.35	0.56
3:D:74:THR:HG22	3:D:75:SER:N	2.19	0.56
3:D:94:TYR:O	3:D:111:GLY:HA2	2.04	0.56
2:C:12:ALA:HA	2:C:111:GLU:O	2.05	0.56
3:D:30:THR:HA	3:D:53:THR:HB	1.87	0.56
2:C:176:ASP:OD2	2:C:178:THR:HG23	2.06	0.56
3:D:173:ALA:HA	3:D:182:LEU:HB3	1.88	0.56
4:M:31:ASP:OD1	4:M:33:LYS:HG3	2.06	0.56
3:B:126:VAL:HB	3:B:211:VAL:HG21	1.87	0.56
1:P:27:GLY:HA3	1:P:43:ARG:NH1	2.20	0.56
3:B:124:PRO:HD3	3:B:204:HIS:HD1	1.70	0.56
4:L:57:HIS:C	4:L:59:LYS:N	2.62	0.56
2:C:67:ARG:O	2:C:81:ILE:HA	2.06	0.56
2:C:60:ARG:CZ	2:C:66:ASP:HA	2.36	0.56
3:D:6:GLN:HG2	3:D:96:CYS:SG	2.46	0.56
3:B:151:PHE:CB	3:B:152:PRO:CD	2.81	0.56
4:L:60:VAL:HG22	4:L:60:VAL:O	2.06	0.56
2:A:19:VAL:HG22	2:A:20:THR:N	2.20	0.55
4:L:42:THR:O	4:L:43:PHE:C	2.49	0.55
2:C:53:LEU:HB2	2:C:54:ILE:HD12	1.87	0.55
2:C:89:GLN:HE22	2:C:172:GLN:NE2	2.03	0.55
2:C:131:LEU:HD11	2:C:136:ALA:HB2	1.88	0.55
3:B:206:ALA:C	3:B:208:SER:H	2.13	0.55
3:D:21:SER:HB3	3:D:80:TYR:CE1	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:74:THR:O	3:D:76:ALA:N	2.39	0.55
4:M:24:LYS:HB2	4:M:74:HIS:CD2	2.40	0.55
1:Q:31:VAL:HG21	3:D:35:HIS:CE1	2.39	0.55
2:A:180:SER:HG	3:B:169:HIS:CE1	2.25	0.55
3:B:13:LYS:HA	3:B:117:SER:O	2.06	0.55
3:B:98:ARG:HB3	3:B:107:VAL:CG1	2.37	0.55
2:C:45:LYS:HB2	2:C:48:GLN:NE2	2.21	0.55
4:L:51:TYR:OH	4:M:68:LEU:HD11	2.07	0.55
3:D:2:ILE:HD13	3:D:98:ARG:NH2	2.22	0.55
3:D:13:LYS:H	3:D:13:LYS:CD	2.18	0.55
2:C:53:LEU:O	2:C:60:ARG:HA	2.07	0.55
3:D:97:ALA:HB1	3:D:105:PHE:HB3	1.87	0.55
3:D:158:THR:HG23	3:D:201:ASN:ND2	2.21	0.55
2:A:24:LYS:HD3	2:A:24:LYS:O	2.06	0.55
2:C:188:THR:HG23	2:C:191:GLU:CD	2.31	0.55
3:D:134:ALA:O	3:D:135:ALA:HB3	2.07	0.55
4:L:25:VAL:HA	4:L:75:MET:O	2.07	0.55
2:C:84:VAL:CG1	2:C:110:LEU:HD21	2.36	0.55
2:C:123:ILE:HD13	2:C:124:PHE:N	2.22	0.55
3:D:97:ALA:HA	3:D:107:VAL:O	2.07	0.55
4:M:64:TRP:HZ3	4:M:66:ALA:HB2	1.72	0.55
3:B:161:SER:H	3:B:201:ASN:ND2	2.04	0.55
3:D:126:VAL:HG21	3:D:211:VAL:HG11	1.89	0.55
2:A:173:ASP:HB3	2:A:176:ASP:OD2	2.06	0.55
3:B:2:ILE:HA	3:B:26:GLY:HA3	1.88	0.55
3:D:84:ASN:O	3:D:85:SER:C	2.50	0.54
3:B:215:ILE:N	3:B:215:ILE:HD12	2.23	0.54
2:C:193:GLU:HA	2:C:217:ARG:NH2	2.22	0.54
3:D:61:ALA:HB3	3:D:64:PHE:HD1	1.72	0.54
2:C:37:ASN:ND2	2:C:57:ALA:HB2	2.23	0.54
4:L:57:HIS:C	4:L:59:LYS:H	2.15	0.54
3:D:58:PRO:HB2	3:D:60:TYR:HE2	1.72	0.54
4:L:68:LEU:H	4:L:68:LEU:CD2	2.21	0.54
2:A:201:GLU:HG2	2:A:212:VAL:HG22	1.89	0.54
3:B:139:SER:HA	3:B:190:SER:OG	2.08	0.54
4:L:68:LEU:HB2	4:M:66:ALA:HB3	1.89	0.54
3:D:27:TYR:O	3:D:29:PHE:N	2.41	0.54
1:P:29:GLN:HE22	3:B:53:THR:N	1.98	0.53
2:A:130:GLN:HG2	2:A:135:GLY:O	2.08	0.53
2:C:142:LEU:HD11	2:C:152:VAL:CG1	2.38	0.53
3:B:106:ASP:OD2	3:B:107:VAL:HG12	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:48:MET:HA	3:B:64:PHE:CD1	2.43	0.53
3:B:93:THR:HB	3:B:113:THR:HB	1.89	0.53
2:A:116:ASP:OD2	2:A:116:ASP:N	2.40	0.53
4:L:36:THR:HG22	4:L:37:ALA:N	2.22	0.53
3:D:35:HIS:CG	3:D:50:TRP:HB3	2.44	0.53
3:D:126:VAL:HG21	3:D:211:VAL:CG1	2.39	0.53
2:A:129:GLU:O	2:A:132:THR:HG22	2.09	0.53
3:B:84:ASN:O	3:B:85:SER:C	2.51	0.53
2:C:117:ALA:O	2:C:206:THR:HG21	2.08	0.53
2:C:121:VAL:HG21	2:C:142:LEU:HD22	1.90	0.53
4:M:52:ARG:O	4:M:56:LEU:HB2	2.08	0.53
1:Q:35:TYR:O	1:Q:35:TYR:HD1	1.92	0.53
3:B:190:SER:HB3	5:B:297:HOH:O	2.09	0.53
4:L:47:THR:O	4:L:51:TYR:HD1	1.92	0.53
3:D:65:LYS:HG3	3:D:66:GLY:N	2.24	0.53
2:A:56:TRP:O	2:A:58:SER:N	2.41	0.53
2:A:119:PRO:HB3	2:A:145:PHE:CD2	2.44	0.53
4:L:16:GLU:CD	4:L:17:PRO:HD2	2.33	0.53
2:C:33:ARG:HG3	2:C:33:ARG:HH11	1.74	0.53
2:C:131:LEU:O	2:C:189:LYS:HD2	2.09	0.53
2:C:150:ILE:HG12	2:C:151:ASN:H	1.72	0.53
3:D:20:ILE:HG12	3:D:81:LEU:HB3	1.91	0.53
3:D:204:HIS:NE2	3:D:206:ALA:HB3	2.24	0.53
1:Q:37:LEU:O	1:Q:37:LEU:HD13	2.09	0.52
2:A:18:LYS:CG	2:A:82:SER:HA	2.35	0.52
2:C:55:TYR:O	2:C:56:TRP:C	2.52	0.52
2:A:65:PRO:C	2:A:67:ARG:H	2.17	0.52
4:L:68:LEU:HD22	4:L:68:LEU:N	2.24	0.52
2:C:43:GLN:OE1	2:C:45:LYS:HG3	2.09	0.52
3:D:61:ALA:HB3	3:D:64:PHE:CD1	2.44	0.52
4:M:15:GLU:O	4:M:16:GLU:HB2	2.08	0.52
3:B:35:HIS:O	3:B:96:CYS:HA	2.10	0.52
3:B:124:PRO:HB3	3:B:150:TYR:CB	2.40	0.52
3:D:51:VAL:HG22	3:D:52:ASN:N	2.25	0.52
3:D:209:THR:CG2	3:D:210:LYS:N	2.72	0.52
4:L:15:GLU:CG	4:L:16:GLU:H	2.19	0.52
4:L:68:LEU:HD21	4:M:68:LEU:CD1	2.39	0.52
4:M:44:GLU:O	4:M:45:GLU:C	2.52	0.52
2:C:102:LEU:HD11	3:D:99:PHE:CE2	2.45	0.52
2:A:172:GLN:HE21	2:A:177:SER:HB3	1.75	0.52
2:C:31:ASN:ND2	2:C:98:TYR:OH	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:22:VAL:O	1:P:23:LYS:CB	2.58	0.52
4:L:17:PRO:O	4:L:18:LYS:HG3	2.09	0.52
2:C:13:VAL:CG2	2:C:84:VAL:HG21	2.38	0.52
2:C:186:THR:O	2:C:187:LEU:HD23	2.10	0.52
2:C:195:HIS:O	2:C:217:ARG:NH2	2.43	0.52
2:C:199:THR:HG22	2:C:214:SER:HB2	1.91	0.52
3:D:49:GLY:HA3	3:D:70:PHE:HE1	1.74	0.52
2:C:172:GLN:NE2	2:C:177:SER:O	2.42	0.52
3:D:157:VAL:O	3:D:158:THR:HB	2.10	0.52
2:A:176:ASP:CG	2:A:178:THR:HG23	2.35	0.51
2:C:42:TYR:CE1	2:C:95:LYS:HB2	2.44	0.51
2:C:44:GLN:HE21	2:C:50:PRO:HD3	1.75	0.51
2:C:99:ILE:CG1	2:C:101:PRO:HD2	2.40	0.51
3:D:65:LYS:CD	3:D:66:GLY:H	2.22	0.51
2:A:168:SER:OG	3:B:172:PRO:HD2	2.11	0.51
3:B:152:PRO:O	3:B:154:PRO:CD	2.57	0.51
2:C:67:ARG:HH11	2:C:85:GLN:CG	2.22	0.51
2:C:156:ILE:HD11	2:C:161:ARG:HG3	1.93	0.51
3:D:158:THR:HG22	3:D:201:ASN:O	2.10	0.51
3:D:193:TRP:CD2	3:D:194:PRO:HA	2.45	0.51
4:M:82:LYS:NZ	4:M:82:LYS:CB	2.72	0.51
3:B:124:PRO:CB	3:B:150:TYR:HB3	2.41	0.51
4:L:23:ILE:N	4:L:23:ILE:CD1	2.74	0.51
3:D:98:ARG:O	3:D:105:PHE:HA	2.11	0.51
2:C:13:VAL:HG11	2:C:19:VAL:CG2	2.41	0.51
1:Q:35:TYR:O	1:Q:36:LEU:HB3	2.09	0.51
2:A:56:TRP:C	2:A:58:SER:H	2.18	0.51
3:B:11:LEU:HD12	3:B:152:PRO:HG3	1.93	0.51
3:D:67:ARG:HH22	3:D:90:ASP:CG	2.19	0.51
2:A:2:ILE:CG2	2:A:96:GLN:HG2	2.41	0.51
2:A:133:SER:O	2:A:135:GLY:N	2.44	0.51
3:D:76:ALA:C	3:D:78:THR:N	2.67	0.51
3:D:94:TYR:CE2	3:D:114:VAL:HG11	2.46	0.51
3:D:99:PHE:CZ	3:D:103:GLN:HA	2.46	0.51
2:C:188:THR:H	2:C:191:GLU:CD	2.19	0.50
2:C:205:LYS:O	2:C:206:THR:C	2.53	0.50
3:B:39:GLN:NE2	3:B:45:LEU:HD23	2.26	0.50
4:M:22:THR:HA	4:M:40:LYS:HG2	1.93	0.50
4:M:58:ALA:HB1	4:M:62:GLY:O	2.10	0.50
4:M:61:ASN:C	4:M:81:GLY:HA2	2.36	0.50
2:C:156:ILE:C	2:C:158:GLY:H	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:176:GLN:O	3:D:177:SER:HB2	2.10	0.50
1:P:22:VAL:O	1:P:23:LYS:CG	2.59	0.50
2:C:60:ARG:NH1	5:C:242:HOH:O	2.43	0.50
2:C:121:VAL:HG12	2:C:213:LYS:HG3	1.92	0.50
3:D:54:GLU:O	3:D:55:THR:CB	2.59	0.50
4:M:58:ALA:O	4:M:60:VAL:HG12	2.11	0.50
3:B:6:GLN:NE2	3:B:111:GLY:HA2	2.23	0.50
3:D:54:GLU:O	3:D:55:THR:HB	2.11	0.50
3:D:182:LEU:HD12	3:D:182:LEU:O	2.11	0.50
3:D:215:ILE:N	3:D:215:ILE:CD1	2.75	0.50
1:P:31:VAL:HG21	3:B:50:TRP:CE2	2.47	0.50
2:C:19:VAL:HG21	2:C:110:LEU:CD1	2.41	0.50
3:B:123:PRO:HG3	3:B:207:SER:HB2	1.94	0.49
2:A:89:GLN:OE1	2:A:172:GLN:HB3	2.12	0.49
2:A:187:LEU:HD13	2:A:191:GLU:HB2	1.94	0.49
3:B:121:THR:HA	3:B:152:PRO:HD3	1.94	0.49
2:C:33:ARG:HG3	2:C:33:ARG:NH1	2.27	0.49
2:C:148:LYS:HD2	4:M:12:LYS:N	2.27	0.49
3:D:65:LYS:CG	3:D:66:GLY:N	2.75	0.49
2:C:118:ALA:HA	2:C:206:THR:HG21	1.93	0.49
3:D:2:ILE:HD13	3:D:98:ARG:HH22	1.77	0.49
3:D:55:THR:CG2	3:D:57:GLU:HB2	2.40	0.49
3:B:46:ASN:HD22	3:B:47:TRP:N	2.09	0.49
3:D:175:LEU:HD21	3:D:180:TYR:CZ	2.47	0.49
4:L:60:VAL:HG13	4:L:61:ASN:OD1	2.13	0.49
2:C:36:LYS:CG	2:C:56:TRP:HB2	2.43	0.49
2:A:20:THR:HG23	2:A:80:THR:OG1	2.12	0.49
4:L:26:ASN:HB3	4:L:28:ILE:HD11	1.94	0.49
4:M:60:VAL:HG13	4:M:61:ASN:ND2	2.28	0.49
2:A:113:LYS:HA	2:A:146:TYR:HH	1.76	0.49
2:C:42:TYR:HE1	2:C:95:LYS:CB	2.26	0.49
1:Q:37:LEU:HD13	1:Q:37:LEU:C	2.38	0.49
2:A:37:ASN:O	2:A:56:TRP:HA	2.13	0.49
2:A:72:GLY:HA3	2:A:77:PHE:HA	1.95	0.49
3:D:2:ILE:HD13	3:D:98:ARG:NH1	2.27	0.49
3:B:124:PRO:CA	3:B:150:TYR:HB3	2.43	0.49
4:L:48:ALA:CB	4:L:52:ARG:HH21	2.23	0.49
2:C:148:LYS:HE3	4:M:12:LYS:HD2	1.95	0.49
3:B:206:ALA:C	3:B:208:SER:N	2.71	0.48
2:C:102:LEU:HD11	3:D:99:PHE:HE2	1.78	0.48
2:A:166:LEU:HD11	3:B:176:GLN:OE1	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:99:ILE:HD11	2:C:101:PRO:HG2	1.95	0.48
2:C:112:LEU:O	2:C:112:LEU:HD12	2.13	0.48
3:D:102:ARG:HD3	3:D:104:TYR:HE2	1.78	0.48
2:C:96:GLN:HE21	2:C:98:TYR:N	2.11	0.48
3:D:159:TRP:CZ3	3:D:200:CYS:HB3	2.48	0.48
2:A:100:PRO:HA	2:A:101:PRO:C	2.38	0.48
3:B:170:THR:HG23	3:B:184:SER:HB2	1.94	0.48
2:C:131:LEU:CD1	2:C:136:ALA:HB2	2.42	0.48
3:D:117:SER:OG	3:D:118:SER:N	2.46	0.48
2:A:30:LEU:C	2:A:30:LEU:HD23	2.38	0.48
2:C:216:ASN:HB2	2:C:219:GLU:OE2	2.13	0.48
3:D:139:SER:O	3:D:190:SER:HB2	2.13	0.48
3:D:2:ILE:CD1	3:D:98:ARG:HH12	2.26	0.48
3:B:58:PRO:HB2	3:B:60:TYR:CE1	2.29	0.48
2:C:13:VAL:HG23	2:C:14:SER:N	2.28	0.48
3:D:114:VAL:O	3:D:114:VAL:HG22	2.12	0.48
1:P:39:ARG:H	1:P:39:ARG:HG2	1.41	0.48
4:M:21:VAL:HG12	4:M:23:ILE:CD1	2.44	0.48
1:P:28:GLY:N	1:P:30:ILE:HD11	2.28	0.48
2:A:58:SER:HA	2:A:70:GLY:O	2.12	0.48
2:C:53:LEU:O	2:C:64:VAL:HG21	2.13	0.48
3:D:102:ARG:O	3:D:103:GLN:HB2	2.14	0.48
1:P:24:PHE:CG	1:P:25:PRO:CD	2.96	0.47
2:C:199:THR:HB	2:C:214:SER:HB3	1.94	0.47
4:M:61:ASN:O	4:M:81:GLY:HA2	2.14	0.47
2:A:166:LEU:HD21	3:B:176:GLN:OE1	2.14	0.47
4:L:68:LEU:CD1	4:L:75:MET:HE2	2.43	0.47
2:C:34:THR:C	2:C:36:LYS:H	2.21	0.47
2:A:2:ILE:HG21	2:A:96:GLN:HG2	1.96	0.47
2:C:99:ILE:HG13	2:C:101:PRO:CD	2.42	0.47
2:A:6:GLN:CG	2:A:23:CYS:SG	2.94	0.47
2:A:180:SER:OG	3:B:169:HIS:CE1	2.67	0.47
2:A:218:ASN:C	2:A:219:GLU:HG3	2.40	0.47
3:B:89:GLU:HG3	5:B:288:HOH:O	2.14	0.47
3:D:55:THR:C	3:D:57:GLU:H	2.23	0.47
2:C:166:LEU:N	2:C:184:THR:O	2.39	0.47
3:D:120:LYS:HG3	3:D:122:THR:HG22	1.96	0.47
4:M:45:GLU:O	4:M:49:GLU:HG3	2.15	0.47
3:B:159:TRP:O	3:B:160:ASN:C	2.57	0.47
2:C:54:ILE:HG23	2:C:59:THR:H	1.80	0.47
2:C:193:GLU:HA	2:C:217:ARG:CZ	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:199:THR:HG22	2:C:214:SER:HB3	1.96	0.47
3:D:64:PHE:O	3:D:65:LYS:HB3	2.15	0.47
3:D:176:GLN:HB2	3:D:181:THR:HG21	1.97	0.47
2:A:98:TYR:CD2	2:A:99:ILE:HG13	2.49	0.47
2:A:193:GLU:HA	2:A:217:ARG:CZ	2.45	0.47
2:C:89:GLN:HE22	2:C:172:GLN:CD	2.22	0.47
2:C:89:GLN:HE21	2:C:112:LEU:H	1.62	0.47
2:A:86:ALA:HA	2:A:89:GLN:HE21	1.79	0.47
3:B:121:THR:HG23	3:B:152:PRO:CG	2.36	0.47
3:D:124:PRO:HB3	3:D:150:TYR:HB3	1.97	0.47
3:D:195:SER:O	3:D:196:GLU:OE2	2.33	0.47
4:M:52:ARG:CA	4:M:56:LEU:HD13	2.44	0.47
1:Q:40:ARG:HG2	1:Q:40:ARG:HH21	1.79	0.47
2:C:38:TYR:CG	3:D:103:GLN:HG3	2.49	0.47
2:C:67:ARG:HG2	2:C:67:ARG:NH2	2.29	0.47
2:C:161:ARG:HG2	2:C:161:ARG:HH11	1.80	0.47
4:M:64:TRP:CZ3	4:M:66:ALA:HB2	2.49	0.47
1:P:41:GLY:HA2	1:P:42:PRO:HD3	1.70	0.46
2:A:65:PRO:C	2:A:67:ARG:N	2.74	0.46
2:C:15:ALA:C	2:C:17:GLU:H	2.23	0.46
4:M:52:ARG:C	4:M:56:LEU:HD13	2.40	0.46
2:A:95:LYS:HA	2:A:103:THR:O	2.16	0.46
2:C:60:ARG:HG3	2:C:64:VAL:CB	2.38	0.46
2:C:60:ARG:HH22	2:C:66:ASP:HA	1.73	0.46
2:C:92:TYR:N	2:C:92:TYR:CD1	2.83	0.46
3:D:113:THR:HG21	3:D:154:PRO:HD3	1.98	0.46
3:D:162:GLY:C	3:D:164:LEU:N	2.73	0.46
2:A:126:PRO:HD2	2:A:192:TYR:CZ	2.50	0.46
3:B:109:GLY:C	3:B:111:GLY:H	2.23	0.46
2:A:25:SER:OG	2:A:75:THR:HA	2.16	0.46
2:A:137:SER:OG	2:A:186:THR:HG23	2.16	0.46
3:D:126:VAL:O	3:D:213:LYS:HG3	2.16	0.46
4:L:61:ASN:O	4:L:81:GLY:HA2	2.16	0.46
3:D:29:PHE:O	3:D:53:THR:HG21	2.15	0.46
2:A:40:ALA:O	2:A:94:CYS:HA	2.15	0.46
2:A:161:ARG:NH2	2:A:163:ASN:OD1	2.49	0.46
3:B:6:GLN:NE2	3:B:111:GLY:N	2.62	0.46
2:C:113:LYS:HA	2:C:146:TYR:OH	2.16	0.46
2:C:131:LEU:HD12	2:C:135:GLY:O	2.16	0.46
2:C:187:LEU:HB3	2:C:191:GLU:OE1	2.15	0.46
2:A:20:THR:HB	4:L:57:HIS:CE1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:57:HIS:O	4:L:59:LYS:N	2.49	0.46
2:C:44:GLN:HE22	3:D:39:GLN:HE22	1.64	0.46
2:C:117:ALA:C	2:C:206:THR:HG21	2.40	0.46
3:D:150:TYR:N	3:D:179:LEU:HG	2.31	0.46
1:Q:32:GLY:H	3:D:103:GLN:NE2	2.00	0.46
4:L:42:THR:OG1	4:L:45:GLU:HB2	2.16	0.46
2:C:4:MET:SD	2:C:96:GLN:HB2	2.56	0.46
2:C:17:GLU:HG2	4:M:33:LYS:HD3	1.98	0.46
3:D:54:GLU:C	3:D:56:GLY:H	2.24	0.46
4:M:42:THR:O	4:M:43:PHE:C	2.57	0.46
4:M:52:ARG:HA	4:M:56:LEU:HD13	1.98	0.45
3:D:74:THR:C	3:D:76:ALA:N	2.65	0.45
1:Q:35:TYR:HA	2:C:33:ARG:HE	1.81	0.45
3:B:36:TRP:CE2	3:B:81:LEU:HB2	2.51	0.45
3:B:109:GLY:C	3:B:111:GLY:N	2.74	0.45
3:D:52:ASN:N	3:D:52:ASN:OD1	2.49	0.45
3:D:126:VAL:HB	3:D:211:VAL:HG11	1.98	0.45
3:D:194:PRO:O	3:D:196:GLU:N	2.42	0.45
3:B:6:GLN:HE22	3:B:111:GLY:CA	2.28	0.45
3:B:60:TYR:HD1	3:B:60:TYR:N	2.14	0.45
3:B:60:TYR:N	3:B:60:TYR:CD1	2.84	0.45
3:D:24:ALA:O	3:D:25:SER:CB	2.64	0.45
2:A:148:LYS:HG2	5:A:259:HOH:O	2.17	0.45
2:C:99:ILE:CD1	2:C:101:PRO:HD2	2.47	0.45
2:C:144:ASN:OD1	3:D:169:HIS:HE1	2.00	0.45
3:D:206:ALA:C	3:D:208:SER:H	2.24	0.45
2:C:53:LEU:CB	2:C:54:ILE:HD12	2.47	0.45
3:D:176:GLN:O	3:D:177:SER:CB	2.63	0.45
2:C:56:TRP:O	2:C:57:ALA:CB	2.65	0.45
3:D:8:GLY:O	3:D:112:THR:HG23	2.17	0.45
1:P:18:ARG:HD3	1:P:19:PRO:CD	2.46	0.45
3:B:98:ARG:NH1	3:B:106:ASP:OD1	2.49	0.45
2:C:37:ASN:HD22	2:C:57:ALA:CB	2.30	0.45
3:D:99:PHE:HD2	3:D:105:PHE:CE1	2.34	0.45
4:L:48:ALA:O	4:L:49:GLU:C	2.60	0.45
3:D:83:ILE:HG21	3:D:86:LEU:HD23	1.98	0.45
3:D:94:TYR:HE2	3:D:114:VAL:HG11	1.82	0.45
2:A:2:ILE:HA	2:A:26:SER:HB3	1.99	0.45
2:A:168:SER:OG	3:B:171:PHE:HB3	2.17	0.45
2:C:101:PRO:HA	3:D:47:TRP:CZ3	2.52	0.45
1:P:28:GLY:H	1:P:30:ILE:HD11	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:97:ALA:HA	2:A:102:LEU:HD22	1.98	0.44
3:B:126:VAL:O	3:B:213:LYS:HE3	2.17	0.44
2:C:96:GLN:NE2	2:C:98:TYR:CB	2.80	0.44
2:A:131:LEU:C	2:A:133:SER:N	2.74	0.44
3:B:159:TRP:HB2	3:B:164:LEU:HB3	1.99	0.44
2:C:172:GLN:HG2	2:C:179:TYR:CZ	2.52	0.44
1:P:33:GLY:HA2	1:P:36:LEU:CD1	2.47	0.44
2:A:172:GLN:HE21	2:A:177:SER:CB	2.30	0.44
2:C:59:THR:O	2:C:60:ARG:HB3	2.17	0.44
2:A:43:GLN:NE2	5:A:282:HOH:O	2.38	0.44
3:B:152:PRO:C	3:B:154:PRO:HD2	2.42	0.44
3:B:137:THR:O	3:B:139:SER:N	2.51	0.44
2:C:30:LEU:C	2:C:31:ASN:HD22	2.26	0.44
2:C:85:GLN:O	2:C:86:ALA:C	2.60	0.44
2:C:148:LYS:O	2:C:149:ASP:HB3	2.17	0.44
3:D:133:SER:O	3:D:134:ALA:HB2	2.18	0.44
2:A:138:VAL:N	2:A:185:LEU:O	2.46	0.44
3:D:19:LYS:HA	3:D:81:LEU:O	2.17	0.44
3:B:175:LEU:HD21	3:B:178:ASP:HA	1.99	0.44
2:C:32:SER:O	2:C:33:ARG:CB	2.66	0.44
2:C:148:LYS:HD3	2:C:179:TYR:CZ	2.53	0.44
3:D:114:VAL:O	3:D:114:VAL:HG13	2.17	0.44
3:B:129:LEU:O	3:B:144:GLY:N	2.51	0.44
3:B:199:THR:HG22	3:B:214:LYS:HA	1.98	0.44
2:C:166:LEU:HD23	2:C:167:ASN:N	2.33	0.44
2:C:72:GLY:O	2:C:73:SER:HB2	2.18	0.43
2:C:166:LEU:HD23	2:C:166:LEU:C	2.43	0.43
2:C:168:SER:O	2:C:181:MET:HA	2.18	0.43
3:B:91:THR:O	3:B:92:ALA:HB2	2.17	0.43
2:C:32:SER:O	2:C:33:ARG:HB3	2.17	0.43
3:D:199:THR:HG23	3:D:214:LYS:HG2	2.00	0.43
1:P:36:LEU:C	1:P:37:LEU:HD22	2.43	0.43
4:L:68:LEU:HD13	4:L:75:MET:HG3	2.00	0.43
2:C:112:LEU:HD12	2:C:112:LEU:C	2.43	0.43
2:C:145:PHE:O	2:C:178:THR:HB	2.18	0.43
3:D:18:VAL:HG12	3:D:86:LEU:HD11	1.99	0.43
2:C:19:VAL:HG21	2:C:110:LEU:HD13	1.99	0.43
3:D:2:ILE:HD13	3:D:98:ARG:CZ	2.48	0.43
3:D:119:ALA:HB1	5:D:222:HOH:O	2.18	0.43
3:B:29:PHE:CG	3:B:77:SER:HA	2.53	0.43
4:L:16:GLU:CG	4:L:17:PRO:HD2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:151:ASN:O	2:C:202:ALA:HA	2.18	0.43
2:C:172:GLN:HE21	2:C:172:GLN:HB3	1.59	0.43
3:D:48:MET:HG2	3:D:64:PHE:CZ	2.52	0.43
3:D:55:THR:C	3:D:57:GLU:N	2.74	0.43
2:A:18:LYS:HG3	2:A:82:SER:CA	2.40	0.43
2:C:121:VAL:HG22	2:C:142:LEU:CA	2.44	0.43
3:D:5:VAL:HA	5:D:233:HOH:O	2.19	0.43
1:Q:29:GLN:O	1:Q:30:ILE:HG23	2.19	0.43
2:A:67:ARG:HH21	2:A:67:ARG:HB3	1.84	0.43
3:B:108:TRP:CD1	3:B:108:TRP:N	2.87	0.43
4:L:50:ALA:O	4:L:51:TYR:C	2.62	0.43
1:P:42:PRO:HB2	1:P:43:ARG:H	1.69	0.43
2:A:2:ILE:N	2:A:2:ILE:HD12	2.34	0.43
2:A:80:THR:O	2:A:80:THR:HG22	2.17	0.43
2:A:187:LEU:C	2:A:187:LEU:HD12	2.44	0.43
3:B:40:ALA:HB3	3:B:43:LYS:CG	2.49	0.43
2:C:2:ILE:HB	2:C:96:GLN:OE1	2.18	0.43
2:C:4:MET:CE	2:C:96:GLN:HB2	2.49	0.43
3:D:2:ILE:HD13	3:D:98:ARG:HH12	1.84	0.43
3:D:159:TRP:CD1	3:D:159:TRP:N	2.87	0.43
2:A:31:ASN:HB3	2:A:34:THR:OG1	2.19	0.43
2:A:112:LEU:CB	2:A:172:GLN:HE22	2.26	0.43
3:B:126:VAL:HG21	3:B:202:VAL:CG1	2.47	0.43
3:B:160:ASN:ND2	3:B:164:LEU:HD12	2.34	0.43
2:C:129:GLU:CB	5:C:259:HOH:O	2.67	0.43
4:M:27:LEU:O	4:M:34:ILE:HA	2.18	0.43
1:P:17:ARG:O	3:B:57:GLU:OE1	2.36	0.42
2:A:150:ILE:HG23	2:A:181:MET:HE3	2.00	0.42
3:B:6:GLN:NE2	3:B:111:GLY:CA	2.81	0.42
2:C:150:ILE:CG1	2:C:151:ASN:N	2.80	0.42
2:C:199:THR:CG2	2:C:214:SER:HB3	2.49	0.42
3:B:161:SER:HA	3:B:201:ASN:ND2	2.34	0.42
3:D:129:LEU:HB2	3:D:144:GLY:CA	2.49	0.42
4:M:68:LEU:HD23	4:M:75:MET:HG3	2.00	0.42
2:A:95:LYS:HB3	2:A:95:LYS:HZ3	1.84	0.42
3:B:137:THR:HG23	3:B:138:ASN:N	2.34	0.42
3:B:144:GLY:O	3:B:159:TRP:HH2	2.02	0.42
2:A:144:ASN:HA	2:A:178:THR:OG1	2.20	0.42
2:C:155:LYS:HA	2:C:159:SER:O	2.19	0.42
3:D:152:PRO:HD2	3:D:206:ALA:CB	2.50	0.42
1:P:17:ARG:HG2	1:P:18:ARG:HH21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:55:TYR:O	2:A:56:TRP:C	2.63	0.42
2:C:104:PHE:HE1	3:D:47:TRP:HB2	1.83	0.42
2:C:192:TYR:O	2:C:217:ARG:NH2	2.52	0.42
3:D:182:LEU:C	3:D:182:LEU:CD1	2.88	0.42
4:M:20:GLU:CG	4:M:42:THR:HA	2.46	0.42
4:L:55:ALA:HB1	5:L:94:HOH:O	2.19	0.42
2:C:25:SER:C	2:C:27:GLN:H	2.27	0.42
4:L:20:GLU:O	4:L:21:VAL:HG13	2.20	0.42
3:D:73:GLU:O	3:D:74:THR:C	2.62	0.42
2:A:173:ASP:OD2	2:A:174:SER:N	2.53	0.42
2:C:29:LEU:O	2:C:37:ASN:HA	2.19	0.42
3:D:51:VAL:HG23	3:D:57:GLU:C	2.44	0.42
2:A:71:ARG:HH22	2:A:80:THR:HB	1.84	0.42
3:B:20:ILE:HD12	3:B:21:SER:O	2.20	0.42
3:B:87:LYS:HD2	3:B:87:LYS:N	2.34	0.42
3:B:98:ARG:HB3	3:B:107:VAL:HG13	2.01	0.42
3:B:161:SER:N	3:B:201:ASN:ND2	2.60	0.42
2:C:12:ALA:HB3	4:M:36:THR:HB	2.01	0.42
2:C:196:ASN:HD21	2:C:216:ASN:HD22	1.68	0.42
2:A:116:ASP:OD1	2:A:205:LYS:CE	2.67	0.42
3:D:157:VAL:O	3:D:158:THR:CB	2.67	0.42
4:M:53:TYR:O	4:M:57:HIS:CB	2.66	0.42
4:M:69:GLU:O	4:M:70:ASP:HB2	2.19	0.42
2:A:7:SER:HB2	2:A:22:SER:OG	2.20	0.41
2:A:19:VAL:HG12	2:A:84:VAL:HG21	2.02	0.41
3:B:160:ASN:HD22	3:B:164:LEU:HD12	1.84	0.41
4:L:44:GLU:HG3	4:L:45:GLU:N	2.35	0.41
2:A:38:TYR:CD1	3:B:103:GLN:HG3	2.55	0.41
3:B:109:GLY:O	3:B:111:GLY:N	2.54	0.41
4:L:46:ALA:O	4:L:47:THR:C	2.62	0.41
4:L:62:GLY:HA3	4:L:81:GLY:H	1.85	0.41
2:C:150:ILE:CG2	2:C:181:MET:HE3	2.47	0.41
2:C:173:ASP:HB3	2:C:176:ASP:HB3	2.01	0.41
4:M:52:ARG:O	4:M:56:LEU:N	2.44	0.41
3:B:151:PHE:CG	3:B:152:PRO:N	2.87	0.41
3:B:194:PRO:HG2	3:B:217:PRO:HG2	2.02	0.41
2:C:132:THR:HG22	2:C:132:THR:O	2.20	0.41
3:D:7:SER:HG	3:D:21:SER:H	1.62	0.41
3:D:198:VAL:O	3:D:215:ILE:HD13	2.20	0.41
3:D:11:LEU:HD23	3:D:12:LYS:N	2.34	0.41
3:D:30:THR:HG23	3:D:54:GLU:CG	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:175:LEU:HD13	3:D:175:LEU:HA	1.87	0.41
1:P:34:VAL:HG13	1:P:35:TYR:CD1	2.56	0.41
2:A:2:ILE:HD12	2:A:2:ILE:H	1.85	0.41
2:A:150:ILE:CD1	2:A:151:ASN:N	2.74	0.41
3:D:138:ASN:O	3:D:140:MET:N	2.53	0.41
3:D:158:THR:CG2	3:D:201:ASN:O	2.67	0.41
3:D:162:GLY:C	3:D:164:LEU:H	2.26	0.41
3:B:29:PHE:CD2	3:B:77:SER:HA	2.55	0.41
3:B:60:TYR:HE2	3:B:68:PHE:O	2.04	0.41
3:D:199:THR:HG23	3:D:214:LYS:HA	2.02	0.41
4:M:23:ILE:HD12	4:M:23:ILE:N	2.34	0.41
4:M:58:ALA:O	4:M:59:LYS:C	2.63	0.41
2:A:39:LEU:HD13	2:A:39:LEU:C	2.45	0.41
2:C:198:TYR:O	2:C:214:SER:HB2	2.21	0.41
3:D:176:GLN:O	3:D:176:GLN:HG2	2.20	0.41
2:C:6:GLN:HE22	2:C:93:TYR:HA	1.85	0.41
4:M:59:LYS:HB2	5:M:87:HOH:O	2.20	0.41
4:M:60:VAL:H	4:M:82:LYS:HE2	1.83	0.41
2:A:192:TYR:HA	2:A:198:TYR:OH	2.21	0.41
3:B:55:THR:C	3:B:57:GLU:H	2.28	0.41
3:B:97:ALA:HB1	3:B:105:PHE:HB3	2.01	0.41
3:B:193:TRP:CD1	3:B:194:PRO:HA	2.56	0.41
3:D:129:LEU:HD12	3:D:145:CYS:H	1.86	0.41
4:M:59:LYS:O	4:M:60:VAL:CB	2.68	0.41
2:A:121:VAL:HG12	2:A:213:LYS:HG3	2.03	0.41
2:A:122:SER:O	2:A:140:CYS:HA	2.21	0.41
3:B:50:TRP:NE1	3:B:59:THR:HB	2.36	0.41
3:B:193:TRP:CG	3:B:194:PRO:HA	2.56	0.41
3:B:199:THR:HG22	3:B:214:LYS:HG3	2.03	0.41
4:L:70:ASP:HB3	4:L:73:ASN:HB2	2.03	0.41
2:C:141:PHE:CZ	3:D:185:SER:HB3	2.56	0.41
2:C:176:ASP:OD2	2:C:178:THR:CG2	2.70	0.41
2:A:13:VAL:HG11	2:A:19:VAL:HB	2.03	0.40
3:B:115:THR:CB	5:B:248:HOH:O	2.66	0.40
3:B:144:GLY:O	3:B:145:CYS:HB2	2.19	0.40
4:L:62:GLY:HA3	4:L:81:GLY:N	2.35	0.40
2:C:97:ALA:HA	2:C:102:LEU:HD22	2.03	0.40
2:A:11:LEU:HD22	2:A:13:VAL:CG1	2.50	0.40
2:A:11:LEU:CD2	2:A:13:VAL:HG12	2.51	0.40
2:A:19:VAL:CG2	2:A:20:THR:N	2.82	0.40
2:A:39:LEU:HD11	2:A:94:CYS:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:215:ILE:HD12	3:B:215:ILE:H	1.85	0.40
2:C:72:GLY:HA3	2:C:77:PHE:HA	2.04	0.40
2:A:101:PRO:O	5:A:238:HOH:O	2.22	0.40
3:B:27:TYR:CE2	3:B:98:ARG:HD2	2.57	0.40
3:B:134:ALA:O	3:B:135:ALA:HB3	2.20	0.40
4:L:26:ASN:HB2	4:L:76:ASN:HA	2.03	0.40
4:L:81:GLY:O	4:L:82:LYS:HB3	2.22	0.40
2:C:44:GLN:HE22	3:D:39:GLN:NE2	2.20	0.40
3:D:48:MET:HG2	3:D:64:PHE:CE2	2.56	0.40
2:A:24:LYS:C	2:A:24:LYS:CD	2.90	0.40
2:A:131:LEU:O	2:A:133:SER:N	2.55	0.40
3:B:102:ARG:NH1	3:B:102:ARG:HG2	2.37	0.40
2:C:42:TYR:OH	3:D:104:TYR:HB2	2.22	0.40
2:C:61:GLU:O	2:C:64:VAL:HG23	2.21	0.40
2:C:99:ILE:HB	2:C:100:PRO:CD	2.52	0.40
1:P:31:VAL:HG21	3:B:50:TRP:CD2	2.57	0.40
1:P:42:PRO:O	1:P:43:ARG:HB2	2.20	0.40
3:B:18:VAL:O	3:B:82:GLN:HG3	2.22	0.40
4:L:23:ILE:HG22	4:L:25:VAL:HG23	2.02	0.40
2:C:20:THR:O	2:C:20:THR:HG23	2.21	0.40
2:C:140:CYS:HB2	2:C:154:TRP:CH2	2.56	0.40
2:C:153:LYS:CE	2:C:155:LYS:HE3	2.47	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	P	28/44 (64%)	12 (43%)	7 (25%)	9 (32%)	0 0
1	Q	20/44 (46%)	9 (45%)	8 (40%)	3 (15%)	0 0
2	A	218/220 (99%)	191 (88%)	24 (11%)	3 (1%)	9 29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	218/220 (99%)	174 (80%)	28 (13%)	16 (7%)	1	4
3	B	216/218 (99%)	181 (84%)	17 (8%)	18 (8%)	0	3
3	D	216/218 (99%)	152 (70%)	40 (18%)	24 (11%)	0	1
4	L	68/80 (85%)	57 (84%)	7 (10%)	4 (6%)	1	6
4	M	69/80 (86%)	46 (67%)	11 (16%)	12 (17%)	0	0
All	All	1053/1124 (94%)	822 (78%)	142 (14%)	89 (8%)	0	3

All (89) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	18	ARG
1	P	23	LYS
1	P	24	PHE
1	P	42	PRO
2	A	57	ALA
2	A	134	GLY
3	B	136	GLN
3	B	138	ASN
3	B	151	PHE
3	B	152	PRO
3	B	153	GLU
4	L	18	LYS
2	C	36	LYS
3	D	16	GLU
3	D	76	ALA
3	D	153	GLU
3	D	195	SER
4	M	19	GLU
4	M	20	GLU
4	M	56	LEU
4	M	58	ALA
4	M	60	VAL
1	P	28	GLY
1	Q	39	ARG
3	B	195	SER
2	C	28	SER
2	C	32	SER
2	C	57	ALA
2	C	174	SER
3	D	25	SER

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Mol	Chain	Res	Type
3	D	28	THR
3	D	67	ARG
3	D	75	SER
3	D	85	SER
3	D	94	TYR
3	D	111	GLY
3	D	139	SER
3	D	158	THR
3	D	177	SER
4	M	45	GLU
1	P	17	ARG
1	P	20	GLN
1	P	43	ARG
1	Q	29	GLN
3	B	92	ALA
3	B	132	GLY
3	B	137	THR
3	B	145	CYS
4	L	43	PHE
4	L	80	ALA
2	C	33	ARG
2	C	48	GLN
2	C	56	TRP
2	C	59	THR
2	C	99	ILE
2	C	144	ASN
2	C	177	SER
3	D	24	ALA
3	D	74	THR
3	D	91	THR
3	D	145	CYS
1	P	40	ARG
1	Q	44	LEU
3	B	29	PHE
3	B	205	PRO
2	C	206	THR
3	D	78	THR
3	D	136	GLN
4	M	44	GLU
3	B	67	ARG
3	B	110	ALA
3	B	135	ALA

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Mol	Chain	Res	Type
3	B	210	LYS
3	D	17	THR
3	D	29	PHE
4	M	18	LYS
4	M	70	ASP
2	A	73	SER
4	L	16	GLU
2	C	148	LYS
2	C	149	ASP
3	D	149	GLY
4	M	16	GLU
4	M	67	ASP
3	B	217	PRO
3	B	66	GLY
2	C	65	PRO
4	M	34	ILE
3	D	194	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	P	21/37 (57%)	17 (81%)	4 (19%)	1	6
1	Q	14/37 (38%)	12 (86%)	2 (14%)	3	12
2	A	195/195 (100%)	178 (91%)	17 (9%)	9	30
2	C	195/195 (100%)	176 (90%)	19 (10%)	8	26
3	B	187/187 (100%)	169 (90%)	18 (10%)	8	26
3	D	186/187 (100%)	177 (95%)	9 (5%)	23	50
4	L	54/62 (87%)	52 (96%)	2 (4%)	30	57
4	M	55/62 (89%)	52 (94%)	3 (6%)	19	46
All	All	907/962 (94%)	833 (92%)	74 (8%)	10	32

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	23	LYS
1	P	24	PHE
1	P	39	ARG
1	P	40	ARG
1	Q	30	ILE
1	Q	43	ARG
2	A	13	VAL
2	A	23	CYS
2	A	24	LYS
2	A	32	SER
2	A	80	THR
2	A	95	LYS
2	A	103	THR
2	A	116	ASP
2	A	120	THR
2	A	132	THR
2	A	140	CYS
2	A	142	LEU
2	A	150	ILE
2	A	165	VAL
2	A	181	MET
2	A	184	THR
2	A	200	CYS
3	B	11	LEU
3	B	20	ILE
3	B	28	THR
3	B	38	ASN
3	B	45	LEU
3	B	60	TYR
3	B	72	LEU
3	B	74	THR
3	B	93	THR
3	B	114	VAL
3	B	115	THR
3	B	120	LYS
3	B	122	THR
3	B	156	THR
3	B	164	LEU
3	B	182	LEU
3	B	186	VAL
3	B	211	VAL
4	L	68	LEU
4	L	78	LYS

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Mol	Chain	Res	Type
2	C	11	LEU
2	C	33	ARG
2	C	36	LYS
2	C	52	VAL
2	C	59	THR
2	C	61	GLU
2	C	64	VAL
2	C	75	THR
2	C	84	VAL
2	C	95	LYS
2	C	112	LEU
2	C	120	THR
2	C	123	ILE
2	C	131	LEU
2	C	161	ARG
2	C	165	VAL
2	C	172	GLN
2	C	184	THR
2	C	211	ILE
3	D	28	THR
3	D	60	TYR
3	D	122	THR
3	D	155	VAL
3	D	171	PHE
3	D	182	LEU
3	D	201	ASN
3	D	202	VAL
3	D	215	ILE
4	M	34	ILE
4	M	44	GLU
4	M	82	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	P	29	GLN
2	A	27	GLN
2	A	43	GLN
2	A	44	GLN
2	A	89	GLN
2	A	130	GLN
2	A	143	ASN

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Mol	Chain	Res	Type
2	A	162	GLN
2	A	172	GLN
2	A	195	HIS
2	A	196	ASN
2	A	216	ASN
3	B	1	GLN
3	B	6	GLN
3	B	38	ASN
3	B	39	GLN
3	B	46	ASN
3	B	82	GLN
3	B	84	ASN
3	B	88	ASN
3	B	201	ASN
4	L	26	ASN
4	L	35	GLN
2	C	27	GLN
2	C	31	ASN
2	C	44	GLN
2	C	48	GLN
2	C	85	GLN
2	C	89	GLN
2	C	96	GLN
2	C	143	ASN
2	C	162	GLN
2	C	195	HIS
2	C	196	ASN
2	C	218	ASN
3	D	1	GLN
3	D	103	GLN
3	D	169	HIS
4	M	35	GLN
4	M	61	ASN
4	M	74	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	P	30/44 (68%)	0.08	1 (3%) 49 28	23, 146, 199, 200	0
1	Q	22/44 (50%)	0.33	0 100 100	122, 162, 198, 200	0
2	A	220/220 (100%)	-0.64	0 100 100	10, 37, 77, 143	0
2	C	220/220 (100%)	-0.37	1 (0%) 87 72	15, 56, 125, 173	0
3	B	218/218 (100%)	-0.69	0 100 100	10, 32, 78, 189	0
3	D	218/218 (100%)	-0.40	0 100 100	15, 56, 118, 191	0
4	L	70/80 (87%)	-0.46	0 100 100	12, 49, 146, 199	0
4	M	71/80 (88%)	-0.49	0 100 100	12, 44, 167, 200	0
All	All	1069/1124 (95%)	-0.49	2 (0%) 91 83	10, 45, 140, 200	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	30	LEU	2.4
1	P	19	PRO	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.