



Full wwPDB EM Validation Report ⓘ

Jan 26, 2023 – 12:23 PM JST

PDB ID : 8HHZ
EMDB ID : EMD-34808
Title : SARS-CoV-2 Omicron BA.1 Spike in complex with IY-2A
Authors : Chen, X.; Mohapatra, A.; Wu, Y.-M.
Deposited on : 2022-11-17
Resolution : 4.28 Å (reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

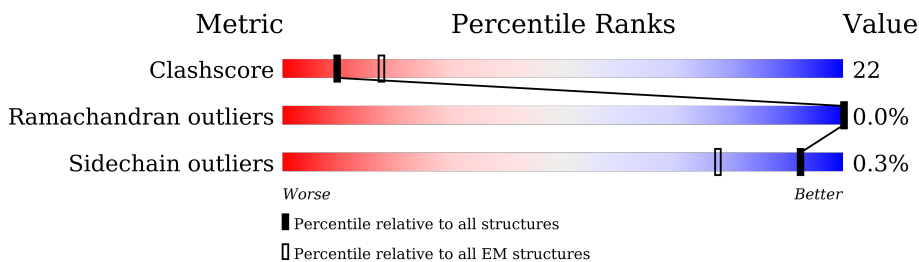
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.28 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)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1261	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">19%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 19%, orange 19%, yellow 46%, green 46%, grey 23%);"></div> <div style="text-align: left;">46%</div> <div style="text-align: right;">32%</div> <div style="text-align: right;">23%</div> </div>
1	B	1261	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">14%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 14%, orange 14%, yellow 46%, green 46%, grey 22%);"></div> <div style="text-align: left;">46%</div> <div style="text-align: right;">31%</div> <div style="text-align: right;">22%</div> </div>
1	C	1261	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">13%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 13%, orange 13%, yellow 45%, green 45%, grey 22%);"></div> <div style="text-align: left;">45%</div> <div style="text-align: right;">33%</div> <div style="text-align: right;">22%</div> </div>
2	E	224	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">56%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 56%, orange 56%, yellow 62%, green 62%, grey 37%);"></div> <div style="text-align: left;">62%</div> <div style="text-align: right;">37%</div> </div>
2	G	224	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">65%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 65%, orange 65%, yellow 67%, green 67%, grey 33%);"></div> <div style="text-align: left;">67%</div> <div style="text-align: right;">33%</div> </div>
2	I	224	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">30%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 30%, orange 30%, yellow 65%, green 65%, grey 34%);"></div> <div style="text-align: left;">65%</div> <div style="text-align: right;">34%</div> </div>
3	F	216	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">49%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 49%, orange 49%, yellow 66%, green 66%, grey 32%, grey 32%);"></div> <div style="text-align: left;">66%</div> <div style="text-align: right;">32%</div> <div style="text-align: right;">•</div> </div>
3	H	216	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">83%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 83%, orange 83%, yellow 76%, green 76%, grey 22%, grey 22%);"></div> <div style="text-align: left;">76%</div> <div style="text-align: right;">22%</div> <div style="text-align: right;">•</div> </div>

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Mol	Chain	Length	Quality of chain
3	J	216	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left, a green segment in the middle, and a yellow segment on the right. Above the red segment is the label '60%'. Below the green segment is the label '62%'. Below the yellow segment is the label '36%'. A small grey square is located at the far right end of the bar.</p>

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 32020 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	977	7429	4770	1227	1401	31	0	0
1	B	981	7424	4762	1229	1401	32	0	0
1	C	980	7438	4785	1227	1394	32	0	0

There are 330 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	initiating methionine	UNP P0DTC2
A	-4	LYS	-	expression tag	UNP P0DTC2
A	-3	VAL	-	expression tag	UNP P0DTC2
A	-2	LYS	-	expression tag	UNP P0DTC2
A	-1	LEU	-	expression tag	UNP P0DTC2
A	0	LEU	-	expression tag	UNP P0DTC2
A	1	VAL	-	expression tag	UNP P0DTC2
A	2	LEU	-	expression tag	UNP P0DTC2
A	3	LEU	-	expression tag	UNP P0DTC2
A	4	CYS	-	expression tag	UNP P0DTC2
A	5	THR	-	expression tag	UNP P0DTC2
A	6	PHE	-	expression tag	UNP P0DTC2
A	7	THR	-	expression tag	UNP P0DTC2
A	8	ALA	-	expression tag	UNP P0DTC2
A	9	THR	-	expression tag	UNP P0DTC2
A	10	TYR	-	expression tag	UNP P0DTC2
A	11	ALA	-	expression tag	UNP P0DTC2
A	12	GLY	-	expression tag	UNP P0DTC2
A	13	THR	-	expression tag	UNP P0DTC2
A	67	VAL	ALA	variant	UNP P0DTC2
A	?	-	HIS	deletion	UNP P0DTC2
A	?	-	VAL	deletion	UNP P0DTC2
A	95	ILE	THR	variant	UNP P0DTC2
A	142	ASP	GLY	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	VAL	deletion	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	210A	ILE	LEU	variant	UNP P0DTC2
A	210D	GLU	-	insertion	UNP P0DTC2
A	210E	PRO	-	insertion	UNP P0DTC2
A	210F	GLU	-	insertion	UNP P0DTC2
A	339	ASP	GLY	variant	UNP P0DTC2
A	371	LEU	SER	variant	UNP P0DTC2
A	373	PRO	SER	variant	UNP P0DTC2
A	375	PHE	SER	variant	UNP P0DTC2
A	417	ASN	LYS	variant	UNP P0DTC2
A	440	LYS	ASN	variant	UNP P0DTC2
A	446	SER	GLY	variant	UNP P0DTC2
A	477	ASN	SER	variant	UNP P0DTC2
A	478	LYS	THR	variant	UNP P0DTC2
A	484	ALA	GLU	variant	UNP P0DTC2
A	493	ARG	GLN	variant	UNP P0DTC2
A	496	SER	GLY	variant	UNP P0DTC2
A	498	ARG	GLN	variant	UNP P0DTC2
A	501	TYR	ASN	variant	UNP P0DTC2
A	505	HIS	TYR	variant	UNP P0DTC2
A	547	LYS	THR	variant	UNP P0DTC2
A	614	GLY	ASP	variant	UNP P0DTC2
A	655	TYR	HIS	variant	UNP P0DTC2
A	679	LYS	ASN	variant	UNP P0DTC2
A	681	HIS	PRO	variant	UNP P0DTC2
A	682	GLY	ARG	variant	UNP P0DTC2
A	683	SER	ARG	variant	UNP P0DTC2
A	685	SER	ARG	variant	UNP P0DTC2
A	764	LYS	ASN	variant	UNP P0DTC2
A	796	TYR	ASP	variant	UNP P0DTC2
A	856	LYS	ASN	variant	UNP P0DTC2
A	954	HIS	GLN	variant	UNP P0DTC2
A	969	LYS	ASN	variant	UNP P0DTC2
A	981	PHE	LEU	variant	UNP P0DTC2
A	986	PRO	LYS	variant	UNP P0DTC2
A	987	PRO	VAL	variant	UNP P0DTC2
A	1211	LYS	-	expression tag	UNP P0DTC2
A	1212	ASP	-	expression tag	UNP P0DTC2
A	1213	ILE	-	expression tag	UNP P0DTC2
A	1214	ARG	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1215	SER	-	expression tag	UNP P0DTC2
A	1216	LEU	-	expression tag	UNP P0DTC2
A	1217	VAL	-	expression tag	UNP P0DTC2
A	1218	PRO	-	expression tag	UNP P0DTC2
A	1219	ARG	-	expression tag	UNP P0DTC2
A	1220	GLY	-	expression tag	UNP P0DTC2
A	1221	SER	-	expression tag	UNP P0DTC2
A	1222	PRO	-	expression tag	UNP P0DTC2
A	1223	GLY	-	expression tag	UNP P0DTC2
A	1224	SER	-	expression tag	UNP P0DTC2
A	1225	GLY	-	expression tag	UNP P0DTC2
A	1226	TYR	-	expression tag	UNP P0DTC2
A	1227	ILE	-	expression tag	UNP P0DTC2
A	1228	PRO	-	expression tag	UNP P0DTC2
A	1229	GLU	-	expression tag	UNP P0DTC2
A	1230	ALA	-	expression tag	UNP P0DTC2
A	1231	PRO	-	expression tag	UNP P0DTC2
A	1232	ARG	-	expression tag	UNP P0DTC2
A	1233	ASP	-	expression tag	UNP P0DTC2
A	1234	GLY	-	expression tag	UNP P0DTC2
A	1235	GLN	-	expression tag	UNP P0DTC2
A	1236	ALA	-	expression tag	UNP P0DTC2
A	1237	TYR	-	expression tag	UNP P0DTC2
A	1238	VAL	-	expression tag	UNP P0DTC2
A	1239	ARG	-	expression tag	UNP P0DTC2
A	1240	LYS	-	expression tag	UNP P0DTC2
A	1241	ASP	-	expression tag	UNP P0DTC2
A	1242	GLY	-	expression tag	UNP P0DTC2
A	1243	GLU	-	expression tag	UNP P0DTC2
A	1244	TRP	-	expression tag	UNP P0DTC2
A	1245	VAL	-	expression tag	UNP P0DTC2
A	1246	LEU	-	expression tag	UNP P0DTC2
A	1247	LEU	-	expression tag	UNP P0DTC2
A	1248	SER	-	expression tag	UNP P0DTC2
A	1249	THR	-	expression tag	UNP P0DTC2
A	1250	PHE	-	expression tag	UNP P0DTC2
A	1251	LEU	-	expression tag	UNP P0DTC2
A	1252	GLY	-	expression tag	UNP P0DTC2
A	1253	HIS	-	expression tag	UNP P0DTC2
A	1254	HIS	-	expression tag	UNP P0DTC2
A	1255	HIS	-	expression tag	UNP P0DTC2
A	1256	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1257	HIS	-	expression tag	UNP P0DTC2
A	1258	HIS	-	expression tag	UNP P0DTC2
B	-5	MET	-	initiating methionine	UNP P0DTC2
B	-4	LYS	-	expression tag	UNP P0DTC2
B	-3	VAL	-	expression tag	UNP P0DTC2
B	-2	LYS	-	expression tag	UNP P0DTC2
B	-1	LEU	-	expression tag	UNP P0DTC2
B	0	LEU	-	expression tag	UNP P0DTC2
B	1	VAL	-	expression tag	UNP P0DTC2
B	2	LEU	-	expression tag	UNP P0DTC2
B	3	LEU	-	expression tag	UNP P0DTC2
B	4	CYS	-	expression tag	UNP P0DTC2
B	5	THR	-	expression tag	UNP P0DTC2
B	6	PHE	-	expression tag	UNP P0DTC2
B	7	THR	-	expression tag	UNP P0DTC2
B	8	ALA	-	expression tag	UNP P0DTC2
B	9	THR	-	expression tag	UNP P0DTC2
B	10	TYR	-	expression tag	UNP P0DTC2
B	11	ALA	-	expression tag	UNP P0DTC2
B	12	GLY	-	expression tag	UNP P0DTC2
B	13	THR	-	expression tag	UNP P0DTC2
B	67	VAL	ALA	variant	UNP P0DTC2
B	?	-	HIS	deletion	UNP P0DTC2
B	?	-	VAL	deletion	UNP P0DTC2
B	95	ILE	THR	variant	UNP P0DTC2
B	142	ASP	GLY	variant	UNP P0DTC2
B	?	-	VAL	deletion	UNP P0DTC2
B	?	-	TYR	deletion	UNP P0DTC2
B	?	-	TYR	deletion	UNP P0DTC2
B	210A	ILE	LEU	variant	UNP P0DTC2
B	210D	GLU	-	insertion	UNP P0DTC2
B	210E	PRO	-	insertion	UNP P0DTC2
B	210F	GLU	-	insertion	UNP P0DTC2
B	339	ASP	GLY	variant	UNP P0DTC2
B	371	LEU	SER	variant	UNP P0DTC2
B	373	PRO	SER	variant	UNP P0DTC2
B	375	PHE	SER	variant	UNP P0DTC2
B	417	ASN	LYS	variant	UNP P0DTC2
B	440	LYS	ASN	variant	UNP P0DTC2
B	446	SER	GLY	variant	UNP P0DTC2
B	477	ASN	SER	variant	UNP P0DTC2
B	478	LYS	THR	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	484	ALA	GLU	variant	UNP P0DTC2
B	493	ARG	GLN	variant	UNP P0DTC2
B	496	SER	GLY	variant	UNP P0DTC2
B	498	ARG	GLN	variant	UNP P0DTC2
B	501	TYR	ASN	variant	UNP P0DTC2
B	505	HIS	TYR	variant	UNP P0DTC2
B	547	LYS	THR	variant	UNP P0DTC2
B	614	GLY	ASP	variant	UNP P0DTC2
B	655	TYR	HIS	variant	UNP P0DTC2
B	679	LYS	ASN	variant	UNP P0DTC2
B	681	HIS	PRO	variant	UNP P0DTC2
B	682	GLY	ARG	variant	UNP P0DTC2
B	683	SER	ARG	variant	UNP P0DTC2
B	685	SER	ARG	variant	UNP P0DTC2
B	764	LYS	ASN	variant	UNP P0DTC2
B	796	TYR	ASP	variant	UNP P0DTC2
B	856	LYS	ASN	variant	UNP P0DTC2
B	954	HIS	GLN	variant	UNP P0DTC2
B	969	LYS	ASN	variant	UNP P0DTC2
B	981	PHE	LEU	variant	UNP P0DTC2
B	986	PRO	LYS	variant	UNP P0DTC2
B	987	PRO	VAL	variant	UNP P0DTC2
B	1211	LYS	-	expression tag	UNP P0DTC2
B	1212	ASP	-	expression tag	UNP P0DTC2
B	1213	ILE	-	expression tag	UNP P0DTC2
B	1214	ARG	-	expression tag	UNP P0DTC2
B	1215	SER	-	expression tag	UNP P0DTC2
B	1216	LEU	-	expression tag	UNP P0DTC2
B	1217	VAL	-	expression tag	UNP P0DTC2
B	1218	PRO	-	expression tag	UNP P0DTC2
B	1219	ARG	-	expression tag	UNP P0DTC2
B	1220	GLY	-	expression tag	UNP P0DTC2
B	1221	SER	-	expression tag	UNP P0DTC2
B	1222	PRO	-	expression tag	UNP P0DTC2
B	1223	GLY	-	expression tag	UNP P0DTC2
B	1224	SER	-	expression tag	UNP P0DTC2
B	1225	GLY	-	expression tag	UNP P0DTC2
B	1226	TYR	-	expression tag	UNP P0DTC2
B	1227	ILE	-	expression tag	UNP P0DTC2
B	1228	PRO	-	expression tag	UNP P0DTC2
B	1229	GLU	-	expression tag	UNP P0DTC2
B	1230	ALA	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1231	PRO	-	expression tag	UNP P0DTC2
B	1232	ARG	-	expression tag	UNP P0DTC2
B	1233	ASP	-	expression tag	UNP P0DTC2
B	1234	GLY	-	expression tag	UNP P0DTC2
B	1235	GLN	-	expression tag	UNP P0DTC2
B	1236	ALA	-	expression tag	UNP P0DTC2
B	1237	TYR	-	expression tag	UNP P0DTC2
B	1238	VAL	-	expression tag	UNP P0DTC2
B	1239	ARG	-	expression tag	UNP P0DTC2
B	1240	LYS	-	expression tag	UNP P0DTC2
B	1241	ASP	-	expression tag	UNP P0DTC2
B	1242	GLY	-	expression tag	UNP P0DTC2
B	1243	GLU	-	expression tag	UNP P0DTC2
B	1244	TRP	-	expression tag	UNP P0DTC2
B	1245	VAL	-	expression tag	UNP P0DTC2
B	1246	LEU	-	expression tag	UNP P0DTC2
B	1247	LEU	-	expression tag	UNP P0DTC2
B	1248	SER	-	expression tag	UNP P0DTC2
B	1249	THR	-	expression tag	UNP P0DTC2
B	1250	PHE	-	expression tag	UNP P0DTC2
B	1251	LEU	-	expression tag	UNP P0DTC2
B	1252	GLY	-	expression tag	UNP P0DTC2
B	1253	HIS	-	expression tag	UNP P0DTC2
B	1254	HIS	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	HIS	-	expression tag	UNP P0DTC2
C	-5	MET	-	initiating methionine	UNP P0DTC2
C	-4	LYS	-	expression tag	UNP P0DTC2
C	-3	VAL	-	expression tag	UNP P0DTC2
C	-2	LYS	-	expression tag	UNP P0DTC2
C	-1	LEU	-	expression tag	UNP P0DTC2
C	0	LEU	-	expression tag	UNP P0DTC2
C	1	VAL	-	expression tag	UNP P0DTC2
C	2	LEU	-	expression tag	UNP P0DTC2
C	3	LEU	-	expression tag	UNP P0DTC2
C	4	CYS	-	expression tag	UNP P0DTC2
C	5	THR	-	expression tag	UNP P0DTC2
C	6	PHE	-	expression tag	UNP P0DTC2
C	7	THR	-	expression tag	UNP P0DTC2
C	8	ALA	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	9	THR	-	expression tag	UNP P0DTC2
C	10	TYR	-	expression tag	UNP P0DTC2
C	11	ALA	-	expression tag	UNP P0DTC2
C	12	GLY	-	expression tag	UNP P0DTC2
C	13	THR	-	expression tag	UNP P0DTC2
C	67	VAL	ALA	variant	UNP P0DTC2
C	?	-	HIS	deletion	UNP P0DTC2
C	?	-	VAL	deletion	UNP P0DTC2
C	95	ILE	THR	variant	UNP P0DTC2
C	142	ASP	GLY	variant	UNP P0DTC2
C	?	-	VAL	deletion	UNP P0DTC2
C	?	-	TYR	deletion	UNP P0DTC2
C	?	-	TYR	deletion	UNP P0DTC2
C	210A	ILE	LEU	variant	UNP P0DTC2
C	210D	GLU	-	insertion	UNP P0DTC2
C	210E	PRO	-	insertion	UNP P0DTC2
C	210F	GLU	-	insertion	UNP P0DTC2
C	339	ASP	GLY	variant	UNP P0DTC2
C	371	LEU	SER	variant	UNP P0DTC2
C	373	PRO	SER	variant	UNP P0DTC2
C	375	PHE	SER	variant	UNP P0DTC2
C	417	ASN	LYS	variant	UNP P0DTC2
C	440	LYS	ASN	variant	UNP P0DTC2
C	446	SER	GLY	variant	UNP P0DTC2
C	477	ASN	SER	variant	UNP P0DTC2
C	478	LYS	THR	variant	UNP P0DTC2
C	484	ALA	GLU	variant	UNP P0DTC2
C	493	ARG	GLN	variant	UNP P0DTC2
C	496	SER	GLY	variant	UNP P0DTC2
C	498	ARG	GLN	variant	UNP P0DTC2
C	501	TYR	ASN	variant	UNP P0DTC2
C	505	HIS	TYR	variant	UNP P0DTC2
C	547	LYS	THR	variant	UNP P0DTC2
C	614	GLY	ASP	variant	UNP P0DTC2
C	655	TYR	HIS	variant	UNP P0DTC2
C	679	LYS	ASN	variant	UNP P0DTC2
C	681	HIS	PRO	variant	UNP P0DTC2
C	682	GLY	ARG	variant	UNP P0DTC2
C	683	SER	ARG	variant	UNP P0DTC2
C	685	SER	ARG	variant	UNP P0DTC2
C	764	LYS	ASN	variant	UNP P0DTC2
C	796	TYR	ASP	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	856	LYS	ASN	variant	UNP P0DTC2
C	954	HIS	GLN	variant	UNP P0DTC2
C	969	LYS	ASN	variant	UNP P0DTC2
C	981	PHE	LEU	variant	UNP P0DTC2
C	986	PRO	LYS	variant	UNP P0DTC2
C	987	PRO	VAL	variant	UNP P0DTC2
C	1211	LYS	-	expression tag	UNP P0DTC2
C	1212	ASP	-	expression tag	UNP P0DTC2
C	1213	ILE	-	expression tag	UNP P0DTC2
C	1214	ARG	-	expression tag	UNP P0DTC2
C	1215	SER	-	expression tag	UNP P0DTC2
C	1216	LEU	-	expression tag	UNP P0DTC2
C	1217	VAL	-	expression tag	UNP P0DTC2
C	1218	PRO	-	expression tag	UNP P0DTC2
C	1219	ARG	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	SER	-	expression tag	UNP P0DTC2
C	1222	PRO	-	expression tag	UNP P0DTC2
C	1223	GLY	-	expression tag	UNP P0DTC2
C	1224	SER	-	expression tag	UNP P0DTC2
C	1225	GLY	-	expression tag	UNP P0DTC2
C	1226	TYR	-	expression tag	UNP P0DTC2
C	1227	ILE	-	expression tag	UNP P0DTC2
C	1228	PRO	-	expression tag	UNP P0DTC2
C	1229	GLU	-	expression tag	UNP P0DTC2
C	1230	ALA	-	expression tag	UNP P0DTC2
C	1231	PRO	-	expression tag	UNP P0DTC2
C	1232	ARG	-	expression tag	UNP P0DTC2
C	1233	ASP	-	expression tag	UNP P0DTC2
C	1234	GLY	-	expression tag	UNP P0DTC2
C	1235	GLN	-	expression tag	UNP P0DTC2
C	1236	ALA	-	expression tag	UNP P0DTC2
C	1237	TYR	-	expression tag	UNP P0DTC2
C	1238	VAL	-	expression tag	UNP P0DTC2
C	1239	ARG	-	expression tag	UNP P0DTC2
C	1240	LYS	-	expression tag	UNP P0DTC2
C	1241	ASP	-	expression tag	UNP P0DTC2
C	1242	GLY	-	expression tag	UNP P0DTC2
C	1243	GLU	-	expression tag	UNP P0DTC2
C	1244	TRP	-	expression tag	UNP P0DTC2
C	1245	VAL	-	expression tag	UNP P0DTC2
C	1246	LEU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1247	LEU	-	expression tag	UNP P0DTC2
C	1248	SER	-	expression tag	UNP P0DTC2
C	1249	THR	-	expression tag	UNP P0DTC2
C	1250	PHE	-	expression tag	UNP P0DTC2
C	1251	LEU	-	expression tag	UNP P0DTC2
C	1252	GLY	-	expression tag	UNP P0DTC2
C	1253	HIS	-	expression tag	UNP P0DTC2
C	1254	HIS	-	expression tag	UNP P0DTC2
C	1255	HIS	-	expression tag	UNP P0DTC2
C	1256	HIS	-	expression tag	UNP P0DTC2
C	1257	HIS	-	expression tag	UNP P0DTC2
C	1258	HIS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called IY-2A Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	223	1650	1052	271	323	4	0	0
2	G	223	1650	1052	271	323	4	0	0
2	I	223	1650	1052	271	323	4	0	0

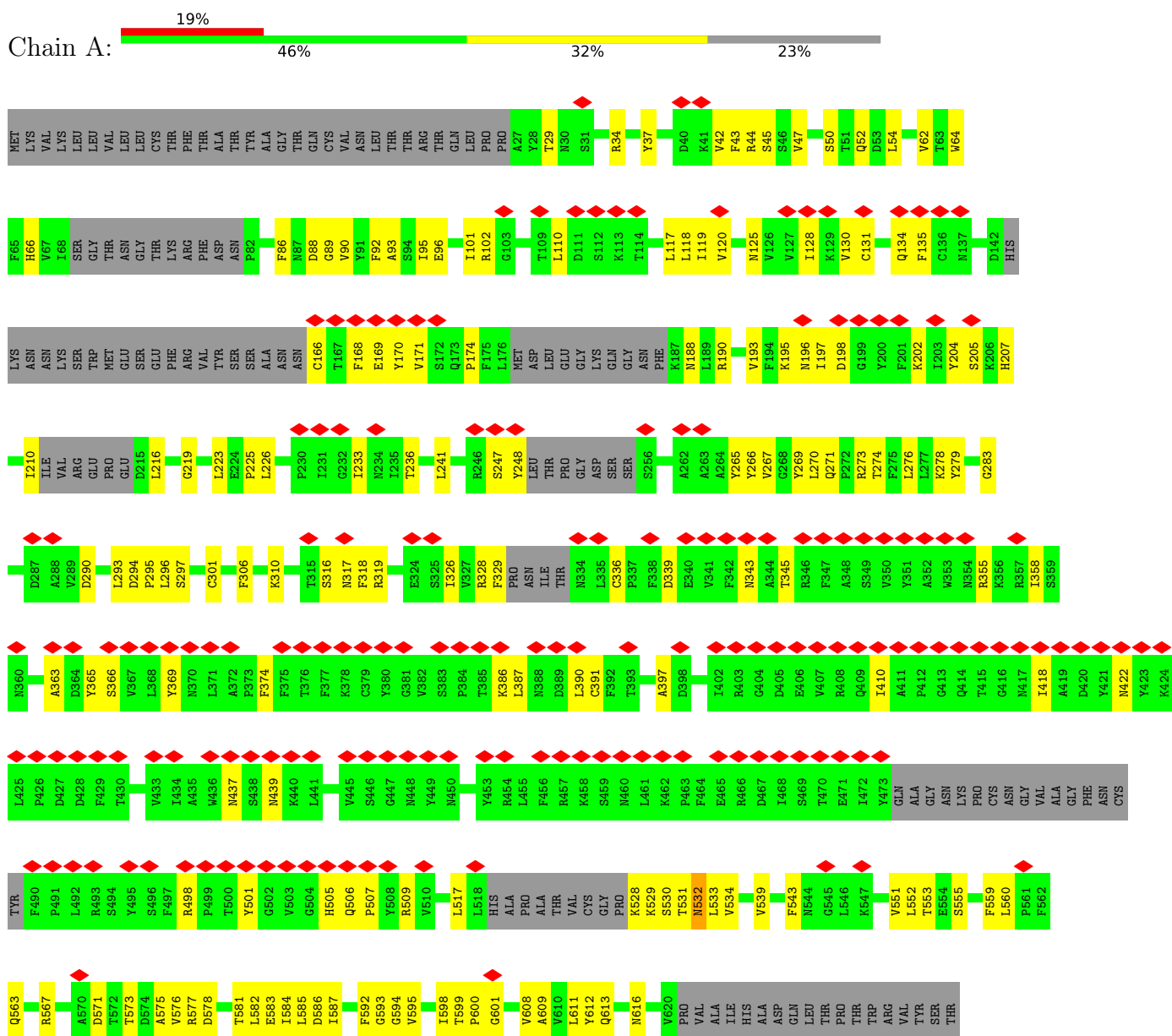
- Molecule 3 is a protein called IY-2A Fab light chain.

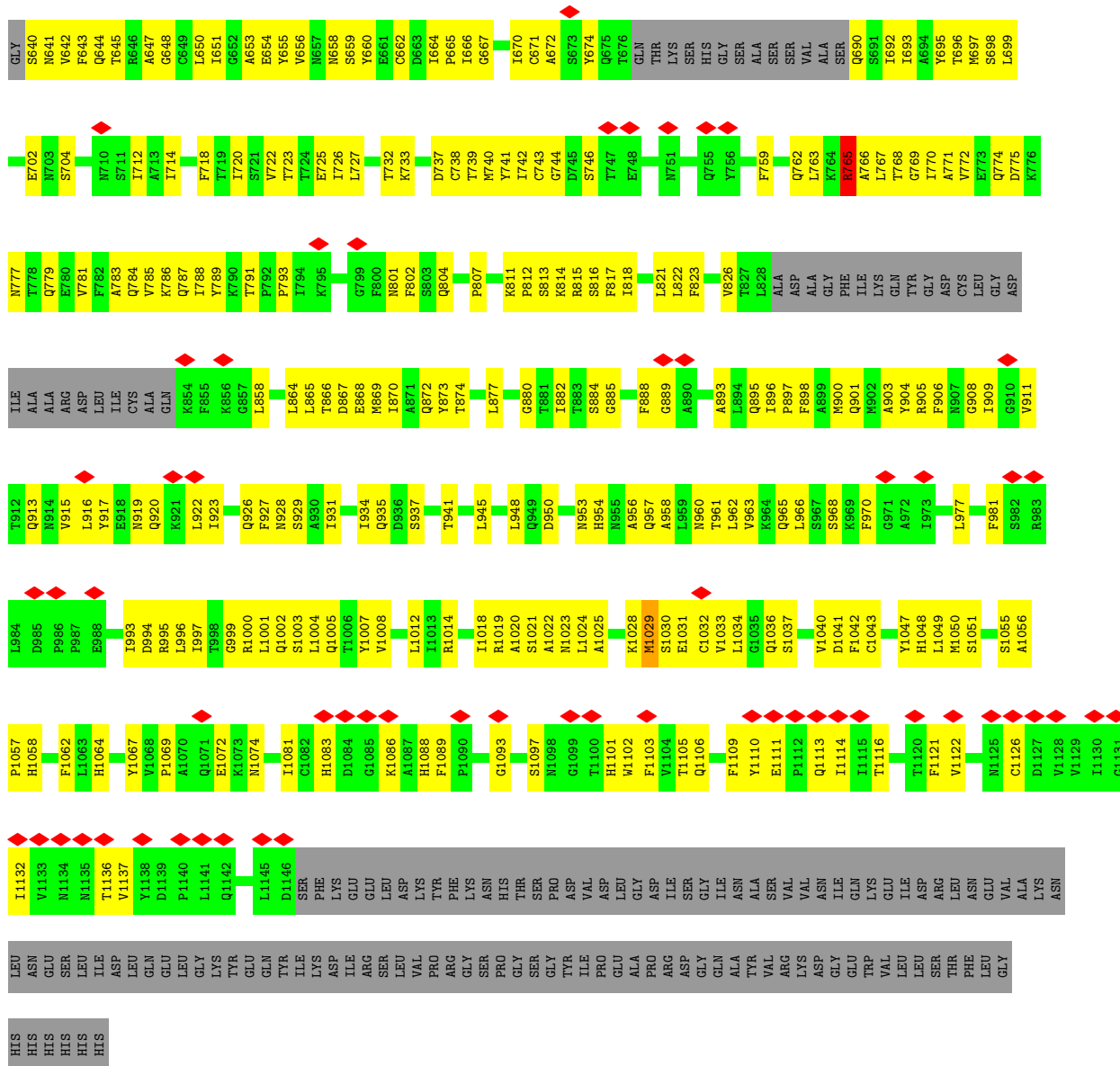
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	F	212	1593	992	265	331	5	0	0
3	H	212	1593	992	265	331	5	0	0
3	J	212	1593	992	265	331	5	0	0

3 Residue-property plots [i](#)

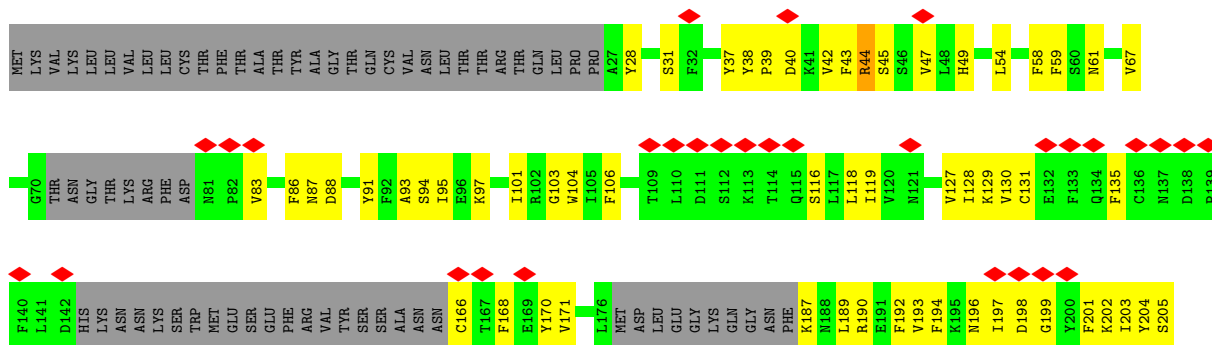
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: Spike glycoprotein





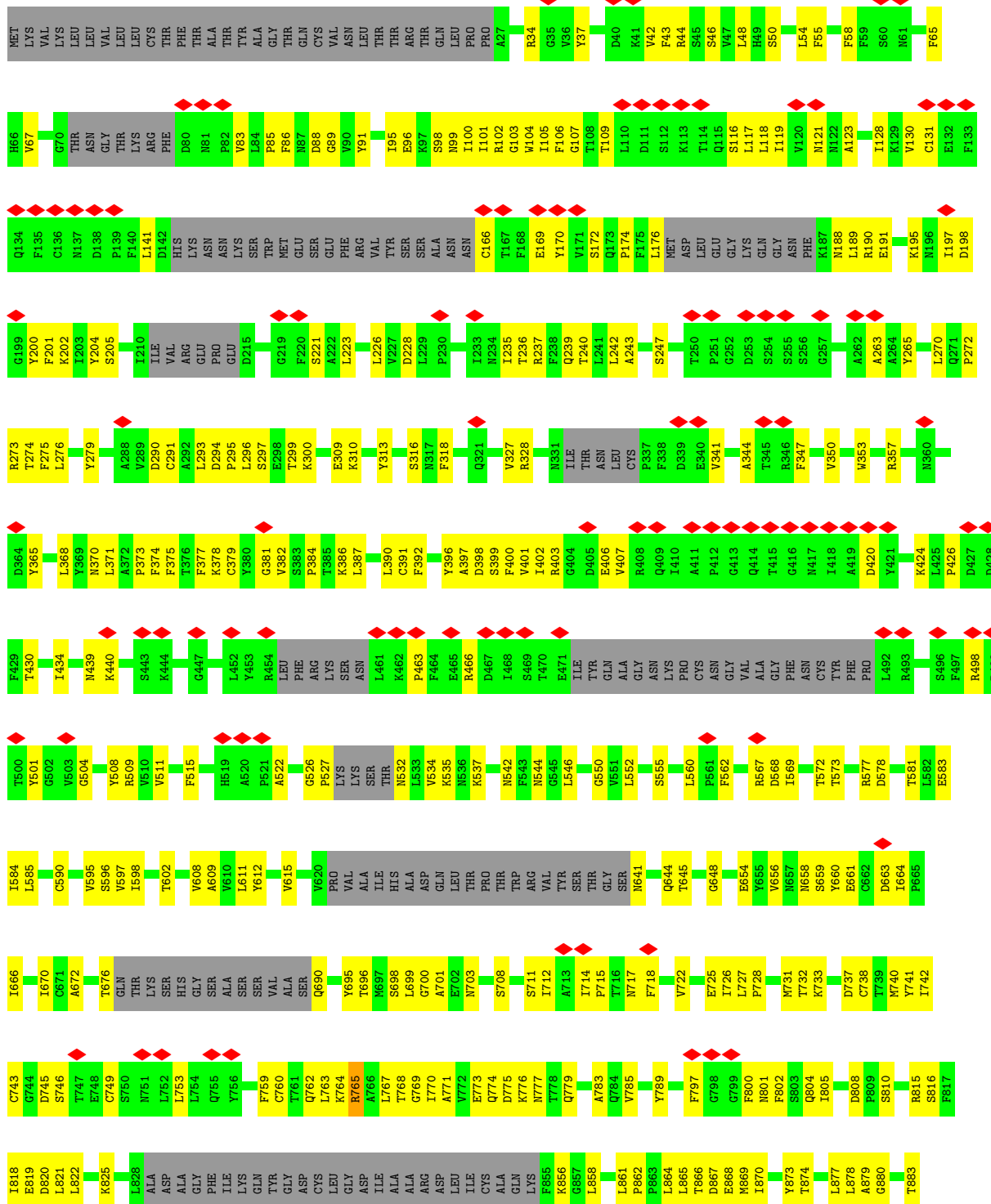
- Molecule 1: Spike glycoprotein

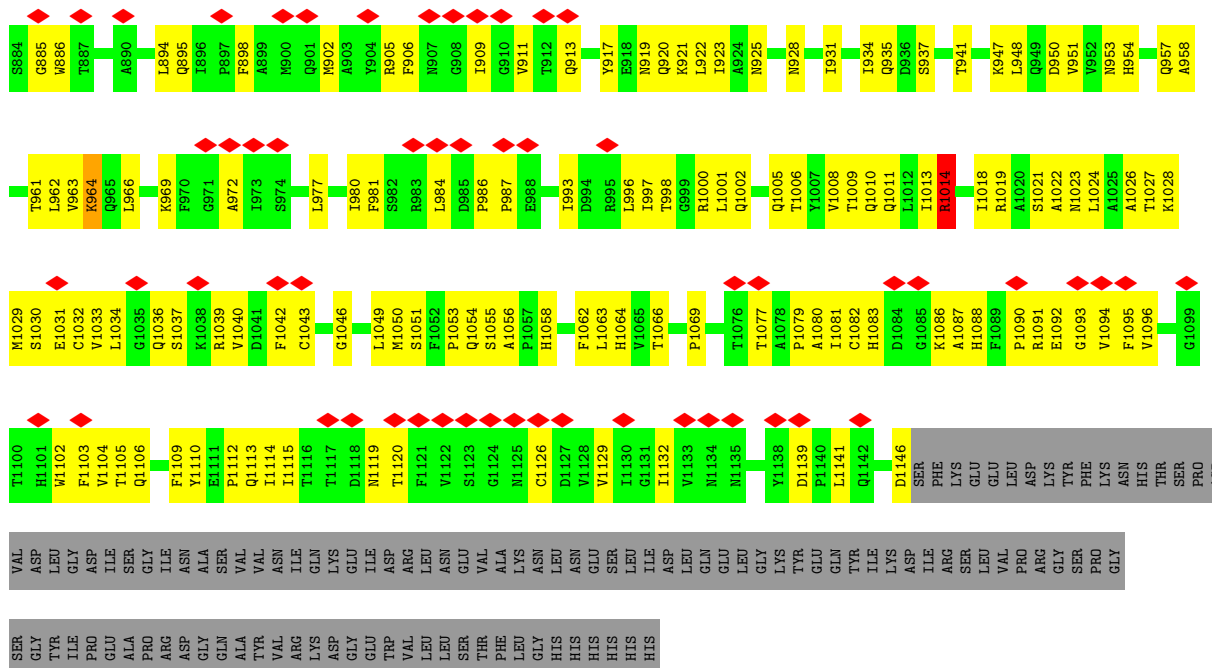


GLU	L1034	T961	T887	R815	G671	T588	V503	S443	A363	L293	I210
ILE	G1035	L962	F888	S816	A672	S891	G504	K444	D364	D294	ILE
ARG	Q1036	L963	G889	F817	A673	S892	H505	K445	P295	D295	VAL
ARG	R1039	K964	A890	F818	T676	F992	Q506	V445	V365	L296	ARG
ASN	V1040	Q965	G891	E819	THR	G594	F507	S446	S566	E298	GLU
VAL	D1041	L966	A892	D820	LYS	G595	F508	M447	V367	T299	PRO
ALA	F1042	K969	A893	L822	SER	V598	R509	M448	V368	K300	GLU
LYS	H1048	F970	R894	L823	HIS	T599	S514	Y449	Y369	D215	LYS
ASN	L1049	G971	L895	A609	GLY	P600	F515	M450	N370	L216	LYS
LEU	M1050	A972	R896	A609	VAL	G601	H519	M451	N371	L223	LYS
ASN	S1051	I973	F897	A609	ALA	V608	A520	Y451	N372	L226	LYS
GLU	F1052	S974	P897	A609	SER	V608	A521	Y452	A372	L227	LYS
LEU	S1055	S975	Q901	A609	SER	V608	A522	Y453	F373	V227	LYS
LEU	A1056	N976	L894	A609	ALA	V610	T523	Y454	F374	D228	LYS
ASP	F1057	L977	L894	A609	SER	V611	V524	Y455	G381	I231	LYS
LEU	H1058	R978	L895	A609	SER	V612	P527	Y455	V382	G232	LYS
GLN	I1058	D979	L895	A609	VAL	Q613	LYS	Y455	S316	I233	LYS
GLU	G1059	R979	L895	A609	VAL	G614	SER	Y455	R319	N234	LYS
LEU	V1060	F981	L895	A609	ALA	G614	SER	Y455	V320	I235	LYS
LEU	V1061	S982	L895	A609	SER	V615	THR	Y455	Q321	I236	LYS
GLY	F1062	R983	L895	A609	SER	V615	THR	Y455	E324	R237	LYS
LYS	L1063	R983	L895	A609	SER	V615	THR	Y455	S325	F238	LYS
TYR	H1064	L984	L895	A609	SER	V615	THR	Y455	I326	Q239	LYS
GLU	Y1067	D985	L895	A609	SER	V615	THR	Y455	V327	T240	LYS
GLN	Y1067	P986	L895	A609	SER	V615	THR	Y455	R328	L241	LYS
TYR	D1146	P987	L895	A609	SER	V615	THR	Y455	F329	Y248	LYS
ILE	SER	E988	L895	A609	SER	V615	THR	Y455	PRO	L249	LYS
LYS	PHE	A989	L895	A609	SER	V615	THR	Y455	ASN	L249	LYS
ASP	E1072	A990	L895	A609	SER	V615	THR	Y455	ILE	P250	LYS
ILE	K1073	E990	L895	A609	SER	V615	THR	Y455	THR	P251	LYS
ARG	N1074	V991	L895	A609	SER	V615	THR	Y455	ASN	G252	LYS
SER	GLU	Q992	L895	A609	SER	V615	THR	Y455	ASN	G253	LYS
LEU	LEU	Q992	L895	A609	SER	V615	THR	Y455	ASN	S254	LYS
VAL	ASP	A930	L895	A609	SER	V615	THR	Y455	ASN	T259	LYS
VAL	LYS	R931	L895	A609	SER	V615	THR	Y455	ASN	A263	LYS
PRO	TYR	G932	L895	A609	SER	V615	THR	Y455	ASN	A264	LYS
ARG	PHE	A1080	L895	A609	SER	V615	THR	Y455	ASN	Y265	LYS
GLY	I1081	L996	L895	A609	SER	V615	THR	Y455	ASN	Y266	LYS
LYS	I1081	I997	L895	A609	SER	V615	THR	Y455	ASN	L270	LYS
SER	C1082	I997	L895	A609	SER	V615	THR	Y455	ASN	R273	LYS
PRO	H1083	R1000	L895	A609	SER	V615	THR	Y455	ASN	T274	LYS
GLY	THR	L1001	L895	A609	SER	V615	THR	Y455	ASN	L276	LYS
SER	SER	Q1002	L895	A609	SER	V615	THR	Y455	ASN	Y279	LYS
GLY	PRO	S1003	L895	A609	SER	V615	THR	Y455	ASN	I285	LYS
TYR	ASP	L1004	L895	A609	SER	V615	THR	Y455	ASN	V289	LYS
ILE	VAL	Q1005	L895	A609	SER	V615	THR	Y455	ASN	D290	LYS
PRO	VAL	T1006	L895	A609	SER	V615	THR	Y455	ASN	C291	LYS
PRO	ASP	T1006	L895	A609	SER	V615	THR	Y455	ASN	A292	LYS
ALA	H1088	Y1007	L895	A609	SER	V615	THR	Y455	ASN		LYS
ALA	F1089	V1008	L895	A609	SER	V615	THR	Y455	ASN		LYS
ARG	P1090	Q872	L895	A609	SER	V615	THR	Y455	ASN		LYS
ASP	R1091	Y873	L895	A609	SER	V615	THR	Y455	ASN		LYS
ASP	ILE	T874	L895	A609	SER	V615	THR	Y455	ASN		LYS
ASP	SER	L877	L895	A609	SER	V615	THR	Y455	ASN		LYS
GLY	V1096	L878	L895	A609	SER	V615	THR	Y455	ASN		LYS
GLN	S1097	L878	L895	A609	SER	V615	THR	Y455	ASN		LYS
ALA	ILE	R1014	L895	A609	SER	V615	THR	Y455	ASN		LYS
TYR	ASN	I1018	L895	A609	SER	V615	THR	Y455	ASN		LYS
VAL	ALA	L1018	L895	A609	SER	V615	THR	Y455	ASN		LYS
VAL	SER	T883	L895	A609	SER	V615	THR	Y455	ASN		LYS
ARG	VAL	S884	L895	A609	SER	V615	THR	Y455	ASN		LYS
LYS	VAL	K1028	L895	A609	SER	V615	THR	Y455	ASN		LYS
LYS	VAL	M1029	L895	A609	SER	V615	THR	Y455	ASN		LYS
ASP	VAL	S1030	L895	A609	SER	V615	THR	Y455	ASN		LYS
ASP	ASN	E1031	L895	A609	SER	V615	THR	Y455	ASN		LYS
GLN	ASN	Y1110	L895	A609	SER	V615	THR	Y455	ASN		LYS
LYS	ASN	C1032	L895	A609	SER	V615	THR	Y455	ASN		LYS
GLN	ASN	V1033	L895	A609	SER	V615	THR	Y455	ASN		LYS

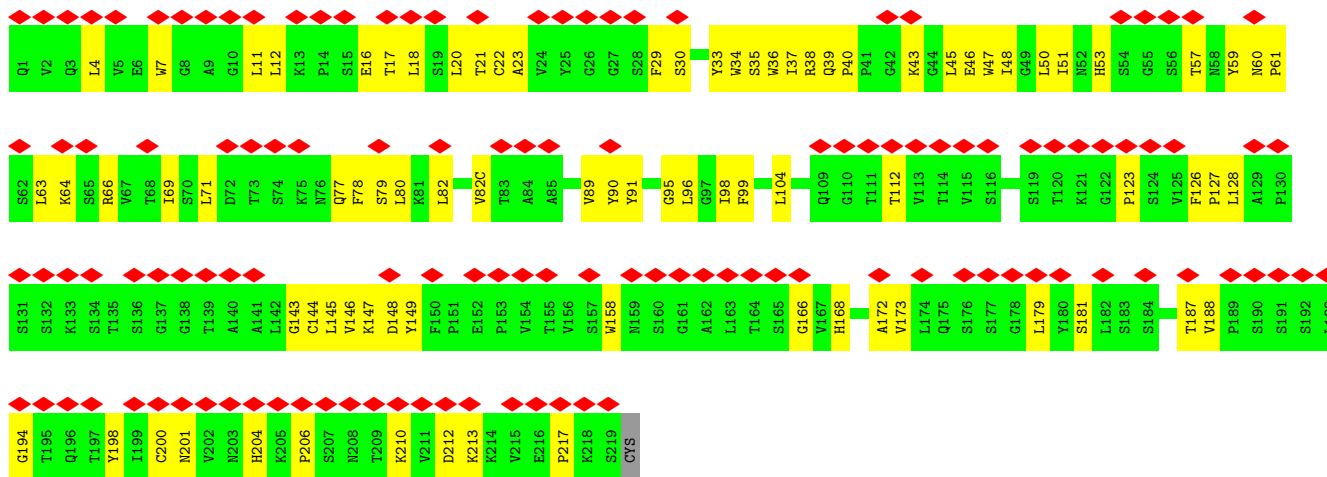
GLY
GLU
TRP
VAL
LEU
LEU
SER
THR
PHE
GLY
GLY
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Spike glycoprotein

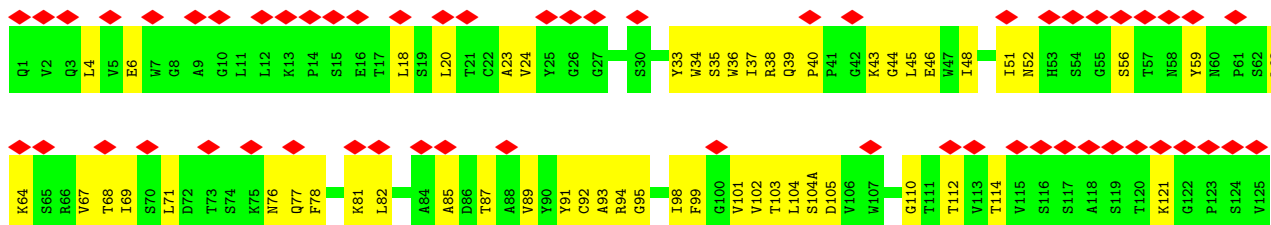


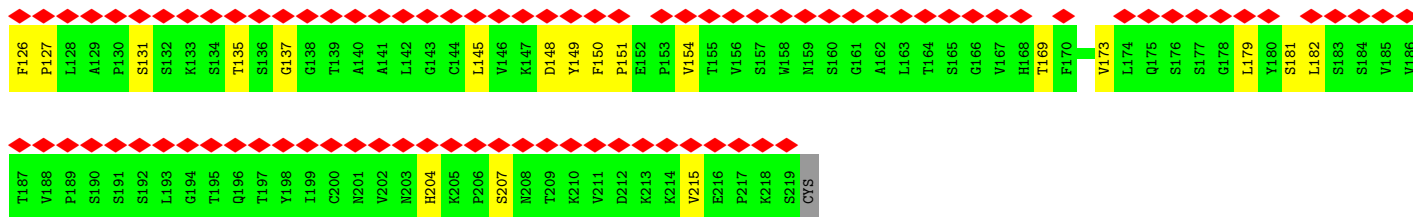


• Molecule 2: IY-2A Fab heavy chain

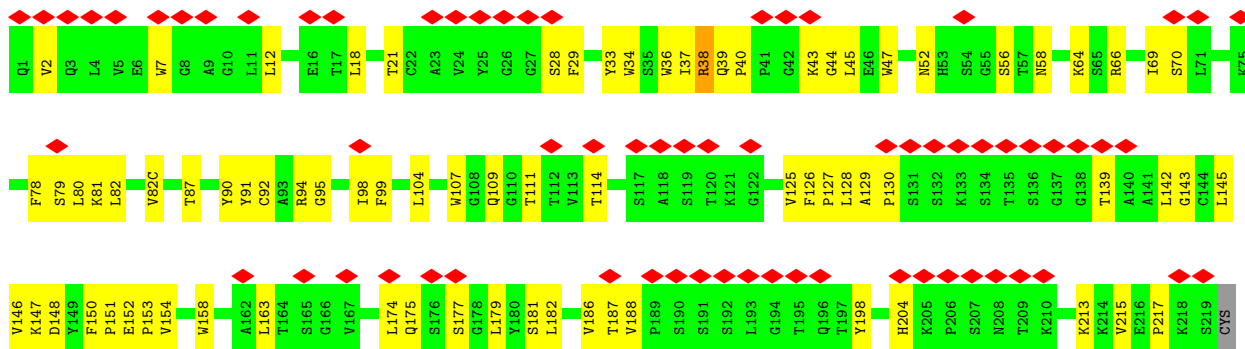


• Molecule 2: IY-2A Fab heavy chain

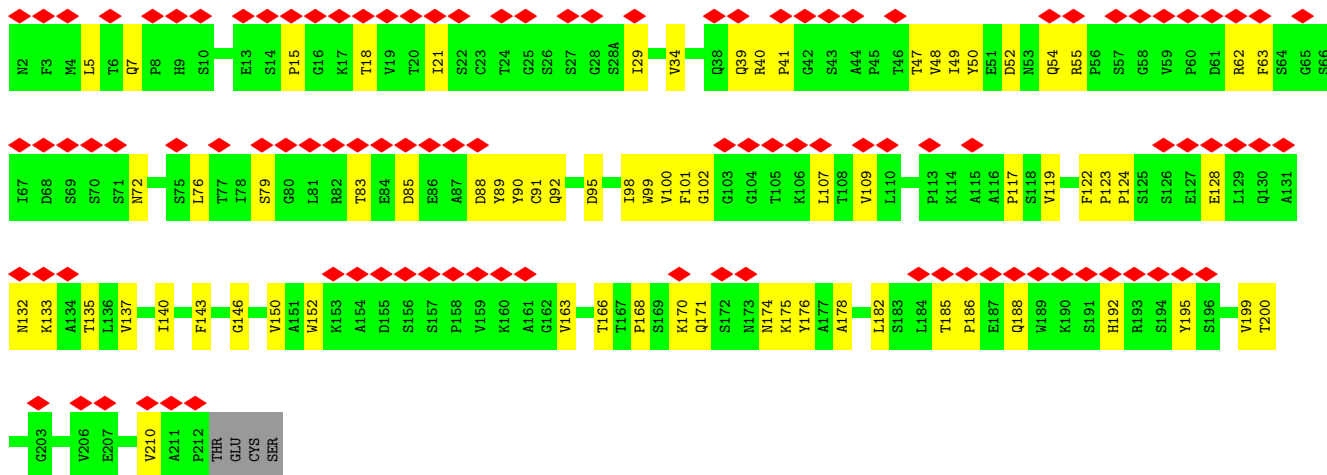




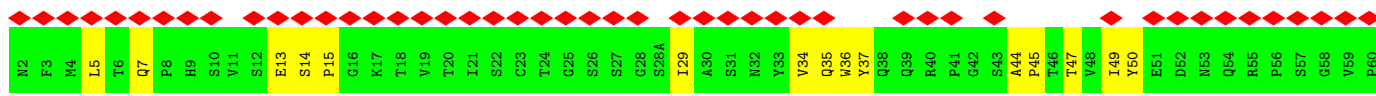
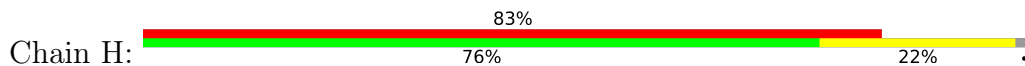
• Molecule 2: IY-2A Fab heavy chain

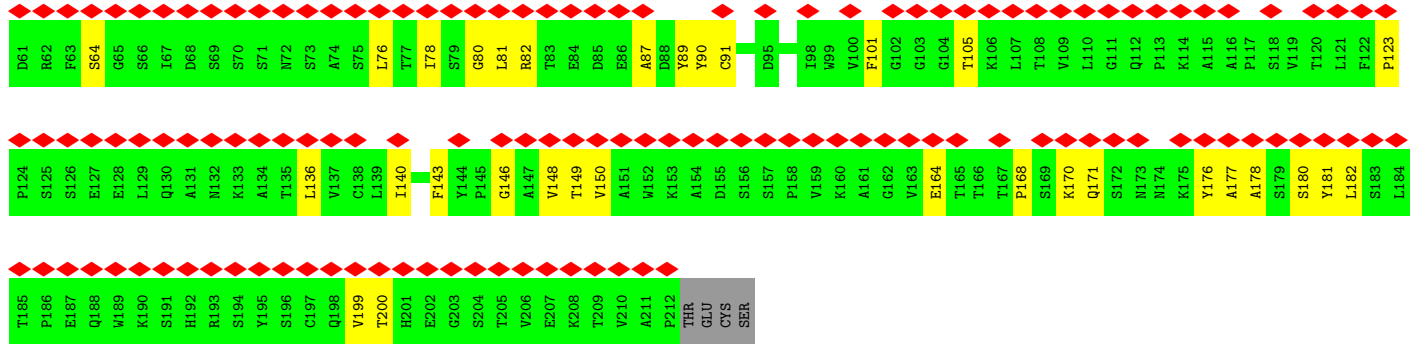


• Molecule 3: IY-2A Fab light chain

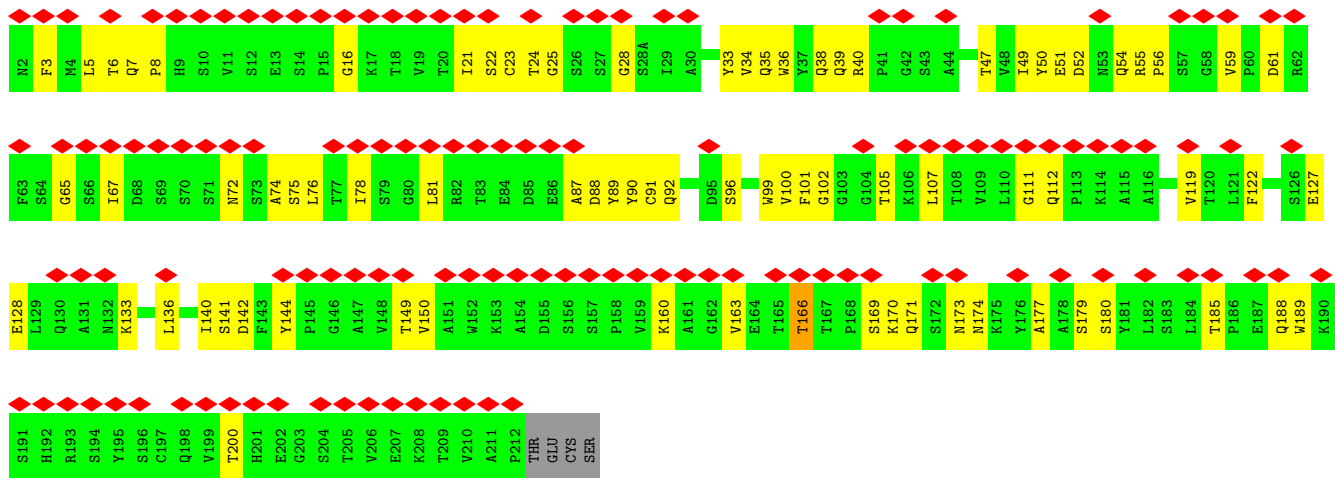


• Molecule 3: IY-2A Fab light chain





• Molecule 3: IY-2A Fab light chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	67276	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.1	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.044	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0037	Depositor
Map size (\AA)	343.43997, 343.43997, 343.43997	wwPDB
Map dimensions	324, 324, 324	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.31	0/7599	0.53	2/10368 (0.0%)
1	B	0.31	0/7595	0.53	0/10366
1	C	0.31	0/7610	0.53	1/10381 (0.0%)
2	E	0.26	0/1692	0.51	0/2314
2	G	0.26	0/1692	0.52	0/2314
2	I	0.26	0/1692	0.50	0/2314
3	F	0.27	0/1633	0.49	0/2231
3	H	0.25	0/1633	0.49	0/2231
3	J	0.27	0/1633	0.50	1/2231 (0.0%)
All	All	0.30	0/32779	0.52	4/44750 (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	C	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	765	ARG	CB-CG-CD	6.64	128.88	111.60
3	J	166	THR	C-N-CA	5.82	136.25	121.70
1	A	1029	MET	CG-SD-CE	-5.45	91.47	100.20
1	C	1014	ARG	CG-CD-NE	-5.01	101.27	111.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	1014	ARG	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	7429	0	7032	373	0
1	B	7424	0	7026	335	0
1	C	7438	0	7090	377	0
2	E	1650	0	1640	75	0
2	G	1650	0	1640	62	0
2	I	1650	0	1640	75	0
3	F	1593	0	1519	62	0
3	H	1593	0	1519	37	0
3	J	1593	0	1519	66	0
All	All	32020	0	30625	1383	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 22.

All (1383) 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:95:ILE:CG1	1:C:189:LEU:HD13	1.29	1.61
1:B:981:PHE:CZ	1:B:993:ILE:HG13	1.59	1.36
1:C:95:ILE:CG1	1:C:189:LEU:CD1	2.09	1.30
1:A:977:LEU:O	1:A:981:PHE:CD2	1.83	1.29
1:A:387:LEU:O	1:A:530:SER:HB3	1.24	1.29
1:A:981:PHE:CZ	1:A:993:ILE:HD12	1.66	1.29
1:C:95:ILE:HG13	1:C:189:LEU:CD1	1.61	1.27
1:A:977:LEU:HB3	1:A:981:PHE:CE2	1.69	1.26
1:A:981:PHE:CE1	1:A:993:ILE:HD12	1.72	1.23
1:C:95:ILE:CD1	1:C:189:LEU:HD13	1.71	1.18
1:A:977:LEU:O	1:A:981:PHE:HD2	1.14	1.14
1:A:387:LEU:O	1:A:530:SER:CB	1.98	1.10
1:A:977:LEU:CB	1:A:981:PHE:HE2	1.64	1.10
1:B:67:VAL:CG2	1:B:265:TYR:HE2	1.66	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:ILE:HG13	1:C:189:LEU:HD13	1.15	1.08
1:B:981:PHE:CE1	1:B:993:ILE:HG13	1.91	1.05
1:C:95:ILE:HG12	1:C:189:LEU:HD13	1.39	1.04
1:B:981:PHE:CZ	1:B:993:ILE:CG1	2.42	1.02
1:A:977:LEU:HB3	1:A:981:PHE:HE2	0.86	1.01
1:A:981:PHE:CE1	1:A:993:ILE:CD1	2.43	1.00
1:B:977:LEU:O	1:B:981:PHE:HD2	1.48	0.96
1:B:67:VAL:CG2	1:B:265:TYR:CE2	2.49	0.96
1:B:977:LEU:O	1:B:981:PHE:CD2	2.19	0.94
1:A:781:VAL:HG13	1:A:1029:MET:HE1	1.49	0.93
1:A:981:PHE:CZ	1:A:993:ILE:CD1	2.51	0.92
2:G:39:GLN:HB2	2:G:45:LEU:HD23	1.53	0.91
1:B:977:LEU:HB3	1:B:981:PHE:HE2	1.36	0.91
1:A:1028:LYS:O	1:A:1032:CYS:HB2	1.72	0.90
1:B:748:GLU:CD	1:B:981:PHE:HE1	1.76	0.89
1:C:95:ILE:HD11	1:C:189:LEU:HD13	1.54	0.89
1:B:95:ILE:HG13	1:B:189:LEU:HD13	1.55	0.88
1:B:541:PHE:O	1:B:547:LYS:HA	1.74	0.87
1:C:95:ILE:HG13	1:C:189:LEU:HD12	1.56	0.87
1:C:95:ILE:HG12	1:C:189:LEU:CD1	1.98	0.87
1:B:1116:THR:HB	1:B:1140:PRO:HD3	1.57	0.86
1:A:958:ALA:HB2	1:A:1014:ARG:HH22	1.41	0.86
1:C:774:GLN:HA	1:C:777:ASN:HD22	1.39	0.85
1:B:572:THR:OG1	1:C:856:LYS:HE2	1.77	0.85
1:C:733:LYS:NZ	1:C:862:PRO:O	2.10	0.84
1:C:931:ILE:HG13	1:C:935:GLN:HE22	1.41	0.84
1:B:981:PHE:CE2	1:B:993:ILE:CD1	2.61	0.84
1:C:905:ARG:HH22	1:C:1050:MET:HB2	1.41	0.84
1:B:67:VAL:HG22	1:B:265:TYR:HE2	1.41	0.83
1:A:714:ILE:O	1:A:1072:GLU:HA	1.78	0.83
1:C:931:ILE:O	1:C:935:GLN:NE2	2.12	0.83
1:A:64:TRP:CE3	1:A:66:HIS:CE1	2.67	0.82
1:A:788:ILE:HD11	1:C:699:LEU:HB2	1.61	0.81
1:A:787:GLN:NE2	1:A:789:TYR:OH	2.13	0.81
1:A:1031:GLU:HB3	1:A:1037:SER:HB2	1.61	0.81
1:B:713:ALA:HB1	1:B:1072:GLU:HB2	1.61	0.81
1:A:290:ASP:O	1:A:297:SER:OG	1.98	0.81
1:A:977:LEU:C	1:A:981:PHE:HD2	1.84	0.81
1:B:1006:THR:HG22	1:B:1010:GLN:HE22	1.46	0.80
3:H:164:GLU:HB2	3:H:181:TYR:HB2	1.61	0.80
1:B:1006:THR:O	1:B:1010:GLN:NE2	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:SER:HA	1:C:279:TYR:O	1.81	0.79
2:G:38:ARG:NH2	2:G:85:ALA:O	2.16	0.79
1:C:1006:THR:O	1:C:1010:GLN:NE2	2.17	0.78
1:B:1002:GLN:HE21	1:C:1002:GLN:HE22	1.29	0.78
3:F:39:GLN:HB3	3:F:88:ASP:HB2	1.64	0.78
1:A:777:ASN:HD21	1:A:1022:ALA:HB3	1.49	0.78
1:A:699:LEU:HG	1:B:788:ILE:HG13	1.65	0.78
1:A:656:VAL:HG22	1:A:658:ASN:H	1.46	0.78
1:B:93:ALA:HB1	1:B:189:LEU:HD11	1.64	0.78
1:B:1091:ARG:NH2	1:B:1118:ASP:O	2.16	0.78
1:B:319:ARG:HH12	1:B:321:GLN:HA	1.49	0.77
1:C:567:ARG:NH1	1:C:573:THR:OG1	2.17	0.77
2:E:96:LEU:HB2	2:E:104:LEU:HB3	1.65	0.77
1:A:977:LEU:C	1:A:981:PHE:CD2	2.56	0.77
1:C:426:PRO:HB3	1:C:463:PRO:HB3	1.66	0.77
1:A:641:ASN:ND2	1:A:654:GLU:OE2	2.18	0.76
1:A:762:GLN:O	1:A:765:ARG:HD3	1.85	0.76
1:A:765:ARG:HH21	1:C:957:GLN:HE22	1.32	0.76
1:C:950:ASP:O	1:C:954:HIS:ND1	2.18	0.76
2:G:52:ASN:HD21	2:G:56:SER:HB2	1.50	0.76
3:H:35:GLN:HE21	3:H:49:ILE:H	1.33	0.76
1:B:736:VAL:HG22	1:B:858:LEU:HG	1.66	0.76
1:B:324:GLU:H	1:B:539:VAL:HG13	1.51	0.76
1:C:386:LYS:HG3	1:C:390:LEU:HG	1.67	0.75
1:A:762:GLN:HB3	1:A:765:ARG:HH11	1.50	0.75
1:B:980:ILE:HG23	1:B:984:LEU:HD12	1.69	0.74
1:B:732:THR:OG1	1:B:955:ASN:ND2	2.19	0.74
1:A:880:GLY:O	1:A:885:GLY:N	2.19	0.74
2:E:71:LEU:HD12	2:E:78:PHE:HB3	1.70	0.74
1:C:1028:LYS:O	1:C:1032:CYS:HB2	1.87	0.74
1:B:656:VAL:HB	1:B:695:TYR:HB3	1.69	0.74
1:A:64:TRP:CD2	1:A:66:HIS:CE1	2.76	0.74
1:B:591:SER:HB2	1:B:615:VAL:HG13	1.69	0.74
1:B:865:LEU:HD12	1:B:873:TYR:HE2	1.51	0.74
3:H:35:GLN:HG3	3:H:49:ILE:HB	1.69	0.74
1:A:1028:LYS:NZ	1:A:1042:PHE:O	2.20	0.73
2:E:166:GLY:HA3	2:E:187:THR:H	1.54	0.73
1:A:880:GLY:HA2	1:A:884:SER:HB2	1.70	0.73
1:B:1028:LYS:NZ	1:B:1042:PHE:O	2.17	0.73
1:B:540:ASN:HA	1:B:548:GLY:O	1.89	0.72
1:C:327:VAL:HA	1:C:542:ASN:HB3	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:VAL:HB	1:B:168:PHE:HB3	1.71	0.72
1:A:674:TYR:HH	1:A:690:GLN:N	1.86	0.72
1:A:779:GLN:O	1:A:783:ALA:N	2.22	0.72
2:I:38:ARG:HD3	2:I:40:PRO:HD3	1.72	0.72
1:A:733:LYS:HE3	1:A:771:ALA:HB1	1.72	0.72
1:A:317:ASN:HB2	1:A:319:ARG:HH11	1.55	0.71
2:I:125:VAL:HB	2:I:213:LYS:HE3	1.72	0.71
1:B:1126:CYS:HB2	1:B:1132:ILE:HD13	1.72	0.71
2:I:146:VAL:HB	2:I:182:LEU:HB3	1.73	0.71
1:C:921:LYS:O	1:C:925:ASN:ND2	2.20	0.71
2:G:45:LEU:HD11	3:H:45:PRO:HB2	1.71	0.71
2:G:94:ARG:NH1	2:G:105:ASP:OD1	2.22	0.71
1:C:106:PHE:HB3	1:C:235:ILE:HD13	1.71	0.71
1:A:310:LYS:HG3	1:A:664:ILE:HD11	1.72	0.71
1:A:870:ILE:HA	1:A:873:TYR:HD2	1.56	0.71
1:B:353:TRP:HZ3	1:B:355:ARG:HB2	1.55	0.71
1:B:802:PHE:HB3	1:B:806:LEU:HD13	1.72	0.71
1:B:1041:ASP:HB3	1:C:1030:SER:HB3	1.71	0.71
1:B:44:ARG:NH2	1:B:279:TYR:OH	2.24	0.71
2:E:20:LEU:HB2	2:E:80:LEU:HB3	1.73	0.71
1:C:205:SER:HB3	1:C:226:LEU:HD12	1.73	0.70
1:B:95:ILE:CG1	1:B:189:LEU:HD13	2.21	0.70
1:C:309:GLU:O	1:C:313:TYR:OH	2.08	0.70
1:B:789:TYR:OH	1:B:891:GLY:O	2.10	0.70
3:F:7:GLN:NE2	3:F:89:TYR:O	2.24	0.70
1:B:748:GLU:OE2	1:B:981:PHE:HE1	1.74	0.70
1:C:767:LEU:HD23	1:C:770:ILE:HD12	1.73	0.70
1:C:774:GLN:NE2	1:C:775:ASP:OD1	2.25	0.70
1:C:611:LEU:HD22	1:C:666:ILE:HG23	1.74	0.70
1:A:666:ILE:HD11	1:A:672:ALA:HB2	1.74	0.70
2:I:145:LEU:HD21	2:I:147:LYS:HE2	1.73	0.69
1:B:903:ALA:HB1	1:B:913:GLN:HG2	1.74	0.69
1:C:195:LYS:HD2	1:C:202:LYS:HD2	1.74	0.69
3:J:28:GLY:O	3:J:72:ASN:ND2	2.26	0.69
1:A:326:ILE:HD13	1:A:534:VAL:HG12	1.74	0.69
1:A:739:THR:O	1:A:744:GLY:N	2.20	0.69
1:B:804:GLN:HG2	1:B:805:ILE:HG23	1.75	0.69
2:I:21:THR:HA	2:I:79:SER:HA	1.75	0.69
1:A:343:ASN:HB2	1:A:369:TYR:HD1	1.58	0.69
1:B:906:PHE:HB3	1:B:911:VAL:HB	1.74	0.69
1:B:977:LEU:HB3	1:B:981:PHE:CE2	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:805:ILE:HG13	1:B:806:LEU:HD12	1.75	0.68
1:C:86:PHE:N	1:C:236:THR:O	2.24	0.68
1:C:774:GLN:HA	1:C:777:ASN:ND2	2.07	0.68
1:A:763:LEU:HD21	1:A:1005:GLN:HE21	1.58	0.68
1:A:1028:LYS:O	1:A:1032:CYS:CB	2.41	0.68
3:F:48:VAL:HG23	3:F:49:ILE:HD12	1.75	0.68
1:A:931:ILE:O	1:A:935:GLN:NE2	2.25	0.68
3:F:55:ARG:NE	3:F:63:PHE:O	2.27	0.68
1:B:67:VAL:HG23	1:B:265:TYR:CE2	2.27	0.68
1:C:644:GLN:NE2	1:C:648:GLY:O	2.27	0.68
1:C:802:PHE:HD1	1:C:805:ILE:HD11	1.58	0.68
1:B:642:VAL:HG22	1:B:651:ILE:HG12	1.76	0.67
1:B:822:LEU:HD22	1:B:945:LEU:HD21	1.76	0.67
1:C:101:ILE:HB	1:C:190:ARG:HH21	1.59	0.67
1:B:598:ILE:HB	1:B:609:ALA:HB3	1.76	0.67
1:A:54:LEU:HD12	1:A:195:LYS:HD2	1.76	0.67
1:B:290:ASP:HB3	1:B:293:LEU:HD23	1.76	0.67
1:A:928:ASN:HA	1:A:931:ILE:HD12	1.76	0.67
1:C:1024:LEU:O	1:C:1028:LYS:HG2	1.94	0.67
1:A:784:GLN:NE2	1:A:889:GLY:O	2.25	0.67
1:C:1026:ALA:O	1:C:1030:SER:OG	2.13	0.67
2:G:87:THR:HG23	2:G:114:THR:HA	1.77	0.67
1:A:102:ARG:HB2	1:A:241:LEU:HB2	1.77	0.67
1:A:714:ILE:HG21	1:A:1110:TYR:HB2	1.76	0.67
1:B:969:LYS:NZ	1:B:974:SER:O	2.28	0.67
1:B:981:PHE:CZ	1:B:993:ILE:CD1	2.78	0.67
1:C:300:LYS:NZ	1:C:602:THR:OG1	2.28	0.66
1:B:905:ARG:NH2	1:B:1049:LEU:O	2.29	0.66
3:F:168:PRO:HB2	3:F:176:TYR:HD2	1.58	0.66
3:J:5:LEU:HD22	3:J:102:GLY:HA2	1.76	0.66
2:E:145:LEU:HD21	2:E:147:LYS:HE2	1.77	0.66
1:B:572:THR:OG1	1:C:856:LYS:CE	2.43	0.66
1:C:577:ARG:HH11	1:C:578:ASP:H	1.44	0.66
2:G:93:ALA:HB1	2:G:104(A):SER:HB3	1.77	0.66
1:A:767:LEU:HA	1:A:770:ILE:HD12	1.78	0.66
1:A:1000:ARG:O	1:A:1003:SER:OG	2.13	0.66
1:A:195:LYS:HB3	1:A:202:LYS:HB3	1.78	0.65
2:E:96:LEU:HD12	2:E:104:LEU:HD22	1.78	0.65
2:I:87:THR:HG23	2:I:114:THR:HA	1.78	0.65
1:C:1114:ILE:O	1:C:1119:ASN:ND2	2.29	0.65
3:F:92:GLN:HE22	3:F:99:TRP:HA	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:126:PHE:HB2	2:I:145:LEU:HB3	1.77	0.65
2:G:59:TYR:HD2	2:G:64:LYS:HD2	1.62	0.65
3:H:37:TYR:HB3	3:H:45:PRO:HB3	1.79	0.65
1:C:37:TYR:HB3	1:C:223:LEU:HD23	1.77	0.65
3:F:170:LYS:NZ	3:F:174:ASN:OD1	2.28	0.65
1:C:577:ARG:NH1	1:C:578:ASP:O	2.30	0.65
1:A:64:TRP:CD2	1:A:66:HIS:ND1	2.65	0.65
1:A:290:ASP:HB3	1:A:293:LEU:HB2	1.79	0.65
1:A:963:VAL:HA	1:A:966:LEU:HD13	1.78	0.65
1:B:611:LEU:HD11	1:B:666:ILE:HG23	1.79	0.65
1:B:889:GLY:HA3	1:B:1034:LEU:HD21	1.79	0.65
1:A:712:ILE:O	1:A:1074:ASN:HA	1.97	0.64
1:B:767:LEU:HA	1:B:770:ILE:HD12	1.79	0.64
1:C:273:ARG:NH2	1:C:290:ASP:OD2	2.30	0.64
1:C:821:LEU:O	1:C:825:LYS:HB2	1.97	0.64
1:A:611:LEU:HD22	1:A:666:ILE:HG22	1.80	0.64
3:J:166:THR:HG1	3:J:179:SER:H	1.44	0.64
1:A:328:ARG:HB2	1:A:543:PHE:HD1	1.62	0.64
1:B:981:PHE:CE2	1:B:993:ILE:HD11	2.33	0.64
1:C:865:LEU:HD12	1:C:873:TYR:HE2	1.62	0.64
2:I:40:PRO:HG2	2:I:43:LYS:HB2	1.78	0.64
1:B:356:LYS:HB3	1:B:397:ALA:HB3	1.79	0.64
1:C:1029:MET:SD	1:C:1053:PRO:HB3	2.37	0.64
3:H:149:THR:HG1	3:H:200:THR:HG1	1.40	0.64
1:C:762:GLN:HG2	1:C:763:LEU:HD12	1.80	0.64
1:A:1126:CYS:HB2	1:A:1132:ILE:HG21	1.80	0.64
1:C:104:TRP:HA	1:C:240:THR:HA	1.79	0.64
1:C:880:GLY:O	1:C:885:GLY:N	2.30	0.64
3:J:6:THR:N	3:J:24:THR:O	2.26	0.64
1:B:95:ILE:HG12	1:B:189:LEU:HB2	1.80	0.64
2:E:89:VAL:HG12	2:E:112:THR:HA	1.80	0.64
2:G:149:TYR:OH	2:G:204:HIS:ND1	2.26	0.64
1:A:576:VAL:HG22	1:A:587:ILE:HD11	1.79	0.64
1:A:1083:HIS:HB3	1:A:1088:HIS:CE1	2.32	0.64
1:A:273:ARG:HH12	1:A:274:THR:HG22	1.62	0.63
1:B:237:ARG:HD3	1:B:239:GLN:HE22	1.62	0.63
1:C:659:SER:OG	1:C:696:THR:O	2.13	0.63
1:C:740:MET:HA	1:C:745:ASP:H	1.63	0.63
1:A:802:PHE:HE1	1:A:927:PHE:HE2	1.47	0.63
1:B:767:LEU:HD23	1:B:770:ILE:HD12	1.79	0.63
1:B:1086:LYS:HE2	1:B:1088:HIS:HE1	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:ILE:HD12	1:A:533:LEU:HD12	1.80	0.63
1:C:54:LEU:HD12	1:C:195:LYS:HG3	1.80	0.63
3:F:7:GLN:HG3	3:F:102:GLY:HA3	1.81	0.63
1:A:600:PRO:HG3	1:A:692:ILE:HD11	1.81	0.63
1:B:981:PHE:CE2	1:B:993:ILE:HD12	2.33	0.63
1:B:1002:GLN:HE21	1:C:1002:GLN:NE2	1.97	0.63
1:C:34:ARG:HH12	1:C:221:SER:HB3	1.62	0.63
2:E:18:LEU:HB3	2:E:82:LEU:HB3	1.81	0.63
2:E:20:LEU:HD13	2:E:80:LEU:HD22	1.81	0.63
1:A:387:LEU:C	1:A:530:SER:HB3	2.16	0.62
1:C:905:ARG:NH2	1:C:1050:MET:HB2	2.14	0.62
1:C:1126:CYS:HB2	1:C:1132:ILE:HD13	1.81	0.62
3:F:150:VAL:HG22	3:F:199:VAL:HG12	1.81	0.62
1:B:338:PHE:HE1	1:B:358:ILE:HG21	1.64	0.62
1:A:656:VAL:HG13	1:A:695:TYR:HB3	1.81	0.62
1:A:931:ILE:HA	1:A:934:ILE:HD12	1.80	0.62
1:B:273:ARG:HH12	1:B:292:ALA:H	1.45	0.62
2:I:33:TYR:O	2:I:95:GLY:N	2.31	0.62
1:B:344:ALA:O	1:B:509:ARG:NH2	2.31	0.62
1:B:877:LEU:HD22	1:B:1029:MET:HE2	1.81	0.62
1:B:1001:LEU:HD12	1:B:1004:LEU:HD11	1.82	0.62
1:C:1080:ALA:HB3	1:C:1129:VAL:HG21	1.82	0.62
2:E:194:GLY:HA2	2:E:217:PRO:HG2	1.82	0.62
1:C:1091:ARG:NH1	1:C:1092:GLU:O	2.32	0.62
3:J:149:THR:OG1	3:J:200:THR:OG1	2.16	0.61
1:A:658:ASN:OD1	1:A:659:SER:N	2.33	0.61
1:B:196:ASN:HD22	1:B:235:ILE:H	1.47	0.61
1:B:294:ASP:O	1:B:297:SER:OG	2.13	0.61
1:B:1040:VAL:HG22	1:C:1031:GLU:HG2	1.82	0.61
1:C:913:GLN:HB2	1:C:917:TYR:CZ	2.35	0.61
2:E:38:ARG:HH12	2:E:48:ILE:HB	1.66	0.61
3:J:112:GLN:NE2	3:J:174:ASN:O	2.26	0.61
1:B:28:TYR:HB3	1:B:61:ASN:HB2	1.82	0.61
2:G:91:TYR:HD1	2:G:110:GLY:HA3	1.64	0.61
2:I:151:PRO:O	2:I:204:HIS:NE2	2.33	0.61
1:B:42:VAL:O	1:B:44:ARG:NH1	2.32	0.61
1:B:954:HIS:O	1:B:957:GLN:HG2	2.00	0.61
2:I:213:LYS:NZ	3:J:127:GLU:OE1	2.29	0.61
1:A:294:ASP:H	1:A:297:SER:HB3	1.65	0.61
1:B:993:ILE:O	1:B:997:ILE:HG12	2.01	0.61
1:C:816:SER:OG	1:C:819:GLU:OE1	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:126:PHE:O	2:E:145:LEU:N	2.27	0.61
2:I:128:LEU:HB3	3:J:122:PHE:CG	2.34	0.61
1:C:1113:GLN:OE1	1:C:1119:ASN:ND2	2.33	0.61
3:J:35:GLN:O	3:J:92:GLN:N	2.20	0.61
1:A:117:LEU:HG	1:A:130:VAL:HG22	1.82	0.61
1:B:751:ASN:OD1	1:B:752:LEU:N	2.33	0.61
3:H:140:ILE:HG21	3:H:148:VAL:HG21	1.83	0.61
1:C:905:ARG:HD3	1:C:1049:LEU:HD22	1.83	0.61
1:C:715:PRO:HG3	1:C:1069:PRO:HB2	1.82	0.60
1:B:67:VAL:HG12	1:B:67:VAL:O	2.02	0.60
1:B:981:PHE:HZ	1:B:993:ILE:HG21	1.67	0.60
1:A:994:ASP:HA	1:A:997:ILE:HD12	1.83	0.60
1:C:733:LYS:HE3	1:C:774:GLN:NE2	2.16	0.60
1:A:1083:HIS:CE1	1:A:1137:VAL:H	2.19	0.60
1:A:1097:SER:HB2	1:A:1102:TRP:CE2	2.36	0.60
1:B:342:PHE:O	1:B:509:ARG:NH1	2.34	0.60
1:B:726:ILE:HG22	1:B:1061:VAL:HG22	1.82	0.60
3:J:34:VAL:N	3:J:52:ASP:OD1	2.34	0.60
1:B:205:SER:H	1:B:226:LEU:HD23	1.65	0.60
1:B:353:TRP:O	1:B:466:ARG:NE	2.33	0.60
1:C:532:ASN:HA	2:I:28:SER:HB2	1.82	0.60
1:C:715:PRO:HG2	1:C:1109:PHE:HA	1.83	0.60
1:C:96:GLU:OE1	1:C:99:ASN:N	2.34	0.60
1:A:317:ASN:O	1:A:319:ARG:NH1	2.34	0.60
1:C:773:GLU:O	1:C:777:ASN:ND2	2.35	0.60
1:A:1031:GLU:O	1:A:1037:SER:N	2.35	0.60
1:B:1039:ARG:NE	1:C:1031:GLU:OE2	2.28	0.60
1:C:318:PHE:HZ	1:C:615:VAL:HG21	1.67	0.60
1:A:366:SER:OG	2:G:56:SER:OG	2.19	0.59
3:J:160:LYS:HA	3:J:163:VAL:HB	1.83	0.59
1:B:190:ARG:HB2	1:B:192:PHE:CE2	2.37	0.59
1:A:722:VAL:HG11	1:A:934:ILE:HG12	1.84	0.59
3:F:192:HIS:HB2	3:F:195:TYR:HE1	1.66	0.59
1:B:899:ALA:HB1	1:B:917:TYR:CE1	2.37	0.59
1:C:353:TRP:O	1:C:466:ARG:NE	2.34	0.59
1:C:1036:GLN:HE21	1:C:1049:LEU:HD23	1.67	0.59
2:G:18:LEU:HB3	2:G:82:LEU:HB3	1.85	0.59
2:G:20:LEU:HD23	2:G:36:TRP:HZ3	1.67	0.59
2:G:71:LEU:HD12	2:G:78:PHE:HB3	1.84	0.59
1:C:274:THR:OG1	1:C:291:CYS:HB3	2.02	0.59
1:C:1087:ALA:HB2	1:C:1126:CYS:HA	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:23:CYS:HB3	3:J:74:ALA:HB3	1.85	0.59
1:A:365:TYR:HB3	2:G:99:PHE:CE1	2.37	0.59
1:B:932:GLY:O	1:B:935:GLN:HG3	2.03	0.59
1:C:1091:ARG:NH2	1:C:1092:GLU:HB3	2.18	0.59
3:F:123:PRO:HG3	3:F:210:VAL:HB	1.84	0.59
2:I:44:GLY:HA2	3:J:90:TYR:CZ	2.38	0.59
1:A:345:THR:O	1:A:509:ARG:NH2	2.36	0.59
1:B:599:THR:HB	1:B:608:VAL:HG12	1.84	0.59
1:C:708:SER:HB3	1:C:711:SER:HB3	1.85	0.59
1:B:94:SER:HB3	1:B:190:ARG:HE	1.68	0.59
1:B:878:LEU:O	1:B:882:ILE:HG12	2.03	0.59
1:C:294:ASP:O	1:C:297:SER:OG	2.14	0.59
3:J:87:ALA:HB3	3:J:89:TYR:HE1	1.68	0.59
1:A:953:ASN:O	1:A:957:GLN:N	2.19	0.58
1:B:91:TYR:HB2	1:B:270:LEU:HD21	1.83	0.58
2:G:121:LYS:HD3	2:G:148:ASP:HB3	1.83	0.58
1:B:865:LEU:HD12	1:B:873:TYR:CE2	2.36	0.58
1:B:960:ASN:O	1:B:964:LYS:N	2.30	0.58
1:C:867:ASP:OD1	1:C:868:GLU:N	2.36	0.58
1:C:906:PHE:HB3	1:C:911:VAL:HB	1.85	0.58
1:C:731:MET:HG2	1:C:732:THR:N	2.18	0.58
3:J:166:THR:OG1	3:J:179:SER:N	2.28	0.58
1:C:664:ILE:HB	1:C:672:ALA:HB3	1.85	0.58
1:C:1028:LYS:NZ	1:C:1042:PHE:O	2.31	0.58
3:F:15:PRO:HG3	3:F:109:VAL:HB	1.85	0.58
1:A:785:VAL:HG21	1:A:888:PHE:CE2	2.38	0.58
1:A:977:LEU:CB	1:A:981:PHE:CE2	2.55	0.58
1:C:290:ASP:OD2	1:C:293:LEU:N	2.36	0.58
1:C:371:LEU:O	2:I:58:ASN:ND2	2.37	0.58
2:E:38:ARG:HE	2:E:90:TYR:HE1	1.51	0.58
1:B:820:ASP:O	1:B:824:ASN:ND2	2.36	0.58
1:C:726:ILE:HG23	1:C:948:LEU:HG	1.86	0.58
1:C:805:ILE:HG22	1:C:818:ILE:HD11	1.84	0.58
3:F:92:GLN:NE2	3:F:99:TRP:HA	2.18	0.58
1:A:725:GLU:OE1	1:A:1064:HIS:NE2	2.36	0.58
1:A:1055:SER:OG	1:A:1056:ALA:N	2.35	0.58
1:C:96:GLU:HG2	1:C:100:ILE:HG22	1.84	0.58
2:E:40:PRO:HG2	2:E:43:LYS:HB2	1.86	0.58
1:A:128:ILE:HB	1:A:170:TYR:HD2	1.69	0.58
1:A:767:LEU:HD23	1:A:770:ILE:HD12	1.84	0.58
1:B:300:LYS:NZ	1:B:306:PHE:O	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:GLU:OE1	1:C:98:SER:N	2.37	0.57
1:C:1104:VAL:HB	1:C:1113:GLN:HE21	1.69	0.57
1:A:336:CYS:HB3	1:A:358:ILE:HD11	1.86	0.57
1:A:937:SER:O	1:A:941:THR:N	2.37	0.57
1:C:726:ILE:CG2	1:C:948:LEU:HG	2.33	0.57
2:E:61:PRO:HA	2:E:64:LYS:HE3	1.86	0.57
2:G:103:THR:HA	3:H:47:THR:HB	1.85	0.57
2:I:36:TRP:CD2	2:I:80:LEU:HD22	2.38	0.57
1:C:767:LEU:HA	1:C:770:ILE:HD12	1.85	0.57
1:B:748:GLU:CD	1:B:981:PHE:CE1	2.67	0.57
1:B:930:ALA:O	1:B:934:ILE:HG12	2.04	0.57
1:B:950:ASP:OD1	1:B:951:VAL:N	2.36	0.57
1:B:1055:SER:OG	1:B:1056:ALA:N	2.36	0.57
1:C:197:ILE:HB	1:C:202:LYS:NZ	2.19	0.57
1:A:740:MET:HA	1:A:744:GLY:HA2	1.85	0.57
3:J:36:TRP:O	3:J:47:THR:HA	2.04	0.57
1:C:661:GLU:O	1:C:695:TYR:OH	2.21	0.57
2:I:36:TRP:HE1	2:I:90:TYR:HB3	1.69	0.57
3:J:185:THR:HG23	3:J:188:GLN:H	1.69	0.57
1:B:118:LEU:HB3	1:B:129:LYS:HB3	1.87	0.57
1:B:815:ARG:NE	1:B:820:ASP:OD1	2.36	0.57
1:C:1005:GLN:O	1:C:1009:THR:HG23	2.05	0.57
3:H:15:PRO:HA	3:H:81:LEU:HD23	1.86	0.57
1:A:575:ALA:HA	1:A:585:LEU:O	2.04	0.57
1:A:656:VAL:HG11	1:A:693:ILE:HD12	1.86	0.57
1:B:424:LYS:HB3	1:B:463:PRO:HG3	1.87	0.57
1:B:870:ILE:HA	1:B:873:TYR:HD2	1.70	0.57
1:C:1028:LYS:HA	1:C:1032:CYS:SG	2.44	0.57
2:I:7:TRP:HA	2:I:111:THR:HG21	1.87	0.57
1:A:599:THR:HG22	1:A:601:GLY:H	1.70	0.57
1:A:822:LEU:HD22	1:A:945:LEU:HD21	1.87	0.57
1:B:748:GLU:OE2	1:B:981:PHE:CE1	2.56	0.57
1:C:961:THR:O	1:C:964:LYS:N	2.37	0.57
2:E:29:PHE:HD1	2:E:34:TRP:NE1	2.03	0.57
1:A:278:LYS:HB2	1:A:306:PHE:CE1	2.40	0.57
1:B:1115:ILE:HA	1:B:1119:ASN:HD21	1.70	0.57
3:F:34:VAL:N	3:F:52:ASP:OD1	2.21	0.57
1:A:190:ARG:HG2	1:A:207:HIS:HD1	1.69	0.56
1:A:1106:GLN:OE1	1:A:1113:GLN:NE2	2.38	0.56
1:B:743:CYS:SG	1:B:746:SER:HB3	2.44	0.56
1:C:825:LYS:NZ	1:C:941:THR:O	2.26	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:47:TRP:CE3	3:F:98:ILE:HD13	2.40	0.56
2:E:48:ILE:HA	2:E:60:ASN:HB2	1.86	0.56
2:E:60:ASN:HA	3:F:98:ILE:HD11	1.85	0.56
2:I:143:GLY:HA2	2:I:158:TRP:CZ2	2.40	0.56
1:A:662:CYS:HB2	1:A:697:MET:HG2	1.86	0.56
1:A:919:ASN:OD1	1:A:922:LEU:HB3	2.05	0.56
1:C:1019:ARG:HH12	1:C:1023:ASN:ND2	2.03	0.56
2:G:48:ILE:HG23	2:G:67:VAL:HG21	1.88	0.56
2:I:52:ASN:ND2	2:I:56:SER:HB2	2.21	0.56
1:B:934:ILE:O	1:B:938:LEU:HG	2.06	0.56
1:C:95:ILE:HD11	1:C:189:LEU:CD1	2.31	0.56
1:B:708:SER:OG	1:B:711:SER:O	2.17	0.56
1:C:801:ASN:HD21	1:C:928:ASN:ND2	2.02	0.56
1:A:977:LEU:CA	1:A:981:PHE:HE2	2.17	0.56
1:B:103:GLY:HA3	1:B:119:ILE:O	2.06	0.56
1:C:931:ILE:HG13	1:C:935:GLN:NE2	2.16	0.56
1:A:34:ARG:NH1	1:A:219:GLY:O	2.35	0.56
1:B:821:LEU:HA	1:B:824:ASN:HD21	1.71	0.56
1:B:938:LEU:HD22	1:B:945:LEU:HD11	1.87	0.56
1:C:1115:ILE:HG23	1:C:1120:THR:HG21	1.87	0.56
2:G:135:THR:OG1	2:G:137:GLY:O	2.23	0.56
1:A:273:ARG:NH1	1:A:274:THR:HG22	2.20	0.56
1:A:858:LEU:HD21	1:A:962:LEU:HD23	1.88	0.56
1:B:87:ASN:ND2	1:B:269:TYR:HB3	2.21	0.56
1:B:858:LEU:HD21	1:B:962:LEU:HD23	1.86	0.56
1:C:771:ALA:O	1:C:774:GLN:HG3	2.06	0.56
1:C:1050:MET:HG2	1:C:1051:SER:H	1.70	0.56
3:J:33:TYR:HB3	3:J:51:GLU:HA	1.88	0.56
1:A:666:ILE:HB	1:A:670:ILE:HG13	1.86	0.56
1:B:957:GLN:O	1:B:961:THR:N	2.35	0.56
1:A:555:SER:HA	1:A:586:ASP:HB2	1.88	0.55
2:G:91:TYR:OH	3:H:44:ALA:N	2.37	0.55
3:H:150:VAL:HG22	3:H:199:VAL:HG12	1.89	0.55
1:B:303:LEU:HD11	1:B:313:TYR:CD1	2.42	0.55
1:B:665:PRO:HA	1:B:671:CYS:HB2	1.87	0.55
1:C:666:ILE:HD11	1:C:672:ALA:HB2	1.88	0.55
2:I:128:LEU:HD11	2:I:145:LEU:HB2	1.87	0.55
2:I:150:PHE:HE2	2:I:179:LEU:HD13	1.70	0.55
2:E:4:LEU:HD21	2:E:34:TRP:HZ3	1.71	0.55
3:F:40:ARG:HG2	3:F:41:PRO:HD2	1.88	0.55
1:C:170:TYR:CZ	1:C:172:SER:HB3	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:200:TYR:HB3	1:C:228:ASP:OD1	2.06	0.55
1:C:534:VAL:HB	1:C:552:LEU:HD12	1.88	0.55
2:E:158:TRP:CZ3	2:E:200:CYS:HB3	2.42	0.55
1:A:125:ASN:HA	1:A:174:PRO:HD3	1.88	0.55
1:A:961:THR:O	1:A:965:GLN:HG3	2.06	0.55
1:C:105:ILE:HG22	1:C:118:LEU:HD23	1.87	0.55
1:C:732:THR:HG22	1:C:1058:HIS:NE2	2.21	0.55
3:F:21:ILE:HB	3:F:76:LEU:HB3	1.87	0.55
1:A:119:ILE:HG12	1:A:128:ILE:HG12	1.88	0.55
1:A:977:LEU:CA	1:A:981:PHE:CE2	2.89	0.55
1:B:722:VAL:HA	1:B:1064:HIS:O	2.07	0.55
1:C:379:CYS:HB2	1:C:384:PRO:HG3	1.88	0.55
1:A:64:TRP:CG	1:A:66:HIS:ND1	2.74	0.55
1:A:913:GLN:OE1	1:A:917:TYR:OH	2.18	0.55
1:A:1040:VAL:HG11	1:B:1034:LEU:HB2	1.89	0.55
2:E:33:TYR:N	2:E:95:GLY:O	2.38	0.55
1:A:766:ALA:O	1:A:770:ILE:HG13	2.06	0.55
2:I:29:PHE:HA	2:I:34:TRP:HZ2	1.72	0.55
2:I:70:SER:N	2:I:79:SER:O	2.31	0.55
1:A:96:GLU:O	1:A:188:ASN:CB	2.55	0.55
1:B:715:PRO:HG3	1:C:894:LEU:HD21	1.89	0.55
2:E:21:THR:HA	2:E:79:SER:HA	1.89	0.55
1:A:741:TYR:HD2	1:A:742:ILE:HG13	1.72	0.55
2:E:37:ILE:HG22	2:E:45:LEU:HD22	1.89	0.55
2:E:127:PRO:HA	2:E:144:CYS:HA	1.89	0.55
1:A:1086:LYS:HD2	1:A:1122:VAL:HG11	1.87	0.54
1:B:969:LYS:HE3	1:B:972:ALA:HB3	1.88	0.54
1:C:95:ILE:CD1	1:C:189:LEU:CD1	2.66	0.54
2:E:143:GLY:HA2	2:E:158:TRP:CH2	2.42	0.54
2:I:39:GLN:HE21	2:I:45:LEU:HD21	1.72	0.54
2:I:47:TRP:HB2	3:J:101:PHE:HE2	1.72	0.54
1:A:195:LYS:HE3	1:A:197:ILE:HG21	1.89	0.54
1:A:777:ASN:ND2	1:A:1022:ALA:HB3	2.19	0.54
1:C:534:VAL:HG13	1:C:537:LYS:HZ3	1.72	0.54
1:C:714:ILE:HD12	1:C:1096:VAL:HG21	1.88	0.54
1:A:865:LEU:HA	1:A:869:MET:HE3	1.89	0.54
1:B:758:SER:O	1:B:761:THR:OG1	2.26	0.54
1:C:85:PRO:HA	1:C:237:ARG:HA	1.89	0.54
1:C:294:ASP:OD1	1:C:297:SER:N	2.37	0.54
1:C:328:ARG:HH22	1:C:532:ASN:N	2.05	0.54
1:B:37:TYR:HB3	1:B:223:LEU:HB3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:VAL:HG22	1:B:171:VAL:HG22	1.88	0.54
1:B:128:ILE:HB	1:B:170:TYR:HB3	1.90	0.54
1:A:42:VAL:C	1:A:44:ARG:HH12	2.10	0.54
1:B:965:GLN:HG2	1:B:1003:SER:OG	2.08	0.54
1:C:296:LEU:HB2	1:C:608:VAL:HB	1.90	0.54
2:I:158:TRP:HB3	2:I:163:LEU:HD23	1.88	0.54
1:A:44:ARG:HE	1:A:279:TYR:HE2	1.56	0.54
1:B:360:ASN:HA	1:B:524:VAL:HG21	1.88	0.54
1:B:1030:SER:HA	1:B:1034:LEU:HD13	1.89	0.54
1:A:317:ASN:HA	1:A:594:GLY:HA2	1.90	0.54
1:A:437:ASN:ND2	1:A:506:GLN:OE1	2.41	0.54
1:B:86:PHE:HB2	1:B:238:PHE:HB3	1.88	0.54
1:C:439:ASN:OD1	1:C:440:LYS:N	2.41	0.54
1:C:725:GLU:OE2	1:C:1064:HIS:NE2	2.39	0.54
3:H:87:ALA:HB3	3:H:89:TYR:HE1	1.72	0.54
1:C:1050:MET:HG2	1:C:1051:SER:N	2.22	0.54
1:C:1091:ARG:HG2	1:C:1119:ASN:O	2.07	0.54
3:J:7:GLN:NE2	3:J:22:SER:O	2.40	0.54
1:A:956:ALA:O	1:A:960:ASN:N	2.27	0.53
1:C:1006:THR:O	1:C:1009:THR:OG1	2.18	0.53
2:I:29:PHE:HA	2:I:34:TRP:CZ2	2.43	0.53
1:B:550:GLY:HA3	1:B:587:ILE:HG23	1.91	0.53
1:B:710:ASN:O	1:B:1077:THR:N	2.32	0.53
1:B:775:ASP:O	1:B:778:THR:OG1	2.26	0.53
1:C:95:ILE:CG1	1:C:189:LEU:HD12	2.21	0.53
2:E:47:TRP:CE3	3:F:98:ILE:HA	2.44	0.53
1:C:290:ASP:O	1:C:297:SER:HB2	2.09	0.53
1:C:762:GLN:O	1:C:765:ARG:HD3	2.09	0.53
1:C:819:GLU:HA	1:C:822:LEU:HB2	1.90	0.53
2:G:34:TRP:N	2:G:51:ILE:O	2.42	0.53
3:J:169:SER:N	3:J:177:ALA:O	2.37	0.53
1:C:95:ILE:HG12	1:C:189:LEU:CB	2.39	0.53
1:C:401:VAL:HG22	1:C:509:ARG:HG2	1.90	0.53
1:C:1046:GLY:HA3	1:C:1066:THR:HG23	1.90	0.53
3:F:152:TRP:CD1	3:F:182:LEU:HD13	2.43	0.53
2:G:91:TYR:CD1	2:G:110:GLY:HA3	2.43	0.53
2:G:131:SER:HB2	3:H:123:PRO:HD2	1.91	0.53
1:A:89:GLY:HA3	1:A:270:LEU:HD12	1.91	0.53
1:B:216:LEU:HD21	1:B:266:TYR:CE2	2.43	0.53
1:C:174:PRO:HB2	1:C:176:LEU:HG	1.89	0.53
1:C:1129:VAL:HB	1:C:1132:ILE:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:128:LEU:HD22	3:J:122:PHE:HB3	1.90	0.53
3:J:3:PHE:CZ	3:J:25:GLY:HA3	2.43	0.53
1:A:896:ILE:HD11	1:A:904:TYR:HE2	1.74	0.53
1:B:742:ILE:HG12	1:B:1000:ARG:HH21	1.72	0.53
1:B:992:GLN:O	1:B:995:ARG:HG2	2.09	0.53
1:C:1011:GLN:HA	1:C:1014:ARG:NH1	2.23	0.53
3:F:152:TRP:CD1	3:F:163:VAL:HG22	2.43	0.53
1:A:927:PHE:O	1:A:931:ILE:HG13	2.09	0.53
1:A:957:GLN:O	1:A:961:THR:HG23	2.08	0.53
3:J:16:GLY:H	3:J:81:LEU:HB3	1.73	0.53
1:A:205:SER:H	1:A:226:LEU:HD23	1.74	0.53
1:A:919:ASN:CG	1:A:923:ILE:HG13	2.28	0.53
1:B:870:ILE:O	1:B:874:THR:HG23	2.09	0.53
1:C:1079:PRO:HG2	1:C:1129:VAL:HG13	1.91	0.53
1:C:1141:LEU:HD11	1:C:1146:ASP:HB2	1.90	0.53
2:E:47:TRP:HE3	3:F:98:ILE:HA	1.74	0.53
1:A:718:PHE:HE2	1:A:720:ILE:HG13	1.74	0.53
1:B:977:LEU:C	1:B:981:PHE:HD2	2.10	0.53
1:B:1014:ARG:O	1:B:1018:ILE:HG12	2.08	0.53
1:C:96:GLU:OE2	1:C:190:ARG:NH1	2.41	0.53
1:B:748:GLU:HA	1:B:751:ASN:ND2	2.24	0.52
1:C:957:GLN:O	1:C:961:THR:HG23	2.09	0.52
3:H:168:PRO:HG3	3:H:178:ALA:HB2	1.92	0.52
1:A:595:VAL:HA	1:A:611:LEU:O	2.09	0.52
1:A:999:GLY:O	1:A:1002:GLN:HG3	2.09	0.52
1:B:991:VAL:HG22	1:B:995:ARG:HH21	1.73	0.52
1:A:642:VAL:HG13	1:A:651:ILE:HG22	1.92	0.52
1:B:901:GLN:O	1:B:905:ARG:HG2	2.09	0.52
1:B:950:ASP:O	1:B:954:HIS:ND1	2.42	0.52
1:B:976:VAL:HG12	1:B:979:ASP:H	1.73	0.52
1:C:403:ARG:NH2	1:C:406:GLU:OE2	2.41	0.52
1:B:726:ILE:HB	1:B:948:LEU:HG	1.91	0.52
1:C:598:ILE:HB	1:C:609:ALA:HB3	1.90	0.52
1:C:715:PRO:O	1:C:1110:TYR:N	2.42	0.52
2:G:38:ARG:HB2	2:G:48:ILE:HD11	1.92	0.52
2:I:143:GLY:HA2	2:I:158:TRP:HZ2	1.74	0.52
1:A:387:LEU:O	1:A:530:SER:OG	2.28	0.52
1:B:87:ASN:HD21	1:B:269:TYR:HB3	1.75	0.52
1:B:666:ILE:HD11	1:B:672:ALA:HB2	1.91	0.52
1:C:309:GLU:HG2	1:C:310:LYS:H	1.74	0.52
1:C:738:CYS:O	1:C:742:ILE:HG12	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:762:GLN:HA	1:C:765:ARG:CD	2.40	0.52
1:C:816:SER:N	1:C:819:GLU:OE2	2.27	0.52
1:C:886:TRP:O	1:C:1034:LEU:HD12	2.09	0.52
1:C:1091:ARG:HG3	1:C:1092:GLU:H	1.75	0.52
1:A:86:PHE:N	1:A:236:THR:O	2.27	0.52
1:B:298:GLU:OE1	1:B:298:GLU:HA	2.10	0.52
1:B:770:ILE:HG23	1:B:774:GLN:HE22	1.75	0.52
1:C:95:ILE:HG12	1:C:189:LEU:HB2	1.92	0.52
1:C:808:ASP:OD2	1:C:810:SER:OG	2.22	0.52
1:C:947:LYS:HA	1:C:950:ASP:HB2	1.91	0.52
2:G:104:LEU:HD23	3:H:50:TYR:HB3	1.92	0.52
3:J:5:LEU:HA	3:J:25:GLY:HA2	1.92	0.52
1:A:95:ILE:HG23	1:A:210:ILE:HD11	1.92	0.52
1:A:903:ALA:HB2	1:A:916:LEU:HD22	1.90	0.52
1:C:91:TYR:HB2	1:C:270:LEU:HD21	1.90	0.52
1:C:769:GLY:O	1:C:773:GLU:HB2	2.10	0.52
2:E:168:HIS:NE2	3:F:171:GLN:HG2	2.24	0.52
3:J:166:THR:HG21	3:J:179:SER:HB2	1.92	0.52
1:A:640:SER:OG	1:A:641:ASN:N	2.42	0.52
1:A:905:ARG:HD3	1:A:1049:LEU:O	2.10	0.52
1:C:402:ILE:O	1:C:508:TYR:N	2.30	0.52
1:A:247:SER:OG	1:A:248:TYR:N	2.43	0.52
1:A:560:LEU:N	1:A:563:GLN:OE1	2.37	0.52
1:A:807:PRO:HB2	1:A:814:LYS:HG3	1.92	0.52
1:B:198:ASP:OD1	1:B:199:GLY:N	2.40	0.52
1:B:867:ASP:OD1	1:B:867:ASP:N	2.41	0.52
1:B:1048:HIS:NE2	1:B:1050:MET:O	2.42	0.52
1:C:1019:ARG:HH12	1:C:1023:ASN:HD21	1.57	0.52
1:C:204:TYR:HB2	1:C:223:LEU:HD21	1.92	0.52
3:J:170:LYS:HE2	3:J:174:ASN:HA	1.93	0.52
1:B:97:LYS:HZ2	1:B:187:LYS:N	2.08	0.51
1:B:356:LYS:O	1:B:397:ALA:N	2.44	0.51
1:B:906:PHE:CZ	1:B:923:ILE:HD13	2.45	0.51
1:B:1087:ALA:HB2	1:B:1126:CYS:HA	1.92	0.51
1:C:996:LEU:O	1:C:1000:ARG:NE	2.41	0.51
2:E:126:PHE:HZ	3:F:133:LYS:HD2	1.75	0.51
3:J:55:ARG:NE	3:J:61:ASP:HA	2.25	0.51
1:A:329:PHE:HE1	1:A:528:LYS:HA	1.75	0.51
1:C:299:THR:HG21	1:C:597:VAL:HG11	1.92	0.51
2:I:175:GLN:NE2	2:I:181:SER:OG	2.42	0.51
1:A:577:ARG:HH22	1:A:582:LEU:HB3	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1081:ILE:HB	1:A:1088:HIS:HB2	1.92	0.51
1:B:39:PRO:HD2	1:B:44:ARG:HH12	1.75	0.51
1:C:919:ASN:O	1:C:923:ILE:HG12	2.10	0.51
1:C:998:THR:HA	1:C:1001:LEU:HG	1.91	0.51
1:A:765:ARG:HH21	1:C:957:GLN:NE2	2.05	0.51
1:B:106:PHE:CE1	1:B:238:PHE:HB2	2.46	0.51
1:B:869:MET:HA	1:B:872:GLN:OE1	2.11	0.51
1:C:759:PHE:HA	1:C:762:GLN:CD	2.31	0.51
2:I:18:LEU:HD23	2:I:82:LEU:HB3	1.93	0.51
2:E:148:ASP:HA	2:E:179:LEU:HB3	1.92	0.51
1:B:1074:ASN:OD1	1:C:895:GLN:NE2	2.44	0.51
1:C:555:SER:HB3	1:C:584:ILE:HG13	1.91	0.51
1:C:1077:THR:HG21	1:C:1094:VAL:HG12	1.92	0.51
2:E:128:LEU:HG	3:F:137:VAL:HG21	1.92	0.51
3:H:136:LEU:HD22	3:H:182:LEU:HD23	1.93	0.51
1:A:43:PHE:HE1	1:A:283:GLY:HA3	1.76	0.51
1:A:90:VAL:HG13	1:A:267:VAL:HG23	1.92	0.51
1:B:131:CYS:HA	1:B:166:CYS:HA	1.92	0.51
1:C:201:PHE:CE1	1:C:235:ILE:HD12	2.45	0.51
1:C:722:VAL:HG23	1:C:934:ILE:HD13	1.93	0.51
1:A:552:LEU:HA	1:A:586:ASP:O	2.11	0.51
1:B:822:LEU:HD21	1:B:938:LEU:HD13	1.92	0.51
3:F:62:ARG:NH2	3:F:85:ASP:OD1	2.44	0.51
3:F:90:TYR:HB3	3:F:101:PHE:HD2	1.76	0.51
2:G:6:GLU:OE2	2:G:92:CYS:N	2.40	0.51
3:J:141:SER:HA	3:J:177:ALA:HA	1.92	0.51
1:A:763:LEU:HD21	1:A:1005:GLN:NE2	2.25	0.51
1:B:273:ARG:NH1	1:B:290:ASP:OD1	2.44	0.51
2:G:4:LEU:HD11	2:G:34:TRP:HZ3	1.76	0.51
3:H:7:GLN:OE1	3:H:91:CYS:N	2.44	0.51
2:I:148:ASP:HA	2:I:179:LEU:HD12	1.92	0.51
1:A:789:TYR:HD1	1:C:703:ASN:HB2	1.75	0.50
1:C:357:ARG:HG3	1:C:396:TYR:HE1	1.76	0.50
3:J:21:ILE:HD11	3:J:107:LEU:HB2	1.92	0.50
3:J:128:GLU:HG2	3:J:133:LYS:HB2	1.93	0.50
1:A:926:GLN:O	1:A:929:SER:OG	2.22	0.50
1:C:420:ASP:HA	1:C:424:LYS:HG2	1.93	0.50
1:C:919:ASN:OD1	1:C:922:LEU:HB3	2.11	0.50
2:I:78:PHE:HZ	2:I:92:CYS:HB2	1.76	0.50
1:A:418:ILE:O	1:A:422:ASN:ND2	2.39	0.50
1:A:640:SER:OG	1:A:654:GLU:OE1	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:867:ASP:OD1	1:A:868:GLU:N	2.44	0.50
1:A:996:LEU:O	1:A:1000:ARG:HG2	2.10	0.50
1:A:1025:ALA:HA	1:A:1028:LYS:HG2	1.94	0.50
1:A:1101:HIS:HB3	1:A:1103:PHE:CE2	2.45	0.50
1:B:351:TYR:HE1	1:B:453:TYR:HA	1.77	0.50
1:C:117:LEU:HD21	1:C:128:ILE:HG23	1.93	0.50
3:F:47:THR:HG21	3:F:50:TYR:CD1	2.47	0.50
1:A:781:VAL:CG1	1:A:1029:MET:HE1	2.32	0.50
1:A:950:ASP:O	1:A:954:HIS:ND1	2.43	0.50
1:C:107:GLY:HA2	1:C:235:ILE:HG12	1.92	0.50
1:C:295:PRO:HB2	1:C:608:VAL:HG21	1.93	0.50
1:C:534:VAL:HG13	1:C:537:LYS:NZ	2.27	0.50
1:C:749:CYS:SG	1:C:977:LEU:HG	2.52	0.50
2:E:126:PHE:N	2:E:145:LEU:O	2.42	0.50
3:H:136:LEU:HB2	3:H:182:LEU:HB3	1.92	0.50
3:J:119:VAL:HG22	3:J:140:ILE:HG22	1.93	0.50
1:B:552:LEU:HD23	1:B:585:LEU:HD13	1.93	0.50
2:I:129:ALA:HB1	2:I:217:PRO:HA	1.94	0.50
2:I:130:PRO:HD3	2:I:142:LEU:HB3	1.92	0.50
1:A:1106:GLN:OE1	1:A:1106:GLN:N	2.44	0.50
1:B:714:ILE:HG21	1:B:1110:TYR:HB2	1.93	0.50
1:C:275:PHE:CD1	1:C:290:ASP:HA	2.46	0.50
1:C:1055:SER:OG	1:C:1056:ALA:N	2.44	0.50
2:E:204:HIS:CD2	2:E:206:PRO:HD2	2.47	0.50
3:J:39:GLN:N	3:J:88:ASP:O	2.36	0.50
1:A:609:ALA:HB1	1:A:653:ALA:HB2	1.93	0.50
1:A:869:MET:HA	1:A:872:GLN:OE1	2.11	0.50
2:I:2:VAL:HG21	2:I:94:ARG:NH1	2.27	0.50
1:A:86:PHE:CZ	1:A:89:GLY:HA2	2.47	0.50
1:A:712:ILE:HA	1:B:895:GLN:HE22	1.77	0.50
1:B:216:LEU:HD21	1:B:266:TYR:HE2	1.76	0.50
1:B:382:VAL:HB	1:B:430:THR:HG23	1.93	0.50
1:C:34:ARG:NH2	1:C:191:GLU:OE1	2.44	0.50
1:C:764:LYS:O	1:C:768:THR:HG23	2.12	0.50
1:C:542:ASN:HA	1:C:546:LEU:O	2.11	0.50
2:E:4:LEU:HD21	2:E:34:TRP:CZ3	2.46	0.50
1:A:1021:SER:O	1:A:1024:LEU:HB3	2.11	0.49
1:B:774:GLN:HA	1:B:777:ASN:OD1	2.12	0.49
1:C:1037:SER:OG	1:C:1043:CYS:SG	2.58	0.49
3:F:34:VAL:HA	3:F:92:GLN:O	2.12	0.49
3:H:29:ILE:HD11	3:H:34:VAL:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:905:ARG:HD3	1:A:1050:MET:HB3	1.94	0.49
1:A:909:ILE:HG21	1:A:1047:TYR:HB3	1.94	0.49
1:B:116:SER:HB2	1:B:135:PHE:CZ	2.47	0.49
1:B:614:GLY:N	1:B:647:ALA:O	2.28	0.49
1:C:740:MET:HA	1:C:745:ASP:N	2.26	0.49
1:C:1030:SER:O	1:C:1034:LEU:HB2	2.11	0.49
1:A:339:ASP:HA	1:A:369:TYR:HE1	1.76	0.49
1:A:788:ILE:H	1:A:788:ILE:HD12	1.76	0.49
1:B:67:VAL:HG21	1:B:265:TYR:CE2	2.46	0.49
1:B:737:ASP:OD1	1:B:738:CYS:N	2.45	0.49
1:C:658:ASN:ND2	1:C:660:TYR:OH	2.44	0.49
1:B:347:PHE:HE1	1:B:399:SER:HB2	1.76	0.49
1:B:396:TYR:HB2	1:B:514:SER:HB2	1.94	0.49
1:C:100:ILE:HG13	1:C:242:LEU:HD23	1.94	0.49
1:C:759:PHE:HA	1:C:762:GLN:NE2	2.27	0.49
1:C:958:ALA:O	1:C:961:THR:OG1	2.24	0.49
2:I:69:ILE:HD11	2:I:78:PHE:CD2	2.48	0.49
3:J:5:LEU:HD21	3:J:91:CYS:SG	2.53	0.49
1:A:328:ARG:NH1	1:A:532:ASN:H	2.10	0.49
1:B:725:GLU:OE1	1:B:1064:HIS:NE2	2.45	0.49
1:B:762:GLN:HB2	1:B:765:ARG:HH21	1.77	0.49
1:C:54:LEU:HD21	1:C:197:ILE:HD11	1.94	0.49
1:C:327:VAL:C	1:C:328:ARG:HD2	2.32	0.49
1:C:931:ILE:HA	1:C:934:ILE:HG22	1.95	0.49
3:F:132:ASN:HA	3:F:186:PRO:HG3	1.94	0.49
1:B:273:ARG:NH2	1:B:292:ALA:HB3	2.27	0.49
2:E:35:SER:HB3	2:E:47:TRP:CD1	2.48	0.49
3:H:150:VAL:HG21	3:H:180:SER:HB3	1.95	0.49
1:A:567:ARG:HA	1:A:573:THR:HA	1.95	0.49
1:A:897:PRO:HG2	1:A:900:MET:HB2	1.94	0.49
1:A:1093:GLY:HA3	1:A:1105:THR:O	2.12	0.49
1:B:368:LEU:HG	1:B:372:ALA:HB2	1.95	0.49
1:C:141:LEU:HD21	1:C:247:SER:HB2	1.94	0.49
1:C:783:ALA:HB2	1:C:873:TYR:CE1	2.48	0.49
2:G:6:GLU:HB2	2:G:110:GLY:HA2	1.93	0.49
1:A:130:VAL:H	1:A:168:PHE:HD2	1.60	0.49
1:B:103:GLY:O	1:B:241:LEU:N	2.43	0.49
1:B:328:ARG:HB2	1:B:543:PHE:CE2	2.47	0.49
1:C:83:VAL:HG13	1:C:239:GLN:HB2	1.95	0.49
2:G:89:VAL:HG12	2:G:112:THR:HA	1.94	0.49
3:J:150:VAL:HG11	3:J:180:SER:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:981:PHE:CE1	1:A:993:ILE:HD11	2.43	0.49
1:B:326:ILE:HG22	1:B:532:ASN:HA	1.94	0.49
1:B:1090:PRO:HD3	1:B:1095:PHE:CE2	2.48	0.49
3:J:92:GLN:HA	3:J:100:VAL:O	2.12	0.49
1:A:134:GLN:NE2	1:A:135:PHE:O	2.46	0.49
1:A:563:GLN:HG2	1:B:43:PHE:HB2	1.95	0.49
1:A:667:GLY:O	1:A:670:ILE:HG12	2.13	0.49
1:A:1001:LEU:O	1:A:1004:LEU:N	2.46	0.49
1:B:316:SER:O	1:B:595:VAL:HG22	2.13	0.49
1:B:752:LEU:HD11	1:B:990:GLU:O	2.13	0.49
1:B:769:GLY:O	1:B:772:VAL:HG22	2.12	0.49
1:B:884:SER:OG	1:B:893:ALA:HB1	2.12	0.49
1:C:88:ASP:HB3	1:C:270:LEU:O	2.12	0.49
1:C:906:PHE:O	1:C:911:VAL:N	2.39	0.49
3:F:18:THR:HG23	3:F:79:SER:HA	1.94	0.49
3:F:89:TYR:CE1	3:F:107:LEU:HB3	2.48	0.49
2:G:45:LEU:HB2	3:H:101:PHE:CE2	2.48	0.49
1:A:741:TYR:OH	1:A:1000:ARG:NH2	2.46	0.48
1:A:908:GLY:HA3	1:A:1036:GLN:NE2	2.28	0.48
1:A:1014:ARG:O	1:A:1018:ILE:HD12	2.13	0.48
1:B:664:ILE:O	1:B:671:CYS:HB2	2.13	0.48
1:C:731:MET:HE3	1:C:1014:ARG:HH21	1.78	0.48
2:I:104:LEU:HA	3:J:35:GLN:OE1	2.13	0.48
1:A:216:LEU:HD21	1:A:266:TYR:HE2	1.77	0.48
2:G:51:ILE:HD13	2:G:71:LEU:HB2	1.95	0.48
2:G:169:THR:O	3:H:171:GLN:HG2	2.13	0.48
1:A:118:LEU:HB2	1:A:135:PHE:CZ	2.48	0.48
1:A:498:ARG:HD2	1:A:501:TYR:CZ	2.48	0.48
1:A:1029:MET:HA	1:A:1033:VAL:HG23	1.95	0.48
2:G:63:LEU:O	2:G:67:VAL:N	2.44	0.48
1:B:101:ILE:O	1:B:190:ARG:NH2	2.21	0.48
1:B:349:SER:OG	1:B:452:LEU:O	2.24	0.48
1:B:593:GLY:HA3	1:B:613:GLN:O	2.14	0.48
2:E:30:SER:HA	2:E:53:HIS:ND1	2.29	0.48
2:G:103:THR:HB	3:H:49:ILE:O	2.13	0.48
1:A:723:THR:HG22	1:A:1064:HIS:HB2	1.95	0.48
1:A:958:ALA:O	1:A:961:THR:OG1	2.19	0.48
2:E:173:VAL:HG12	3:F:166:THR:HG23	1.95	0.48
1:B:231:ILE:HG13	1:B:233:ILE:HG12	1.96	0.48
1:B:324:GLU:O	1:B:540:ASN:ND2	2.47	0.48
1:C:67:VAL:HG12	1:C:67:VAL:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:577:ARG:NH2	1:C:581:THR:H	2.12	0.48
1:C:733:LYS:HD3	1:C:771:ALA:HB1	1.95	0.48
1:C:762:GLN:O	1:C:765:ARG:NH1	2.47	0.48
1:C:873:TYR:O	1:C:877:LEU:HG	2.14	0.48
1:C:1029:MET:HE3	1:C:1033:VAL:HG21	1.95	0.48
1:C:1036:GLN:NE2	1:C:1049:LEU:HD23	2.28	0.48
3:H:5:LEU:HB3	3:H:91:CYS:SG	2.54	0.48
2:I:163:LEU:HD21	2:I:186:VAL:HG11	1.96	0.48
1:A:771:ALA:O	1:A:774:GLN:HG3	2.13	0.48
1:C:197:ILE:HB	1:C:202:LYS:HZ2	1.78	0.48
2:E:16:GLU:HG3	2:E:17:THR:N	2.28	0.48
2:E:18:LEU:HB2	2:E:82(C):VAL:HG21	1.96	0.48
2:E:23:ALA:HA	2:E:77:GLN:HG3	1.96	0.48
2:G:46:GLU:HG2	2:G:63:LEU:HD11	1.94	0.48
1:A:559:PHE:HB3	1:A:563:GLN:HB2	1.96	0.48
1:A:811:LYS:HD2	1:A:812:PRO:HD2	1.96	0.48
1:A:1047:TYR:HD2	1:A:1067:TYR:HD2	1.62	0.48
1:A:1069:PRO:HG2	1:B:894:LEU:HD11	1.96	0.48
1:B:559:PHE:HE2	1:B:584:ILE:HG13	1.78	0.48
1:C:577:ARG:HH22	1:C:581:THR:H	1.62	0.48
1:C:819:GLU:HA	1:C:822:LEU:HD12	1.96	0.48
1:A:884:SER:CB	1:A:893:ALA:HB1	2.44	0.48
1:C:67:VAL:HB	1:C:263:ALA:HB3	1.96	0.48
1:C:902:MET:HA	1:C:905:ARG:HG2	1.96	0.48
1:A:732:THR:HG22	1:A:1058:HIS:NE2	2.29	0.47
1:A:762:GLN:HB3	1:A:765:ARG:NH1	2.23	0.47
1:B:40:ASP:OD1	1:B:40:ASP:N	2.46	0.47
1:C:275:PHE:HD1	1:C:290:ASP:HA	1.78	0.47
2:G:173:VAL:HB	2:G:181:SER:HB3	1.96	0.47
1:A:110:LEU:O	1:A:134:GLN:HA	2.13	0.47
1:C:370:ASN:O	1:C:373:PRO:HD3	2.13	0.47
1:C:1009:THR:O	1:C:1013:ILE:HG13	2.14	0.47
2:I:126:PHE:CE1	3:J:128:GLU:HB3	2.48	0.47
2:I:154:VAL:HB	2:I:182:LEU:HD22	1.95	0.47
1:B:563:GLN:HE22	1:C:43:PHE:HD1	1.62	0.47
1:C:109:THR:O	1:C:116:SER:OG	2.30	0.47
1:C:535:LYS:H	1:C:537:LYS:NZ	2.11	0.47
1:C:779:GLN:OE1	1:C:783:ALA:HB3	2.13	0.47
2:G:154:VAL:HB	2:G:182:LEU:HD22	1.96	0.47
3:H:140:ILE:O	3:H:178:ALA:N	2.38	0.47
3:J:36:TRP:CD1	3:J:49:ILE:HB	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:501:TYR:HB3	1:A:505:HIS:ND1	2.29	0.47
1:C:328:ARG:HG3	1:C:527:PRO:HB3	1.96	0.47
3:H:36:TRP:CG	3:H:76:LEU:HB2	2.50	0.47
1:A:128:ILE:O	1:A:170:TYR:HB3	2.14	0.47
1:A:804:GLN:O	1:A:816:SER:HB2	2.15	0.47
1:A:1024:LEU:O	1:A:1028:LYS:HG2	2.13	0.47
1:C:577:ARG:HE	1:C:583:GLU:N	2.13	0.47
3:F:90:TYR:HB3	3:F:101:PHE:CD2	2.49	0.47
1:A:269:TYR:HB2	1:A:271:GLN:HE22	1.79	0.47
1:B:83:VAL:HG22	1:B:239:GLN:HE21	1.78	0.47
1:B:969:LYS:HZ2	1:B:996:LEU:HD21	1.79	0.47
1:A:896:ILE:HG23	1:A:901:GLN:NE2	2.28	0.47
1:A:896:ILE:HG13	1:A:897:PRO:HD2	1.97	0.47
1:B:293:LEU:HD12	1:B:294:ASP:HB2	1.96	0.47
1:B:316:SER:C	1:B:595:VAL:HG22	2.35	0.47
1:B:426:PRO:HG3	1:B:464:PHE:CZ	2.50	0.47
1:B:611:LEU:HD22	1:B:613:GLN:HG3	1.97	0.47
1:C:42:VAL:HG23	1:C:44:ARG:HD2	1.96	0.47
1:C:743:CYS:SG	1:C:746:SER:HB2	2.55	0.47
1:C:1037:SER:HB2	1:C:1039:ARG:HG2	1.95	0.47
3:F:124:PRO:HG3	3:F:135:THR:H	1.79	0.47
2:G:91:TYR:CE2	3:H:44:ALA:HB3	2.50	0.47
1:A:276:LEU:HD22	1:A:301:CYS:HA	1.95	0.47
1:A:598:ILE:CD1	1:A:666:ILE:HG12	2.45	0.47
1:A:769:GLY:HA2	1:A:772:VAL:HG12	1.96	0.47
1:B:54:LEU:HD21	1:B:88:ASP:HB2	1.96	0.47
1:B:800:PHE:HB3	1:B:802:PHE:CZ	2.50	0.47
1:B:954:HIS:HA	1:B:957:GLN:NE2	2.29	0.47
1:B:956:ALA:O	1:B:960:ASN:N	2.33	0.47
1:C:34:ARG:NH1	1:C:221:SER:HB3	2.28	0.47
1:C:48:LEU:HD12	1:C:276:LEU:HD11	1.97	0.47
1:C:365:TYR:HA	2:I:99:PHE:HE1	1.80	0.47
1:C:374:PHE:CE2	1:C:434:ILE:HG23	2.50	0.47
2:E:48:ILE:HD12	2:E:63:LEU:HD22	1.96	0.47
3:F:140:ILE:HB	3:F:178:ALA:HB3	1.95	0.47
1:A:763:LEU:HD13	1:A:1008:VAL:HG11	1.97	0.47
1:B:716:THR:HB	1:B:1071:GLN:HB3	1.96	0.47
1:B:916:LEU:O	1:B:920:GLN:N	2.48	0.47
1:C:239:GLN:HE21	1:C:240:THR:H	1.61	0.47
3:H:143:PHE:CE2	3:H:146:GLY:HA2	2.49	0.47
2:I:142:LEU:HD13	2:I:215:VAL:HB	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:145:LEU:HD12	2:I:182:LEU:O	2.14	0.47
1:A:204:TYR:HB3	1:A:223:LEU:HG	1.95	0.47
1:A:296:LEU:N	1:A:608:VAL:HG11	2.30	0.47
1:A:650:LEU:HG	1:A:653:ALA:HB3	1.96	0.47
1:B:196:ASN:ND2	1:B:235:ILE:H	2.11	0.47
1:B:818:ILE:O	1:B:822:LEU:HG	2.14	0.47
1:C:202:LYS:HG2	1:C:228:ASP:CG	2.35	0.47
3:F:152:TRP:CE2	3:F:182:LEU:HB2	2.50	0.47
1:A:801:ASN:O	1:A:931:ILE:HD13	2.15	0.46
1:B:127:VAL:HA	1:B:170:TYR:O	2.15	0.46
1:B:442:ASP:OD1	1:B:509:ARG:NH2	2.47	0.46
1:B:576:VAL:O	1:B:585:LEU:HG	2.13	0.46
1:B:741:TYR:HE1	1:B:1000:ARG:HG3	1.80	0.46
1:B:780:GLU:O	1:B:784:GLN:NE2	2.48	0.46
1:C:731:MET:HE3	1:C:1014:ARG:NH2	2.30	0.46
2:G:94:ARG:HG2	2:G:95:GLY:H	1.80	0.46
3:J:23:CYS:N	3:J:74:ALA:O	2.48	0.46
3:J:142:ASP:OD1	3:J:171:GLN:NE2	2.43	0.46
1:A:202:LYS:NZ	1:A:204:TYR:OH	2.39	0.46
1:A:439:ASN:HA	1:A:507:PRO:HG2	1.97	0.46
1:A:727:LEU:HD11	1:A:1028:LYS:HG3	1.98	0.46
1:A:877:LEU:HA	1:A:888:PHE:CZ	2.50	0.46
1:A:968:SER:HB2	1:A:970:PHE:CE2	2.50	0.46
1:B:374:PHE:CD2	2:E:99:PHE:HB3	2.50	0.46
1:B:1006:THR:HG22	1:B:1010:GLN:NE2	2.25	0.46
1:C:805:ILE:HA	1:C:818:ILE:HD11	1.97	0.46
1:C:818:ILE:O	1:C:822:LEU:HG	2.15	0.46
3:F:192:HIS:HB2	3:F:195:TYR:CE1	2.48	0.46
1:A:882:ILE:O	1:A:898:PHE:HD2	1.99	0.46
1:B:374:PHE:CG	2:E:99:PHE:HB3	2.50	0.46
1:B:1060:VAL:HG21	1:B:1062:PHE:HE1	1.80	0.46
2:E:172:ALA:O	3:F:166:THR:HG21	2.16	0.46
3:F:29:ILE:H	3:F:72:ASN:CG	2.18	0.46
1:A:578:ASP:HB3	1:A:583:GLU:H	1.80	0.46
1:A:660:TYR:O	1:A:698:SER:HB3	2.15	0.46
1:A:1032:CYS:HB3	1:A:1051:SER:HB3	1.97	0.46
1:B:31:SER:O	1:B:59:PHE:HA	2.15	0.46
1:B:373:PRO:HG2	1:B:436:TRP:HB2	1.97	0.46
1:C:58:PHE:HB2	1:C:293:LEU:HD22	1.97	0.46
1:C:88:ASP:OD2	1:C:272:PRO:HD3	2.15	0.46
1:C:382:VAL:HG11	1:C:515:PHE:HE2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:560:LEU:HB3	1:C:562:PHE:CE2	2.51	0.46
1:C:909:ILE:HG23	1:C:1036:GLN:CD	2.35	0.46
2:G:94:ARG:O	2:G:104(A):SER:OG	2.16	0.46
1:A:88:ASP:O	1:A:270:LEU:HB2	2.15	0.46
1:A:578:ASP:OD2	1:A:581:THR:HG22	2.16	0.46
1:A:643:PHE:HB2	1:A:655:TYR:HB2	1.97	0.46
1:B:67:VAL:HG23	1:B:265:TYR:CD2	2.51	0.46
1:C:102:ARG:HD2	1:C:243:ALA:HB3	1.98	0.46
1:C:937:SER:O	1:C:941:THR:N	2.39	0.46
2:G:68:THR:HB	2:G:81:LYS:HB2	1.97	0.46
1:A:93:ALA:O	1:A:265:TYR:HA	2.16	0.46
1:A:765:ARG:NH2	1:C:957:GLN:HE22	2.07	0.46
1:A:1030:SER:OG	1:C:1040:VAL:O	2.28	0.46
1:B:67:VAL:O	1:B:67:VAL:CG1	2.63	0.46
1:B:779:GLN:OE1	1:B:783:ALA:HB3	2.16	0.46
1:C:777:ASN:HB3	1:C:1022:ALA:HB1	1.98	0.46
1:C:920:GLN:HG2	1:C:921:LYS:N	2.31	0.46
3:F:200:THR:O	3:F:200:THR:OG1	2.33	0.46
1:A:788:ILE:N	1:C:701:ALA:O	2.49	0.46
1:A:1114:ILE:HG22	1:A:1116:THR:HG23	1.96	0.46
1:C:867:ASP:OD1	1:C:868:GLU:HG2	2.15	0.46
3:F:128:GLU:HG2	3:F:133:LYS:O	2.15	0.46
3:J:136:LEU:HD11	3:J:189:TRP:CZ3	2.51	0.46
1:A:204:TYR:CD1	1:A:225:PRO:HA	2.50	0.46
1:A:391:CYS:SG	1:A:529:LYS:CB	3.04	0.46
1:A:865:LEU:HD23	1:A:873:TYR:CE2	2.49	0.46
1:A:958:ALA:HB1	1:A:1007:TYR:HE1	1.80	0.46
1:B:784:GLN:N	1:B:784:GLN:OE1	2.49	0.46
1:B:906:PHE:CE2	1:B:916:LEU:HD13	2.51	0.46
1:C:656:VAL:HG22	1:C:695:TYR:HB3	1.97	0.46
2:E:47:TRP:HB2	3:F:99:TRP:HB2	1.98	0.46
2:E:188:VAL:HG11	2:E:198:TYR:CE1	2.51	0.46
3:F:119:VAL:HG13	3:F:140:ILE:HG13	1.97	0.46
1:C:390:LEU:HD13	1:C:392:PHE:HE2	1.81	0.46
3:F:143:PHE:CE2	3:F:146:GLY:HA2	2.51	0.46
1:A:50:SER:HB3	1:A:276:LEU:HD13	1.98	0.46
1:A:726:ILE:CG2	1:A:948:LEU:HB2	2.46	0.46
1:B:104:TRP:HA	1:B:240:THR:HA	1.97	0.46
1:C:658:ASN:OD1	1:C:659:SER:N	2.49	0.46
2:E:59:TYR:HE1	2:E:69:ILE:HG22	1.81	0.46
3:J:99:TRP:HE3	3:J:101:PHE:HZ	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:576:VAL:HG23	1:A:585:LEU:HD13	1.97	0.45
1:C:387:LEU:HA	1:C:390:LEU:HB2	1.97	0.45
2:E:201:ASN:ND2	2:E:212:ASP:OD1	2.42	0.45
1:A:880:GLY:HA3	1:A:888:PHE:CD1	2.52	0.45
1:A:1043:CYS:HB3	1:A:1048:HIS:CD2	2.51	0.45
1:B:363:ALA:HB1	1:B:365:TYR:CZ	2.50	0.45
1:B:576:VAL:HB	1:B:585:LEU:HD11	1.97	0.45
2:E:38:ARG:O	2:E:45:LEU:HA	2.17	0.45
1:B:699:LEU:HD11	1:C:869:MET:HE3	1.97	0.45
1:B:732:THR:O	1:B:734:THR:N	2.50	0.45
1:C:398:ASP:O	1:C:511:VAL:HA	2.16	0.45
1:C:676:THR:H	1:C:690:GLN:HA	1.80	0.45
1:C:1014:ARG:O	1:C:1018:ILE:HD12	2.16	0.45
2:G:23:ALA:HA	2:G:77:GLN:HG2	1.97	0.45
1:A:374:PHE:CE2	2:G:99:PHE:HB2	2.51	0.45
1:B:997:ILE:HA	1:B:1000:ARG:NE	2.31	0.45
1:C:660:TYR:O	1:C:698:SER:OG	2.32	0.45
2:I:39:GLN:HB2	2:I:91:TYR:HE2	1.81	0.45
1:A:52:GLN:HA	1:A:274:THR:HA	1.98	0.45
1:A:386:LYS:HB3	1:A:390:LEU:HD12	1.99	0.45
1:A:903:ALA:HB1	1:A:913:GLN:HG2	1.98	0.45
1:B:202:LYS:HG2	1:B:228:ASP:OD1	2.17	0.45
1:B:807:PRO:HA	1:B:816:SER:HA	1.97	0.45
1:C:378:LYS:HG3	3:J:33:TYR:CE2	2.51	0.45
2:E:53:HIS:HA	2:E:71:LEU:HD22	1.97	0.45
2:E:149:TYR:HB2	2:E:204:HIS:CE1	2.51	0.45
1:A:645:THR:HG23	1:A:647:ALA:H	1.81	0.45
1:A:1019:ARG:O	1:A:1023:ASN:ND2	2.49	0.45
1:B:969:LYS:NZ	1:B:996:LEU:HD21	2.30	0.45
1:C:316:SER:O	1:C:595:VAL:HG22	2.17	0.45
1:C:498:ARG:HD2	1:C:501:TYR:CZ	2.50	0.45
1:C:728:PRO:HB3	1:C:951:VAL:HG21	1.98	0.45
1:C:797:PHE:HB2	1:C:800:PHE:O	2.16	0.45
1:C:1106:GLN:HG3	1:C:1109:PHE:O	2.17	0.45
2:E:36:TRP:HD1	2:E:69:ILE:HD12	1.81	0.45
2:I:69:ILE:HD11	2:I:78:PHE:HD2	1.82	0.45
1:A:704:SER:HA	1:B:790:LYS:O	2.16	0.45
1:A:873:TYR:O	1:A:877:LEU:HG	2.17	0.45
1:A:1020:ALA:HA	1:A:1023:ASN:HD22	1.81	0.45
1:B:201:PHE:HD2	1:B:203:ILE:HD11	1.80	0.45
1:B:887:THR:HG21	1:B:894:LEU:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1004:LEU:HD12	1:B:1005:GLN:N	2.32	0.45
2:G:59:TYR:CD2	2:G:64:LYS:HD2	2.47	0.45
1:A:759:PHE:O	1:A:763:LEU:HD23	2.16	0.45
1:B:658:ASN:ND2	1:B:660:TYR:OH	2.50	0.45
1:C:641:ASN:HB3	1:C:654:GLU:OE2	2.16	0.45
1:C:717:ASN:OD1	1:C:718:PHE:N	2.46	0.45
1:C:50:SER:HA	1:C:275:PHE:O	2.17	0.45
1:C:779:GLN:NE2	1:C:783:ALA:HB3	2.32	0.45
3:H:149:THR:OG1	3:H:200:THR:OG1	2.14	0.45
1:A:916:LEU:HD12	1:A:920:GLN:HA	1.99	0.45
1:A:1041:ASP:HB3	1:B:1030:SER:HB3	1.98	0.45
1:B:1115:ILE:HG23	1:B:1120:THR:HG21	1.98	0.45
1:C:318:PHE:CE1	1:C:612:TYR:HB3	2.52	0.45
1:C:802:PHE:HZ	1:C:898:PHE:CE1	2.34	0.45
1:C:953:ASN:O	1:C:957:GLN:HG3	2.17	0.45
2:E:37:ILE:O	2:E:91:TYR:N	2.27	0.45
2:I:125:VAL:HA	2:I:145:LEU:O	2.17	0.45
3:J:38:GLN:HE22	3:J:40:ARG:NH2	2.15	0.45
1:A:577:ARG:HH12	1:A:582:LEU:C	2.19	0.44
1:A:789:TYR:CZ	1:A:893:ALA:HB2	2.52	0.44
1:A:906:PHE:HB3	1:A:911:VAL:HB	1.98	0.44
1:A:950:ASP:C	1:A:954:HIS:HD1	2.20	0.44
1:B:67:VAL:HG22	1:B:265:TYR:CE2	2.32	0.44
1:B:732:THR:HG22	1:B:1058:HIS:NE2	2.32	0.44
1:C:534:VAL:O	1:C:552:LEU:HB2	2.17	0.44
1:C:544:ASN:ND2	1:C:578:ASP:OD1	2.50	0.44
1:C:1081:ILE:O	1:C:1088:HIS:HD2	2.00	0.44
2:E:29:PHE:HB2	2:E:53:HIS:HB3	1.98	0.44
2:G:24:VAL:HG22	2:G:76:ASN:O	2.18	0.44
2:G:149:TYR:OH	2:G:207:SER:OG	2.20	0.44
1:A:787:GLN:OE1	1:A:787:GLN:N	2.50	0.44
1:A:896:ILE:O	1:A:901:GLN:NE2	2.45	0.44
1:A:1029:MET:O	1:A:1034:LEU:HG	2.17	0.44
1:C:89:GLY:HA3	1:C:270:LEU:HB2	1.98	0.44
1:C:969:LYS:HZ1	1:C:972:ALA:HB3	1.82	0.44
1:C:1019:ARG:HG3	1:C:1019:ARG:HH11	1.82	0.44
2:I:12:LEU:HD23	2:I:82(C):VAL:HG21	2.00	0.44
2:I:36:TRP:CG	2:I:80:LEU:HD22	2.52	0.44
3:J:8:PRO:O	3:J:105:THR:HG22	2.16	0.44
1:A:616:ASN:HA	1:A:644:GLN:NE2	2.32	0.44
1:A:743:CYS:HB3	1:A:746:SER:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:906:PHE:HD1	1:A:1049:LEU:HD21	1.82	0.44
1:A:917:TYR:CE2	1:C:1090:PRO:HD2	2.52	0.44
1:B:797:PHE:HE2	1:B:883:THR:HG1	1.62	0.44
1:C:341:VAL:HG11	1:C:397:ALA:HB3	1.99	0.44
2:E:123:PRO:HB3	2:E:146:VAL:HG13	2.00	0.44
3:J:3:PHE:CE1	3:J:25:GLY:HA3	2.52	0.44
1:A:658:ASN:HB3	1:A:660:TYR:CE2	2.52	0.44
1:A:768:THR:O	1:A:772:VAL:HG12	2.17	0.44
1:A:977:LEU:C	1:A:981:PHE:CE2	2.91	0.44
1:B:882:ILE:HG13	1:B:883:THR:H	1.81	0.44
1:C:170:TYR:OH	1:C:172:SER:HB3	2.17	0.44
1:A:45:SER:O	1:A:47:VAL:HG23	2.18	0.44
1:A:555:SER:OG	1:A:584:ILE:HG23	2.18	0.44
1:B:539:VAL:HG12	1:B:540:ASN:N	2.33	0.44
1:B:769:GLY:O	1:B:773:GLU:OE1	2.35	0.44
1:C:439:ASN:OD1	1:C:440:LYS:HG3	2.17	0.44
2:E:18:LEU:HD23	2:E:82:LEU:HD23	2.00	0.44
2:G:39:GLN:HG3	2:G:44:GLY:C	2.37	0.44
2:I:66:ARG:HE	2:I:82:LEU:HD11	1.83	0.44
1:A:193:VAL:HB	1:A:204:TYR:HB2	1.99	0.44
1:B:291:CYS:O	1:B:297:SER:OG	2.36	0.44
1:B:551:VAL:HG12	1:B:588:THR:O	2.18	0.44
1:B:906:PHE:O	1:B:911:VAL:N	2.32	0.44
1:C:103:GLY:HA3	1:C:119:ILE:O	2.18	0.44
3:F:117:PRO:HB3	3:F:143:PHE:HB3	1.99	0.44
2:G:150:PHE:HB2	2:G:179:LEU:HD22	1.99	0.44
3:H:13:GLU:OE2	3:H:14:SER:N	2.51	0.44
2:I:109:GLN:OE1	2:I:109:GLN:N	2.42	0.44
2:I:154:VAL:HG22	2:I:204:HIS:CG	2.53	0.44
3:J:34:VAL:O	3:J:50:TYR:HA	2.17	0.44
3:J:36:TRP:CE2	3:J:76:LEU:HB2	2.52	0.44
1:A:916:LEU:O	1:A:920:GLN:N	2.50	0.44
1:A:968:SER:HB3	1:B:759:PHE:HZ	1.82	0.44
1:B:38:TYR:CE1	1:B:285:ILE:HG13	2.52	0.44
1:B:759:PHE:O	1:B:763:LEU:HD23	2.18	0.44
1:C:874:THR:O	1:C:878:LEU:HD23	2.18	0.44
2:E:127:PRO:HG3	2:E:213:LYS:HB3	1.99	0.44
1:A:410:ILE:HD11	1:A:418:ILE:HG22	1.99	0.44
1:A:915:VAL:O	1:A:919:ASN:HB3	2.18	0.44
1:B:882:ILE:HG13	1:B:883:THR:N	2.32	0.44
1:B:1029:MET:SD	1:B:1033:VAL:HG21	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1097:SER:HB2	1:B:1102:TRP:CE2	2.53	0.44
1:C:550:GLY:HA2	1:C:590:CYS:H	1.83	0.44
1:C:963:VAL:O	1:C:966:LEU:HB2	2.17	0.44
1:C:972:ALA:HB3	1:C:996:LEU:HD21	1.99	0.44
3:F:5:LEU:HD13	3:F:91:CYS:SG	2.58	0.44
1:A:811:LYS:HG3	1:A:813:SER:H	1.83	0.44
1:A:884:SER:OG	1:A:893:ALA:HB1	2.17	0.44
1:B:963:VAL:O	1:B:966:LEU:HB2	2.18	0.44
1:B:986:PRO:HA	1:B:989:ALA:HB3	2.00	0.44
1:C:131:CYS:HA	1:C:166:CYS:HA	1.99	0.44
1:C:1083:HIS:HB3	1:C:1088:HIS:NE2	2.33	0.44
1:A:64:TRP:CE2	1:A:66:HIS:CG	3.06	0.43
1:A:770:ILE:HD11	1:A:1012:LEU:HD22	2.00	0.43
1:B:45:SER:O	1:B:47:VAL:HG23	2.18	0.43
1:B:1115:ILE:HG22	1:B:1137:VAL:HG13	2.00	0.43
1:C:906:PHE:HB3	1:C:911:VAL:O	2.18	0.43
1:C:1028:LYS:HB2	1:C:1062:PHE:CE2	2.53	0.43
2:I:139:THR:OG1	2:I:187:THR:OG1	2.36	0.43
1:A:117:LEU:HB2	1:A:233:ILE:HD11	2.01	0.43
1:A:866:THR:H	1:A:869:MET:CE	2.31	0.43
1:A:997:ILE:O	1:A:1001:LEU:HG	2.18	0.43
1:B:193:VAL:HB	1:B:204:TYR:HB2	2.00	0.43
1:C:116:SER:O	1:C:130:VAL:HG23	2.18	0.43
3:F:50:TYR:N	3:F:54:GLN:O	2.50	0.43
2:G:38:ARG:NH1	2:G:40:PRO:HD3	2.33	0.43
2:G:126:PHE:HB2	2:G:145:LEU:HD21	1.99	0.43
2:I:174:LEU:HA	2:I:179:LEU:O	2.18	0.43
3:J:65:GLY:HA2	3:J:75:SER:O	2.17	0.43
1:A:882:ILE:HG23	1:A:898:PHE:CD2	2.54	0.43
1:B:902:MET:HB2	1:B:916:LEU:HD21	2.01	0.43
1:B:1006:THR:O	1:B:1009:THR:OG1	2.29	0.43
1:C:375:PHE:HZ	1:C:407:VAL:HG11	1.83	0.43
1:C:993:ILE:O	1:C:997:ILE:HG12	2.18	0.43
2:E:98:ILE:HG12	2:E:99:PHE:CG	2.53	0.43
3:F:95:ASP:HB3	3:F:98:ILE:HB	2.00	0.43
2:I:36:TRP:NE1	2:I:90:TYR:HB3	2.32	0.43
1:A:316:SER:O	1:A:595:VAL:HG12	2.19	0.43
1:B:725:GLU:O	1:B:1061:VAL:HA	2.18	0.43
1:C:371:LEU:C	2:I:58:ASN:HD21	2.22	0.43
1:C:977:LEU:HD12	1:C:981:PHE:CE2	2.54	0.43
1:C:1104:VAL:HB	1:C:1113:GLN:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:143:GLY:HA2	2:E:158:TRP:HH2	1.82	0.43
1:A:131:CYS:HB2	1:A:166:CYS:HB2	1.63	0.43
1:B:273:ARG:HH2	1:B:292:ALA:HB3	1.84	0.43
1:C:552:LEU:HD13	1:C:585:LEU:HD21	2.00	0.43
1:C:737:ASP:OD2	1:C:740:MET:HG2	2.18	0.43
1:C:902:MET:SD	1:C:905:ARG:HD2	2.58	0.43
1:C:986:PRO:HB2	1:C:987:PRO:HD3	2.00	0.43
3:F:7:GLN:HE22	3:F:90:TYR:HA	1.84	0.43
3:F:175:LYS:HA	3:F:175:LYS:HD3	1.76	0.43
3:H:78:ILE:HD11	3:H:89:TYR:HE2	1.83	0.43
1:A:905:ARG:NH1	1:A:1050:MET:HA	2.34	0.43
1:B:947:LYS:HA	1:B:950:ASP:OD2	2.18	0.43
1:C:375:PHE:HA	3:J:96:SER:HA	1.99	0.43
1:C:879:ALA:O	1:C:883:THR:HG22	2.18	0.43
1:C:1139:ASP:OD1	1:C:1139:ASP:N	2.49	0.43
3:H:37:TYR:HB2	3:H:90:TYR:H	1.84	0.43
1:A:660:TYR:HB2	1:A:695:TYR:CZ	2.54	0.43
1:A:726:ILE:HG21	1:A:948:LEU:HB2	2.00	0.43
1:B:54:LEU:HD22	1:B:197:ILE:HG22	2.00	0.43
1:B:577:ARG:HA	1:B:583:GLU:O	2.18	0.43
1:B:730:SER:OG	1:B:731:MET:N	2.51	0.43
1:C:733:LYS:HG3	1:C:861:LEU:HB2	1.99	0.43
2:G:33:TYR:CD1	2:G:52:ASN:HB3	2.54	0.43
1:A:963:VAL:O	1:A:966:LEU:HB2	2.18	0.43
1:A:965:GLN:HB3	1:A:970:PHE:CZ	2.54	0.43
1:A:1047:TYR:HD2	1:A:1067:TYR:CD2	2.36	0.43
1:B:664:ILE:HG23	1:B:672:ALA:HB3	2.01	0.43
1:B:973:ILE:HD13	1:B:983:ARG:HH2	1.84	0.43
1:C:931:ILE:O	1:C:934:ILE:HG22	2.18	0.43
2:I:18:LEU:O	2:I:81:LYS:HD3	2.19	0.43
2:I:37:ILE:HG21	2:I:107:TRP:HH2	1.84	0.43
3:J:7:GLN:HG2	3:J:23:CYS:HA	2.01	0.43
3:J:67:ILE:HG12	3:J:74:ALA:HA	2.01	0.43
1:A:118:LEU:HD21	1:A:120:VAL:HG13	2.01	0.43
1:A:355:ARG:HA	1:A:397:ALA:O	2.18	0.43
1:A:818:ILE:O	1:A:822:LEU:HG	2.19	0.43
1:A:958:ALA:HB1	1:A:1007:TYR:CE1	2.54	0.43
1:A:977:LEU:O	1:A:981:PHE:CE2	2.60	0.43
1:A:1029:MET:O	1:A:1034:LEU:N	2.30	0.43
1:B:956:ALA:O	1:B:959:LEU:HB2	2.19	0.43
1:C:65:PHE:HB2	1:C:265:TYR:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:785:VAL:HG21	1:C:789:TYR:HE1	1.83	0.43
1:C:886:TRP:HD1	1:C:1034:LEU:O	2.02	0.43
2:G:35:SER:OG	2:G:102:VAL:HG21	2.19	0.43
2:I:47:TRP:HB2	3:J:101:PHE:CE2	2.52	0.43
3:J:36:TRP:N	3:J:49:ILE:O	2.46	0.43
3:J:49:ILE:HG21	3:J:65:GLY:HA3	2.00	0.43
1:A:92:PHE:HZ	1:A:101:ILE:HD13	1.82	0.43
1:A:785:VAL:HG21	1:A:888:PHE:CD2	2.54	0.43
1:B:289:VAL:HG23	1:B:306:PHE:CE2	2.53	0.43
1:B:577:ARG:HE	1:B:582:LEU:C	2.22	0.43
1:C:290:ASP:HB3	1:C:293:LEU:HB2	2.01	0.43
1:C:344:ALA:HB3	1:C:347:PHE:HE1	1.84	0.43
2:G:39:GLN:NE2	2:G:43:LYS:O	2.52	0.43
2:I:177:SER:OG	2:I:179:LEU:HD23	2.19	0.43
1:A:517:LEU:HD23	1:A:517:LEU:HA	1.92	0.42
1:B:274:THR:HG23	1:B:291:CYS:SG	2.59	0.42
1:B:296:LEU:O	1:B:299:THR:OG1	2.25	0.42
1:B:1029:MET:O	1:B:1033:VAL:HB	2.19	0.42
1:C:818:ILE:HG21	1:C:1054:GLN:HG2	2.01	0.42
2:E:47:TRP:HE3	3:F:98:ILE:HD13	1.84	0.42
2:G:63:LEU:O	2:G:67:VAL:HG12	2.19	0.42
2:G:127:PRO:HB3	2:G:215:VAL:HG13	2.01	0.42
1:A:1008:VAL:O	1:A:1012:LEU:HD23	2.18	0.42
1:A:1105:THR:HG1	1:A:1106:GLN:H	1.67	0.42
1:A:1105:THR:HG1	1:A:1111:GLU:H	1.64	0.42
1:C:864:LEU:HG	1:C:865:LEU:HD22	2.01	0.42
1:C:1054:GLN:OE1	1:C:1063:LEU:HD13	2.19	0.42
2:E:39:GLN:HG3	2:E:45:LEU:CD2	2.49	0.42
3:F:34:VAL:HG12	3:F:52:ASP:OD1	2.19	0.42
2:I:2:VAL:HG21	2:I:94:ARG:HH12	1.84	0.42
1:A:66:HIS:CG	1:A:66:HIS:O	2.72	0.42
1:A:567:ARG:HD2	1:A:571:ASP:HA	2.00	0.42
1:B:196:ASN:HD21	1:B:234:ASN:HA	1.85	0.42
1:B:760:CYS:HA	1:B:763:LEU:HB2	2.01	0.42
1:B:805:ILE:HD12	1:B:1052:PHE:HE2	1.84	0.42
1:B:877:LEU:HD12	1:B:878:LEU:N	2.34	0.42
1:B:991:VAL:HG13	1:B:995:ARG:HH21	1.84	0.42
1:C:381:GLY:HA3	1:C:430:THR:HG23	2.01	0.42
1:C:1008:VAL:HA	1:C:1011:GLN:HB2	2.02	0.42
3:J:35:GLN:HG3	3:J:50:TYR:HB3	2.00	0.42
3:J:54:GLN:OE1	3:J:54:GLN:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:PHE:CE1	1:A:196:ASN:HB2	2.53	0.42
1:A:884:SER:HB3	1:A:893:ALA:HB1	2.01	0.42
1:B:47:VAL:HB	1:B:49:HIS:HE1	1.84	0.42
1:C:391:CYS:HB3	1:C:522:ALA:HB3	2.00	0.42
3:H:64:SER:O	3:H:76:LEU:HD12	2.19	0.42
2:I:188:VAL:HG11	2:I:198:TYR:HE2	1.85	0.42
3:J:35:GLN:HB3	3:J:92:GLN:HB3	2.01	0.42
1:A:895:GLN:OE1	1:A:895:GLN:N	2.35	0.42
1:B:296:LEU:O	1:B:300:LYS:HG2	2.20	0.42
1:C:569:ILE:H	1:C:569:ILE:HD12	1.84	0.42
1:C:597:VAL:HG13	1:C:608:VAL:HG23	2.01	0.42
1:C:663:ASP:OD1	1:C:664:ILE:N	2.52	0.42
1:C:1021:SER:HA	1:C:1024:LEU:HD12	2.00	0.42
1:A:642:VAL:HG22	1:A:651:ILE:HG22	2.00	0.42
1:A:1093:GLY:CA	1:A:1105:THR:O	2.68	0.42
1:B:992:GLN:HA	1:B:995:ARG:NE	2.34	0.42
1:C:390:LEU:HD13	1:C:392:PHE:CE2	2.55	0.42
2:E:22:CYS:HB3	2:E:78:PHE:CE2	2.55	0.42
2:E:51:ILE:HG13	2:E:57:THR:HG22	2.00	0.42
3:F:185:THR:HG23	3:F:188:GLN:H	1.83	0.42
1:B:705:VAL:HB	1:C:883:THR:HG21	2.01	0.42
1:B:1084:ASP:HB3	1:B:1086:LYS:HZ2	1.85	0.42
1:C:55:PHE:HB2	1:C:273:ARG:HB2	2.02	0.42
1:C:368:LEU:HD23	1:C:371:LEU:HA	2.02	0.42
1:C:526:GLY:HA2	1:C:527:PRO:HD3	1.89	0.42
2:E:66:ARG:O	2:E:82:LEU:HA	2.20	0.42
2:I:70:SER:O	2:I:79:SER:N	2.34	0.42
1:A:774:GLN:O	1:A:777:ASN:HB3	2.20	0.42
1:A:870:ILE:O	1:A:874:THR:HG23	2.19	0.42
1:B:811:LYS:HG2	1:B:813:SER:H	1.85	0.42
1:B:986:PRO:O	1:B:990:GLU:HG2	2.19	0.42
1:B:1008:VAL:HA	1:B:1011:GLN:HB2	2.00	0.42
1:C:198:ASP:OD1	1:C:198:ASP:N	2.47	0.42
3:F:83:THR:HA	3:F:109:VAL:HG21	2.02	0.42
1:A:660:TYR:HB2	1:A:695:TYR:OH	2.20	0.42
1:A:1083:HIS:CE1	1:A:1136:THR:HA	2.55	0.42
1:B:58:PHE:HB3	1:B:59:PHE:CD2	2.55	0.42
1:B:656:VAL:HG21	1:B:693:ILE:HB	2.01	0.42
1:C:123:ALA:O	1:C:174:PRO:HG3	2.20	0.42
1:C:1083:HIS:O	1:C:1086:LYS:HG2	2.19	0.42
3:J:35:GLN:N	3:J:92:GLN:O	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:ASP:HA	1:A:369:TYR:CE1	2.54	0.42
1:A:659:SER:HB3	1:A:698:SER:OG	2.20	0.42
1:A:1005:GLN:HA	1:A:1008:VAL:HG12	2.02	0.42
1:B:305:SER:OG	1:B:307:THR:O	2.32	0.42
1:B:491:PRO:HB2	1:B:492:LEU:H	1.71	0.42
1:B:973:ILE:HG23	1:B:974:SER:N	2.35	0.42
1:C:295:PRO:HB2	1:C:608:VAL:CG2	2.50	0.42
1:C:726:ILE:O	1:C:727:LEU:HD12	2.20	0.42
1:C:733:LYS:HD2	1:C:861:LEU:HB2	2.02	0.42
3:H:80:GLY:O	3:H:82:ARG:NH1	2.52	0.42
1:A:386:LYS:O	1:A:390:LEU:N	2.53	0.41
1:A:791:THR:O	1:A:793:PRO:HD3	2.20	0.41
1:A:966:LEU:HD12	1:A:1000:ARG:HH22	1.85	0.41
1:B:969:LYS:CE	1:B:972:ALA:HB3	2.50	0.41
2:I:150:PHE:HA	2:I:151:PRO:HA	1.75	0.41
1:A:197:ILE:HG13	1:A:198:ASP:OD2	2.19	0.41
1:A:739:THR:O	1:A:743:CYS:N	2.47	0.41
1:B:732:THR:O	1:B:734:THR:HG23	2.20	0.41
1:B:805:ILE:HG13	1:B:806:LEU:N	2.35	0.41
1:B:896:ILE:HG13	1:B:897:PRO:HD2	2.01	0.41
1:C:102:ARG:O	1:C:121:ASN:N	2.38	0.41
1:C:382:VAL:HG11	1:C:515:PHE:CE2	2.55	0.41
1:C:568:ASP:N	1:C:572:THR:O	2.30	0.41
1:C:645:THR:HB	1:C:670:ILE:HD13	2.01	0.41
2:E:46:GLU:HA	3:F:99:TRP:O	2.19	0.41
2:I:52:ASN:HD21	2:I:56:SER:HB2	1.83	0.41
1:A:96:GLU:O	1:A:188:ASN:HB2	2.18	0.41
1:C:731:MET:CG	1:C:732:THR:N	2.82	0.41
2:E:7:TRP:HH2	2:E:77:GLN:HG2	1.84	0.41
2:G:103:THR:O	2:G:104:LEU:HD22	2.21	0.41
3:H:168:PRO:HA	3:H:177:ALA:O	2.19	0.41
2:I:152:GLU:HG2	2:I:153:PRO:HA	2.02	0.41
1:A:37:TYR:CD2	1:A:204:TYR:HE2	2.38	0.41
1:A:897:PRO:O	1:A:901:GLN:HG3	2.21	0.41
1:A:1106:GLN:HB3	1:A:1113:GLN:HE22	1.86	0.41
1:B:595:VAL:HA	1:B:611:LEU:O	2.19	0.41
1:B:781:VAL:O	1:B:1029:MET:HG2	2.19	0.41
1:B:951:VAL:O	1:B:954:HIS:HB2	2.19	0.41
1:C:552:LEU:HB3	1:C:585:LEU:HD21	2.02	0.41
1:C:969:LYS:HA	1:C:969:LYS:HD2	1.72	0.41
1:C:1103:PHE:CB	1:C:1112:PRO:HB3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:665:PRO:HA	1:A:671:CYS:SG	2.60	0.41
1:A:965:GLN:HB3	1:A:970:PHE:HZ	1.85	0.41
1:A:1109:PHE:CG	1:A:1110:TYR:N	2.89	0.41
1:B:997:ILE:HG23	1:B:1000:ARG:CZ	2.51	0.41
1:C:107:GLY:H	1:C:235:ILE:HG23	1.86	0.41
1:C:532:ASN:HA	2:I:28:SER:CB	2.49	0.41
1:C:773:GLU:O	1:C:776:LYS:HG2	2.20	0.41
1:C:1093:GLY:HA2	1:C:1105:THR:O	2.20	0.41
2:E:35:SER:HB2	2:E:37:ILE:HD11	2.03	0.41
2:G:59:TYR:OH	2:G:69:ILE:HG22	2.20	0.41
1:A:658:ASN:HB3	1:A:660:TYR:CZ	2.55	0.41
1:A:702:GLU:HA	1:B:788:ILE:O	2.19	0.41
1:A:789:TYR:CE2	1:A:893:ALA:HB2	2.56	0.41
1:B:273:ARG:HD3	1:B:290:ASP:OD1	2.20	0.41
1:B:698:SER:C	1:B:700:GLY:H	2.23	0.41
1:C:347:PHE:CE2	1:C:399:SER:HB2	2.55	0.41
1:C:350:VAL:HG23	1:C:400:PHE:CD2	2.56	0.41
1:C:596:SER:HB2	1:C:611:LEU:HD23	2.02	0.41
1:A:169:GLU:OE2	1:A:171:VAL:HG23	2.20	0.41
1:A:195:LYS:HE3	1:A:197:ILE:CG2	2.49	0.41
1:A:612:TYR:O	1:A:648:GLY:HA3	2.20	0.41
1:A:699:LEU:CG	1:B:788:ILE:HG13	2.44	0.41
1:A:737:ASP:OD1	1:A:738:CYS:N	2.53	0.41
1:A:1030:SER:HA	1:A:1034:LEU:HB2	2.03	0.41
1:B:49:HIS:O	1:B:276:LEU:HD12	2.19	0.41
1:B:365:TYR:CD1	2:E:99:PHE:HE1	2.39	0.41
1:C:370:ASN:HD22	1:C:374:PHE:HE1	1.68	0.41
1:C:377:PHE:HE1	2:I:98:ILE:HG13	1.84	0.41
1:C:753:LEU:HD21	1:C:760:CYS:SG	2.60	0.41
1:C:858:LEU:HD13	1:C:962:LEU:HD23	2.02	0.41
1:C:1019:ARG:HG3	1:C:1019:ARG:NH1	2.35	0.41
2:E:33:TYR:CE2	2:E:50:LEU:HD13	2.56	0.41
3:F:29:ILE:N	3:F:72:ASN:OD1	2.44	0.41
2:G:150:PHE:HA	2:G:151:PRO:HA	1.83	0.41
3:J:111:GLY:N	3:J:144:TYR:OH	2.32	0.41
1:A:826:VAL:HG21	1:A:1057:PRO:HG2	2.03	0.41
1:B:347:PHE:CE1	1:B:399:SER:HB2	2.55	0.41
1:C:107:GLY:O	1:C:237:ARG:HG3	2.20	0.41
1:C:577:ARG:HH11	1:C:578:ASP:N	2.15	0.41
1:C:984:LEU:HD23	1:C:984:LEU:HA	1.85	0.41
1:C:1024:LEU:O	1:C:1027:THR:OG1	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1029:MET:HE3	1:C:1029:MET:HA	2.03	0.41
1:C:1095:PHE:HB3	1:C:1102:TRP:CE3	2.55	0.41
2:E:11:LEU:O	2:E:12:LEU:HD22	2.21	0.41
2:E:104:LEU:HG	3:F:50:TYR:OH	2.21	0.41
3:F:98:ILE:HG22	3:F:100:VAL:HB	2.02	0.41
2:G:98:ILE:O	2:G:101:VAL:HG23	2.20	0.41
1:A:817:PHE:O	1:A:821:LEU:HG	2.20	0.41
1:B:498:ARG:HD2	1:B:501:TYR:CZ	2.56	0.41
1:B:715:PRO:HG2	1:B:1108:ASN:HA	2.03	0.41
1:B:905:ARG:HH12	1:B:1036:GLN:N	2.19	0.41
1:B:1030:SER:O	1:B:1034:LEU:HB2	2.21	0.41
1:C:95:ILE:HA	1:C:188:ASN:O	2.20	0.41
1:C:403:ARG:HB2	1:C:504:GLY:O	2.21	0.41
1:C:645:THR:HB	1:C:670:ILE:CD1	2.51	0.41
1:C:712:ILE:HD13	1:C:1077:THR:HG23	2.02	0.41
1:C:804:GLN:OE1	1:C:804:GLN:N	2.46	0.41
1:C:815:ARG:HB2	1:C:820:ASP:OD1	2.20	0.41
1:C:866:THR:O	1:C:870:ILE:HG13	2.20	0.41
1:C:1104:VAL:HG23	1:C:1115:ILE:HG13	2.02	0.41
2:E:36:TRP:HB3	2:E:80:LEU:HD12	2.02	0.41
2:G:37:ILE:HG22	2:G:45:LEU:HD22	2.03	0.41
3:H:146:GLY:HA3	3:H:176:TYR:CD2	2.56	0.41
2:I:39:GLN:HE21	2:I:45:LEU:CD2	2.33	0.41
2:I:127:PRO:HG3	2:I:213:LYS:HD2	2.03	0.41
1:A:43:PHE:CE1	1:A:283:GLY:HA3	2.56	0.41
1:A:363:ALA:HB1	1:A:365:TYR:CE2	2.56	0.41
1:A:763:LEU:HD21	1:A:1005:GLN:HG3	2.02	0.41
1:A:789:TYR:CE2	1:A:888:PHE:HB2	2.57	0.41
1:A:928:ASN:O	1:A:931:ILE:HB	2.21	0.41
1:A:1089:PHE:HB3	1:B:913:GLN:OE1	2.21	0.41
1:B:536:ASN:C	1:B:537:LYS:HD2	2.42	0.41
1:B:664:ILE:CG2	1:B:672:ALA:HB3	2.51	0.41
1:B:868:GLU:HG2	1:B:869:MET:N	2.36	0.41
1:C:714:ILE:HD13	1:C:1105:THR:HG23	2.03	0.41
1:C:733:LYS:HE3	1:C:774:GLN:HE21	1.83	0.41
3:F:122:PHE:HB2	3:F:137:VAL:HB	2.03	0.41
1:A:295:PRO:HB2	1:A:608:VAL:HG21	2.02	0.40
1:A:318:PHE:O	1:A:592:PHE:HB2	2.20	0.40
1:A:714:ILE:HD13	1:A:1110:TYR:HB2	2.02	0.40
1:A:815:ARG:HH22	1:A:823:PHE:HB2	1.86	0.40
1:A:867:ASP:OD1	1:A:868:GLU:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:869:MET:SD	1:C:699:LEU:HD21	2.61	0.40
1:B:430:THR:HG22	1:B:515:PHE:HB2	2.03	0.40
1:B:536:ASN:O	1:B:537:LYS:HD2	2.22	0.40
1:B:1114:ILE:HG22	1:B:1116:THR:HG23	2.03	0.40
1:C:776:LYS:HZ1	1:C:1019:ARG:HH21	1.67	0.40
2:G:20:LEU:HD12	2:G:20:LEU:HA	1.94	0.40
2:I:64:LYS:HE3	2:I:64:LYS:HB2	1.75	0.40
3:J:78:ILE:HD11	3:J:89:TYR:HE2	1.85	0.40
3:J:89:TYR:HB2	3:J:105:THR:OG1	2.21	0.40
1:A:328:ARG:HB2	1:A:543:PHE:CD1	2.51	0.40
1:A:905:ARG:CD	1:A:1050:MET:HB3	2.51	0.40
1:A:1089:PHE:HB2	1:A:1121:PHE:CE1	2.56	0.40
1:B:969:LYS:HD3	1:B:975:SER:N	2.36	0.40
1:C:128:ILE:O	1:C:169:GLU:HA	2.21	0.40
1:C:1082:CYS:HB2	1:C:1126:CYS:HB2	1.99	0.40
3:F:7:GLN:NE2	3:F:90:TYR:HA	2.36	0.40
2:I:34:TRP:CZ3	2:I:94:ARG:HB2	2.57	0.40
3:J:171:GLN:NE2	3:J:173:ASN:OD1	2.45	0.40
1:A:88:ASP:HB3	1:A:270:LEU:O	2.22	0.40
1:A:775:ASP:OD2	1:A:864:LEU:HB3	2.21	0.40
1:A:786:LYS:O	1:C:700:GLY:HA3	2.22	0.40
1:A:789:TYR:CD1	1:C:703:ASN:HB2	2.55	0.40
1:B:194:PHE:HB3	1:B:201:PHE:CZ	2.56	0.40
1:B:328:ARG:HH21	1:B:533:LEU:HG	1.87	0.40
1:B:769:GLY:O	1:B:770:ILE:C	2.60	0.40
1:B:1040:VAL:HG22	1:C:1031:GLU:CG	2.51	0.40
1:C:741:TYR:HD2	1:C:858:LEU:HD21	1.86	0.40
2:E:173:VAL:CG2	2:E:181:SER:HB2	2.52	0.40
2:I:37:ILE:HG21	2:I:107:TRP:CH2	2.56	0.40
3:J:50:TYR:CD1	3:J:56:PRO:HG3	2.57	0.40
1:A:559:PHE:CZ	1:A:575:ALA:HB3	2.57	0.40
1:A:593:GLY:HA3	1:A:613:GLN:O	2.21	0.40
1:A:655:TYR:OH	1:A:696:THR:HG23	2.21	0.40
1:A:727:LEU:HD12	1:A:1062:PHE:CE1	2.57	0.40
1:A:741:TYR:CD2	1:A:742:ILE:HG13	2.53	0.40
1:A:906:PHE:HE1	1:A:1049:LEU:HD11	1.87	0.40
1:A:1097:SER:HB2	1:A:1102:TRP:CD2	2.56	0.40
1:B:894:LEU:H	1:B:894:LEU:HD12	1.86	0.40
1:B:981:PHE:HZ	1:B:993:ILE:CG2	2.34	0.40
1:B:997:ILE:HA	1:B:1000:ARG:CD	2.52	0.40
1:C:762:GLN:HA	1:C:765:ARG:NE	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:89:TYR:N	3:H:105:THR:O	2.48	0.40
2:I:150:PHE:CE2	2:I:179:LEU:HD13	2.54	0.40
3:J:56:PRO:O	3:J:59:VAL:HG22	2.22	0.40
1:A:29:THR:HG23	1:A:62:VAL:HG23	2.03	0.40
1:A:37:TYR:HB3	1:A:223:LEU:HB3	2.04	0.40
1:A:328:ARG:NH1	1:A:531:THR:HB	2.37	0.40
1:A:534:VAL:HG11	1:A:539:VAL:HG11	2.04	0.40
1:A:551:VAL:HG22	1:A:553:THR:HG23	2.02	0.40
1:A:1029:MET:O	1:A:1033:VAL:HB	2.22	0.40
1:A:1105:THR:OG1	1:A:1106:GLN:N	2.54	0.40
1:B:714:ILE:HD13	1:B:1110:TYR:HB2	2.04	0.40
1:B:1067:TYR:OH	1:B:1108:ASN:OD1	2.11	0.40
1:C:980:ILE:HG21	1:C:993:ILE:HG23	2.03	0.40
2:E:210:LYS:HB3	2:E:210:LYS:HE3	1.81	0.40
3:F:188:GLN:O	3:F:195:TYR:OH	2.40	0.40
2:G:33:TYR:HB2	2:G:102:VAL:HG22	2.04	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 PDB entries followed by that with respect to all EM entries.

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	953/1261 (76%)	889 (93%)	63 (7%)	1 (0%)	51	85
1	B	957/1261 (76%)	887 (93%)	70 (7%)	0	100	100
1	C	956/1261 (76%)	884 (92%)	72 (8%)	0	100	100
2	E	221/224 (99%)	208 (94%)	13 (6%)	0	100	100
2	G	221/224 (99%)	206 (93%)	15 (7%)	0	100	100
2	I	221/224 (99%)	216 (98%)	5 (2%)	0	100	100
3	F	210/216 (97%)	199 (95%)	11 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	H	210/216 (97%)	197 (94%)	13 (6%)	0	100	100
3	J	210/216 (97%)	199 (95%)	11 (5%)	0	100	100
All	All	4159/5103 (82%)	3885 (93%)	273 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	532	ASN

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 PDB entries followed by that with respect to all EM entries.

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	788/1098 (72%)	786 (100%)	2 (0%)	92	95
1	B	787/1098 (72%)	784 (100%)	3 (0%)	91	94
1	C	788/1098 (72%)	785 (100%)	3 (0%)	91	94
2	E	188/190 (99%)	188 (100%)	0	100	100
2	G	188/190 (99%)	188 (100%)	0	100	100
2	I	188/190 (99%)	187 (100%)	1 (0%)	88	93
3	F	182/186 (98%)	182 (100%)	0	100	100
3	H	182/186 (98%)	181 (100%)	1 (0%)	88	93
3	J	182/186 (98%)	182 (100%)	0	100	100
All	All	3473/4422 (78%)	3463 (100%)	10 (0%)	92	95

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	765	ARG
1	A	995	ARG
1	B	44	ARG
1	B	408	ARG
1	B	1000	ARG

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Mol	Chain	Res	Type
1	C	765	ARG
1	C	964	LYS
1	C	1014	ARG
3	H	170	LYS
2	I	38	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	409	GLN
1	A	777	ASN
1	A	935	GLN
1	A	1113	GLN
1	B	196	ASN
1	B	658	ASN
1	B	955	ASN
1	B	1002	GLN
1	B	1010	GLN
1	B	1088	HIS
1	C	774	GLN
1	C	777	ASN
1	C	928	ASN
1	C	935	GLN
1	C	1010	GLN
1	C	1036	GLN
1	C	1048	HIS
3	F	92	GLN
2	G	52	ASN
3	H	35	GLN
3	H	92	GLN

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](#)

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.

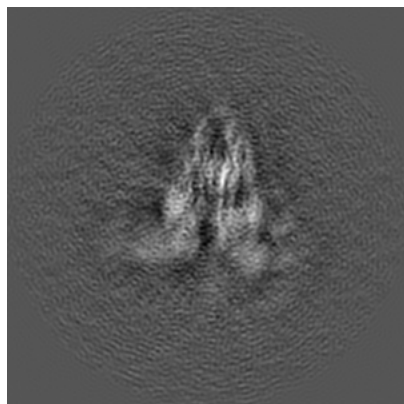
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34808. These allow visual inspection of the internal detail of the map and identification of artifacts.

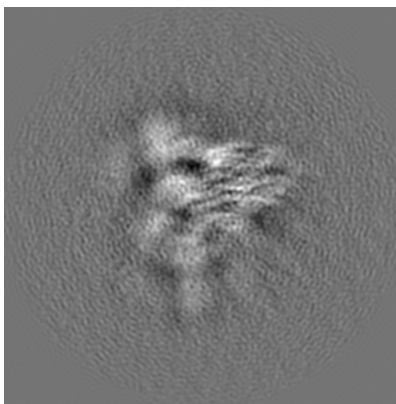
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

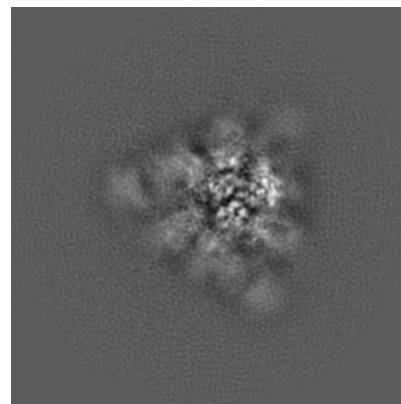
6.1.1 Primary map



X

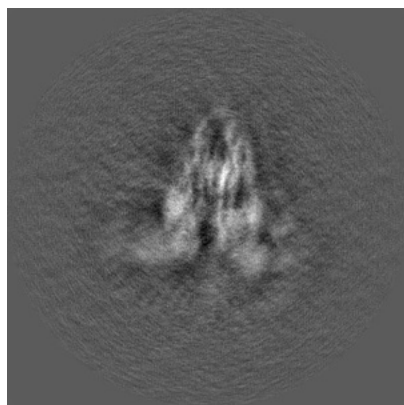


Y

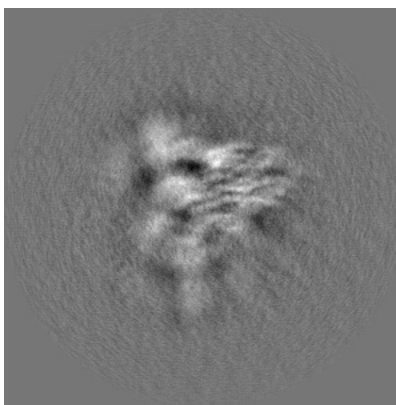


Z

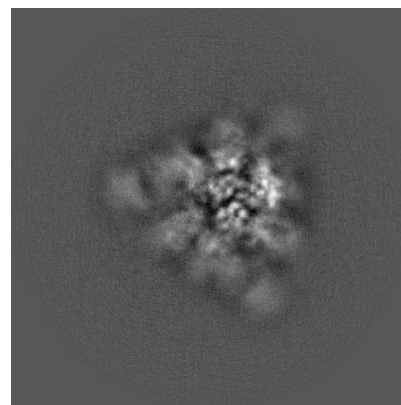
6.1.2 Raw map



X



Y

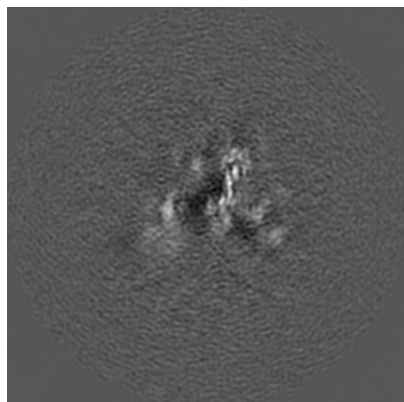


Z

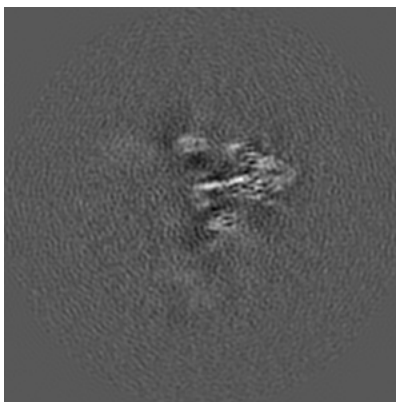
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

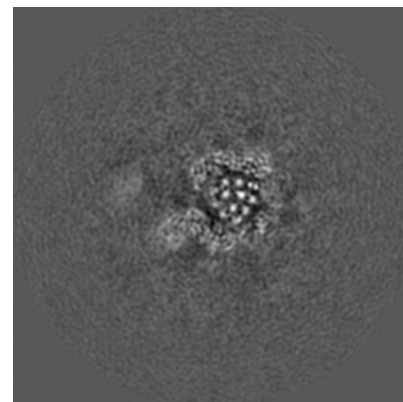
6.2.1 Primary map



X Index: 162

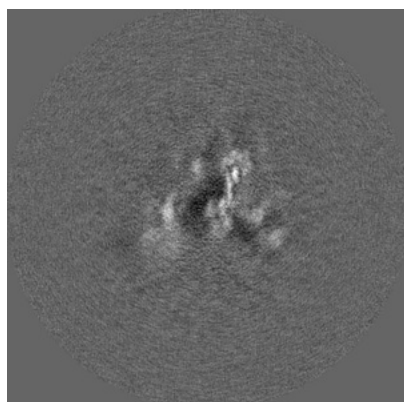


Y Index: 162

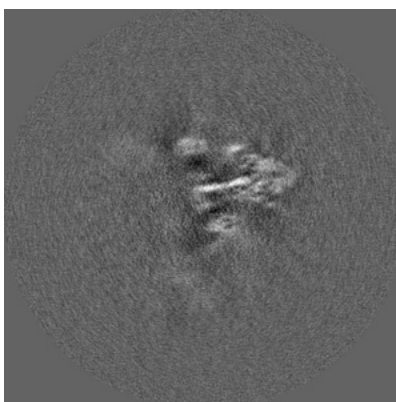


Z Index: 162

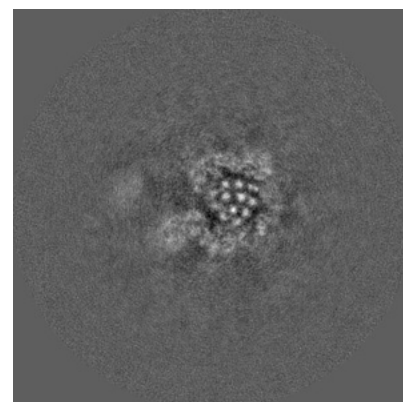
6.2.2 Raw map



X Index: 162



Y Index: 162

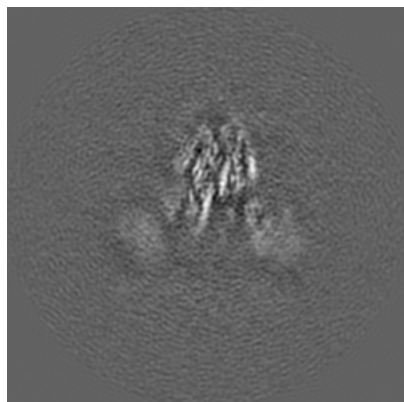


Z Index: 162

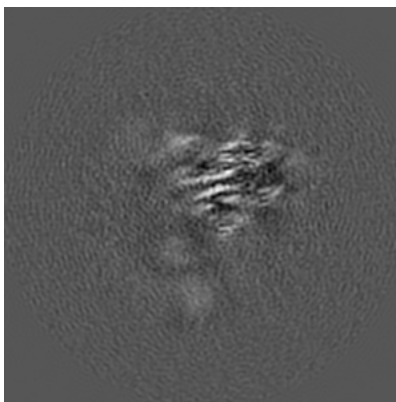
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

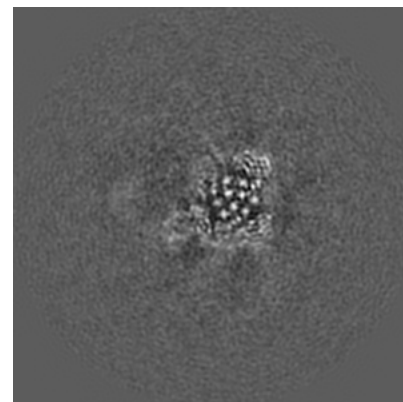
6.3.1 Primary map



X Index: 178

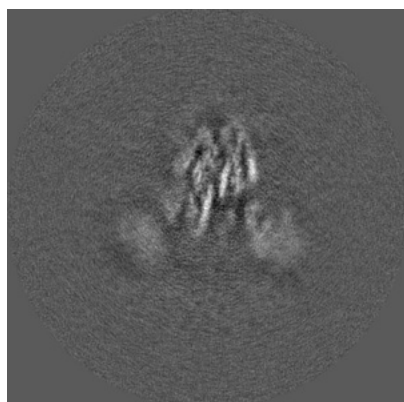


Y Index: 173

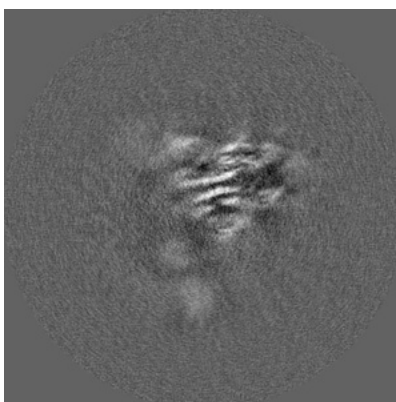


Z Index: 167

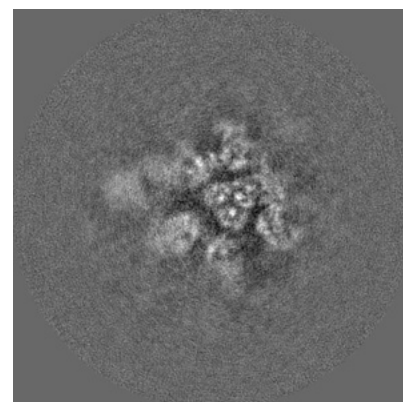
6.3.2 Raw map



X Index: 178



Y Index: 173

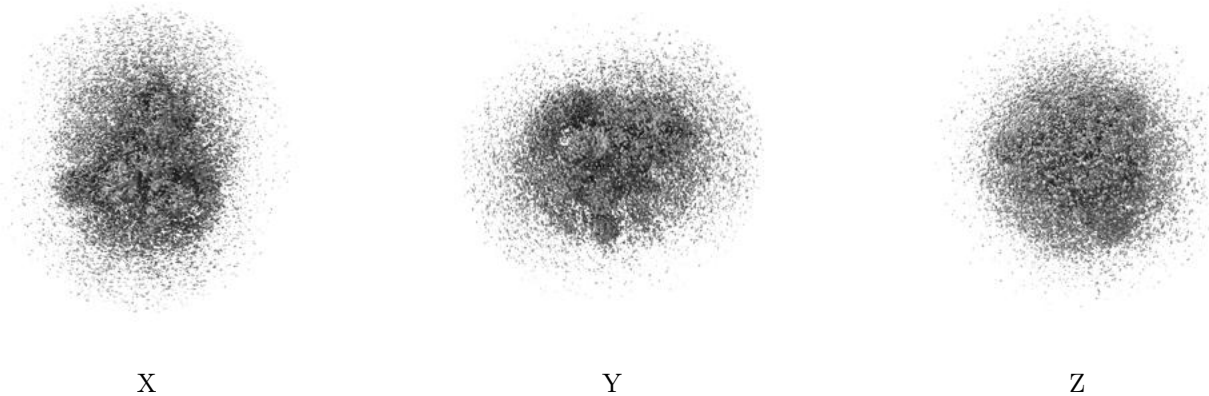


Z Index: 153

The images above show the largest variance slices of the map in three orthogonal directions.

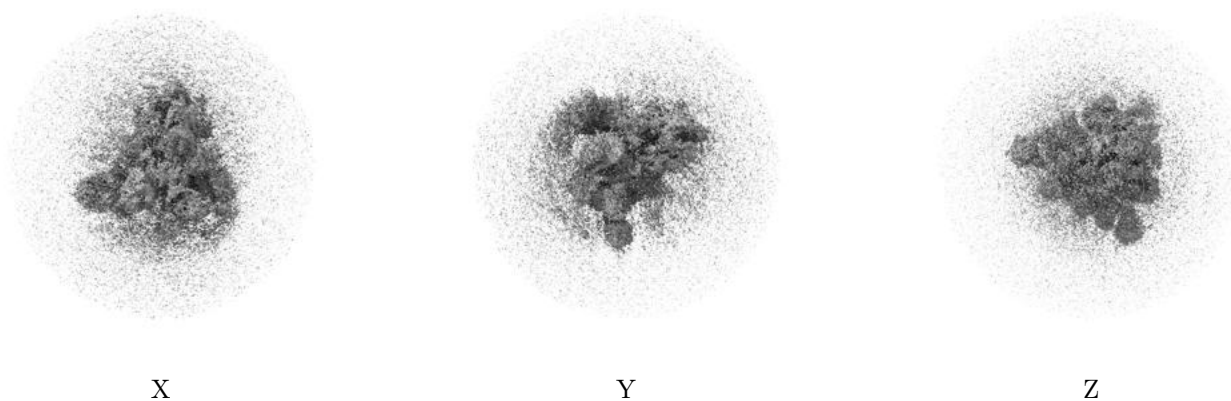
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0037. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

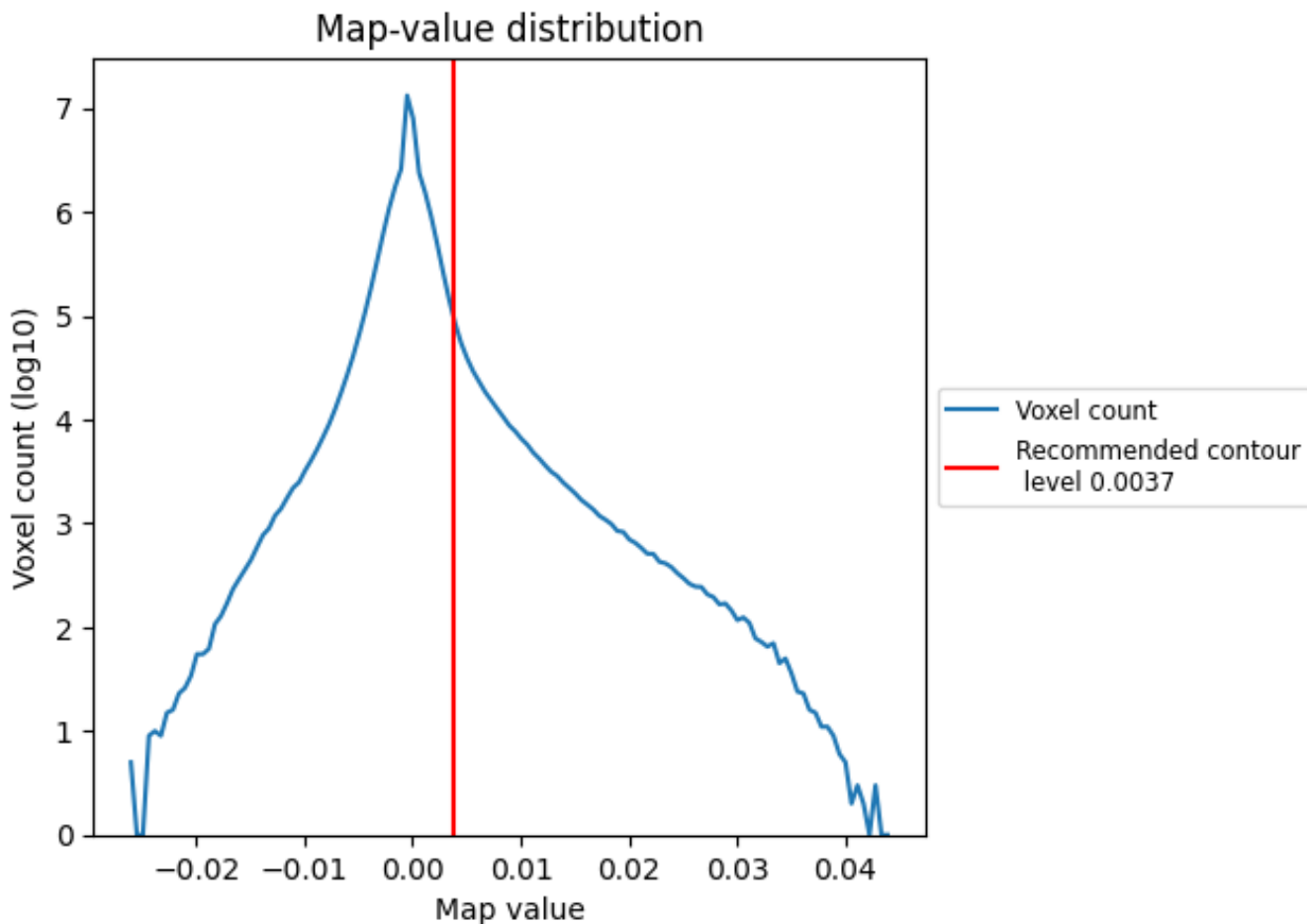
6.5 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

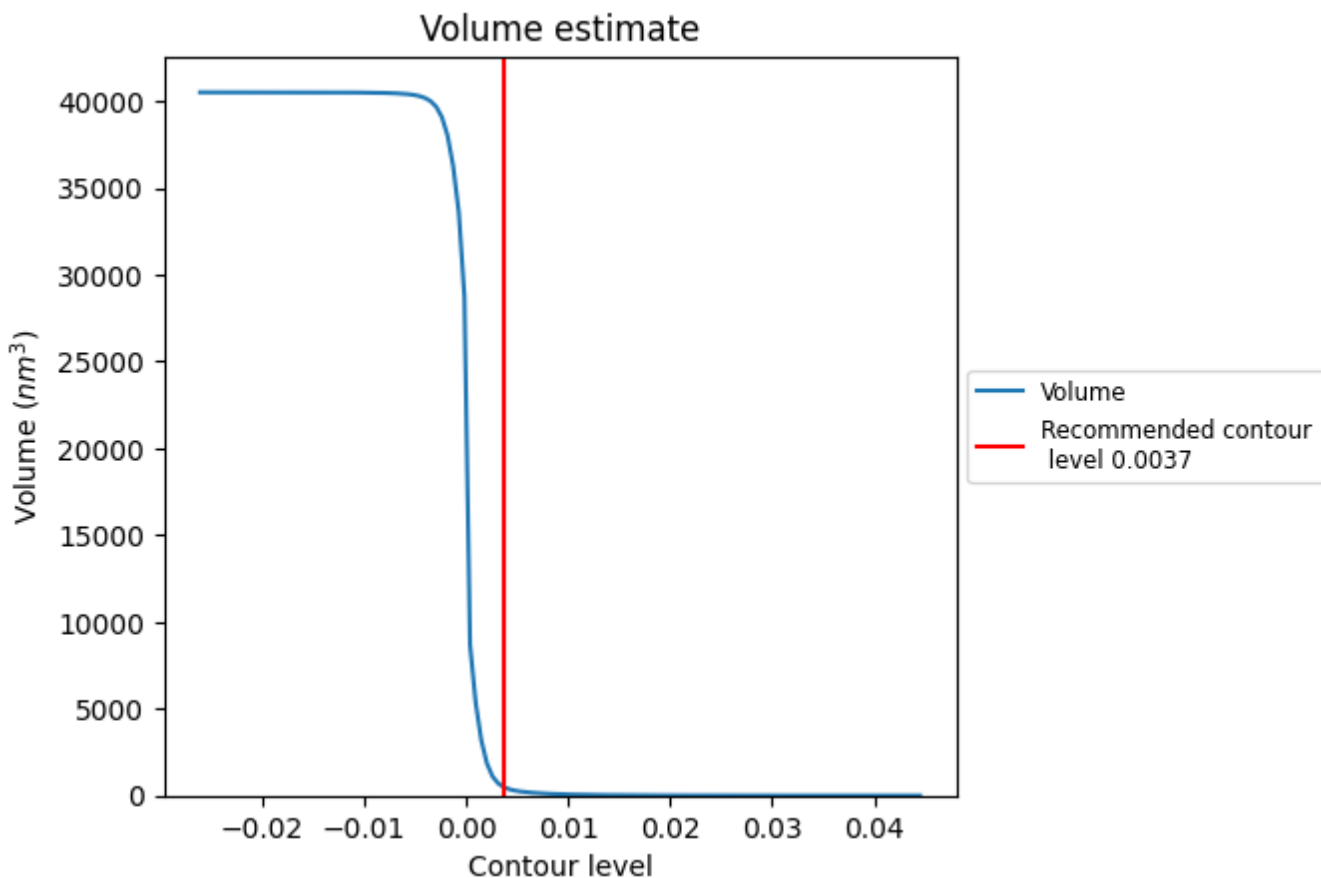
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

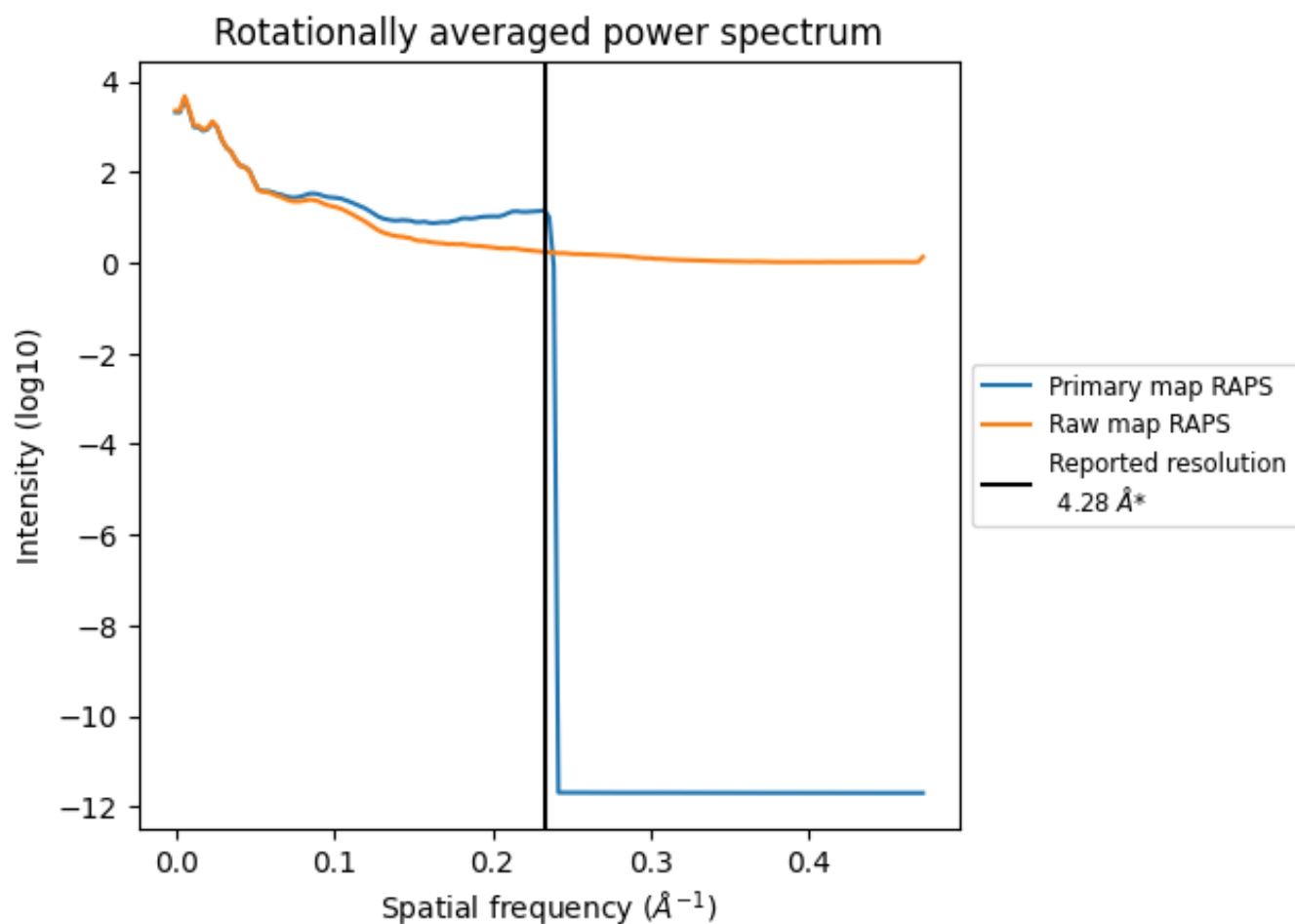
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 487 nm³; this corresponds to an approximate mass of 440 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

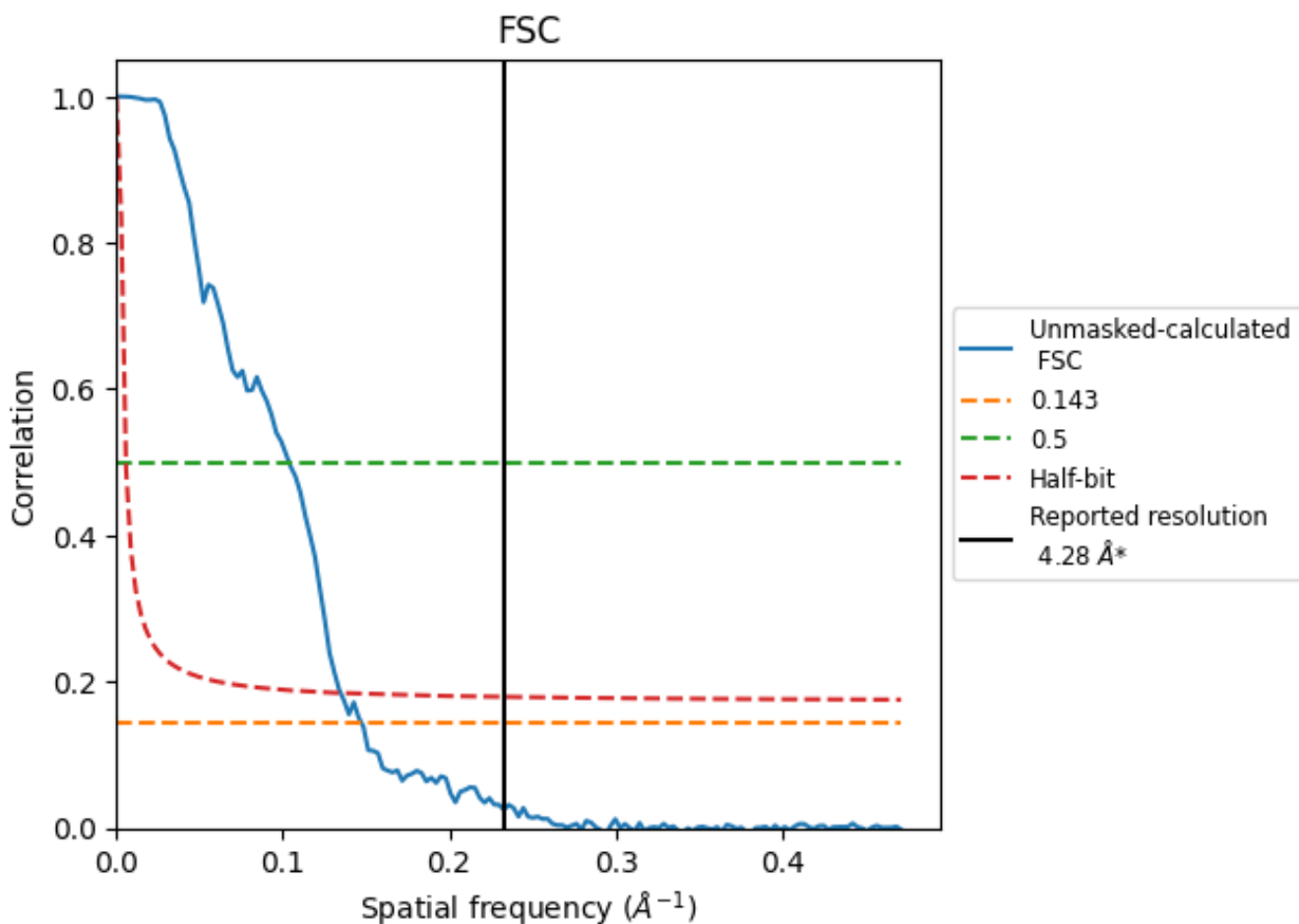


*Reported resolution corresponds to spatial frequency of 0.234 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.234 Å⁻¹

8.2 Resolution estimates [i](#)

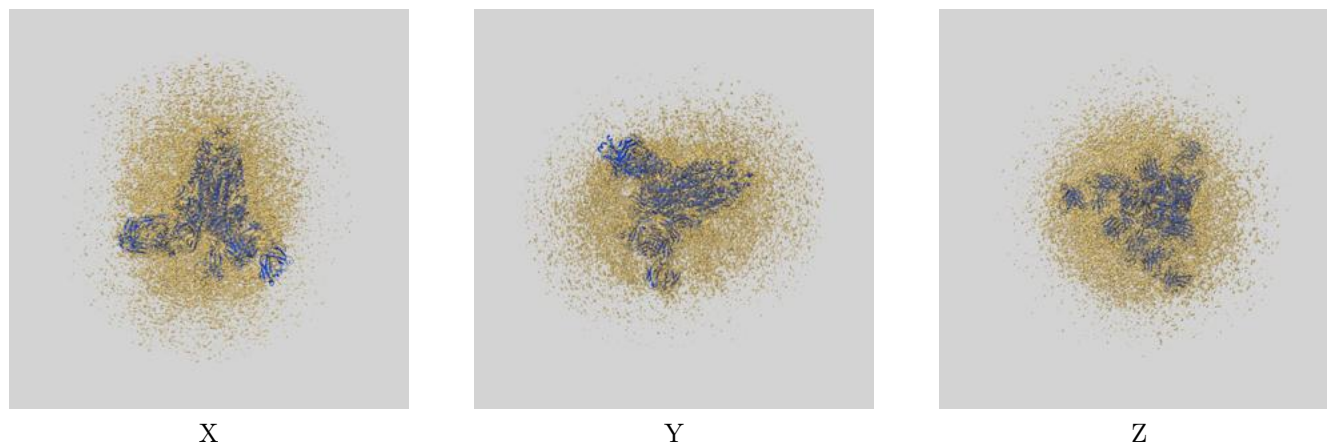
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.28	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.78	9.64	7.42

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.78 differs from the reported value 4.28 by more than 10 %

9 Map-model fit [i](#)

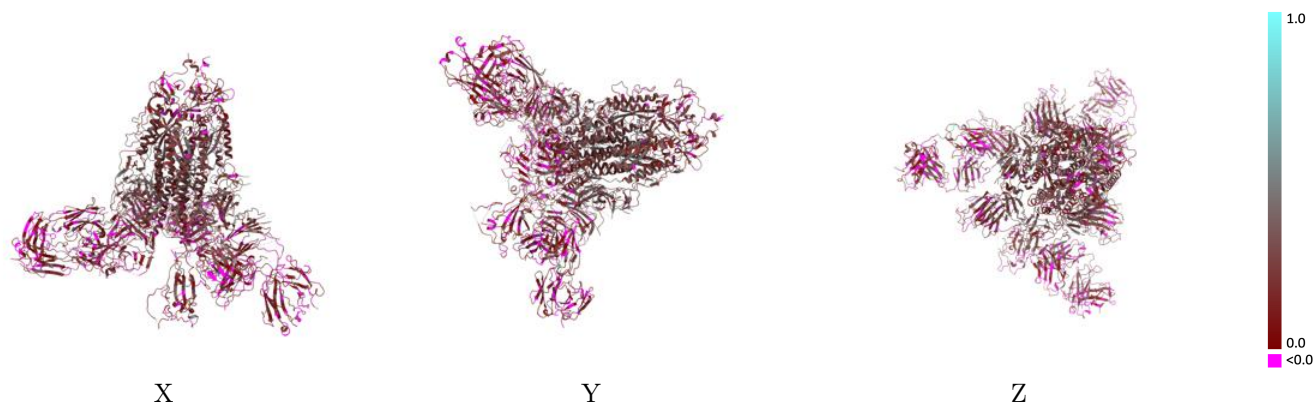
This section contains information regarding the fit between EMDB map EMD-34808 and PDB model 8HHZ. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



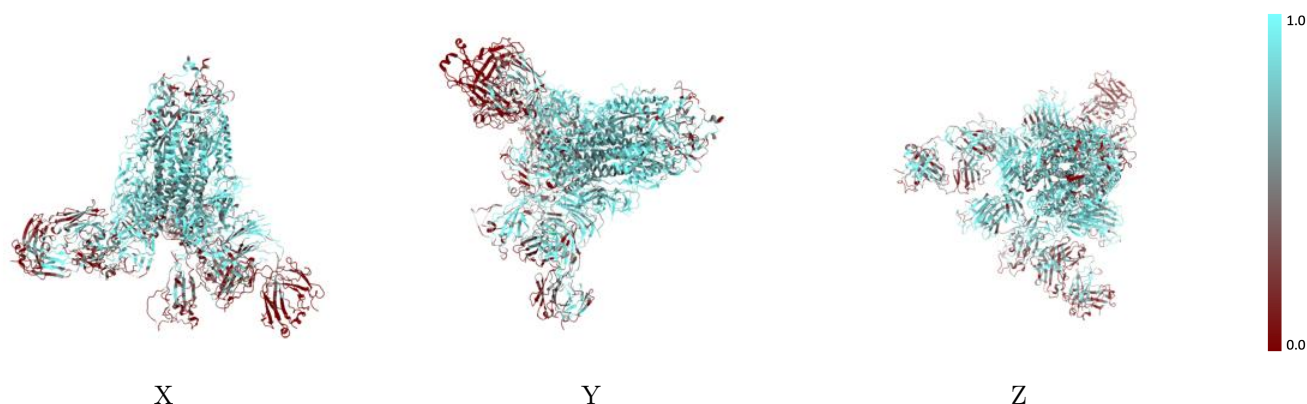
The images above show the 3D surface view of the map at the recommended contour level 0.0037 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



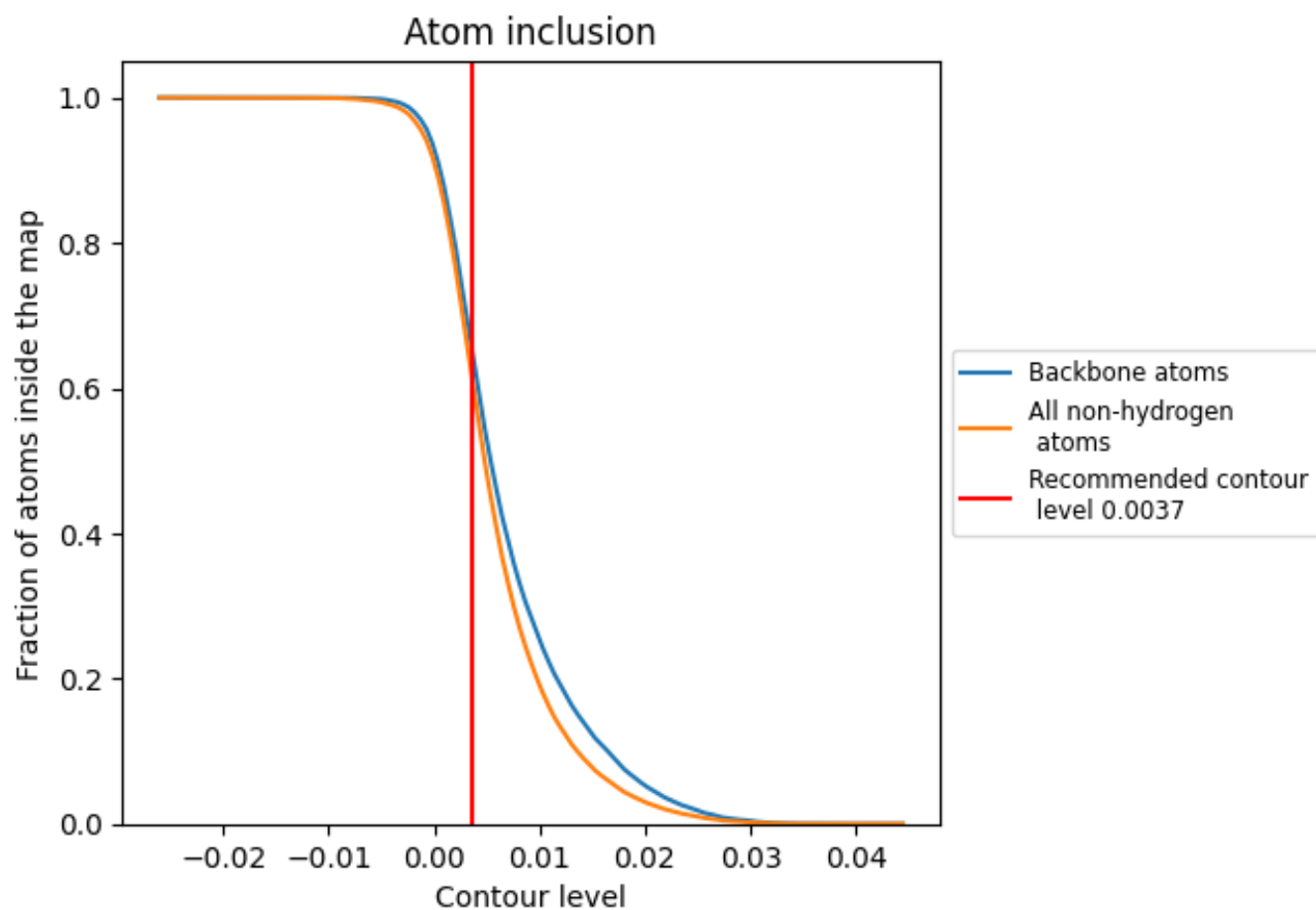
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0037).





















9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0037) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6049	 0.2070
A	 0.6603	 0.2330
B	 0.7096	 0.2470
C	 0.7246	 0.2440
E	 0.4107	 0.1130
F	 0.4506	 0.1460
G	 0.3106	 0.1280
H	 0.1785	 0.1480
I	 0.6102	 0.1300
J	 0.3805	 0.1100

