



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:08 PM UTC

PDB ID : 5UDD / pdb_00005udd
Title : Crystal Structure of RSV F B9320 Bound to MEDI8897
Authors : McLellan, J.S.
Deposited on : 2016-12-26
Resolution : 4.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

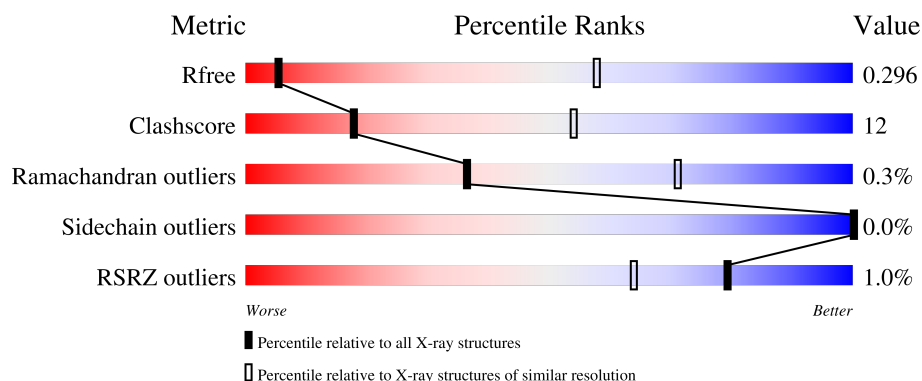
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.30 Å.

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



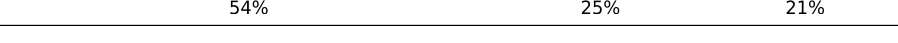
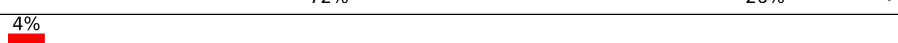
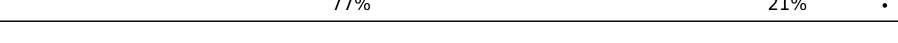
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1052 (4.70-3.90)
Clashscore	190562	1097 (4.70-3.90)
Ramachandran outliers	187476	1001 (4.70-3.90)
Sidechain outliers	187428	1007 (4.72-3.88)
RSRZ outliers	180081	1049 (4.70-3.90)

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

Mol	Chain	Length	Quality of chain
1	A	568	57% 22% 21%
1	B	568	% 56% 24% 20%
1	C	568	% 55% 23% 21%
1	D	568	58% 22% 20%
1	E	568	% 56% 23% 21%

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Mol	Chain	Length	Quality of chain
1	F	568	%  52% 28% 20%
1	G	568	 54% 26% 20%
1	H	568	%  56% 24% 21%
1	I	568	%  54% 25% 21%
2	J	228	 72% 26% .
2	K	228	4%  75% 22% .
2	L	228	 73% 24% .
2	M	228	 76% 21% .
2	N	228	 81% 16% .
2	O	228	4%  71% 24% 5%
3	P	214	%  77% 22% .
3	Q	214	2%  77% 21% .
3	R	214	 77% 21% .
3	S	214	 74% 24% .
3	T	214	 80% 18% .
3	U	214	4%  83% 14% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 51201 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Fusion glycoprotein F0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	449	Total	C	N	O	S	0	0	0
			3489	2201	578	688	22			
1	B	452	Total	C	N	O	S	0	0	0
			3511	2216	581	692	22			
1	C	450	Total	C	N	O	S	0	0	0
			3497	2208	578	689	22			
1	D	455	Total	C	N	O	S	0	0	0
			3532	2229	585	696	22			
1	E	451	Total	C	N	O	S	0	0	0
			3506	2213	580	691	22			
1	F	452	Total	C	N	O	S	0	0	0
			3515	2218	582	693	22			
1	G	453	Total	C	N	O	S	0	0	0
			3518	2221	582	693	22			
1	H	451	Total	C	N	O	S	0	0	0
			3502	2211	579	690	22			
1	I	448	Total	C	N	O	S	0	0	0
			3483	2199	576	686	22			

There are 531 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	155	CYS	SER	engineered mutation	UNP Q6V2E7
A	190	PHE	SER	engineered mutation	UNP Q6V2E7
A	207	LEU	VAL	engineered mutation	UNP Q6V2E7
A	290	CYS	SER	engineered mutation	UNP Q6V2E7
A	514	SER	-	expression tag	UNP Q6V2E7
A	515	ALA	-	expression tag	UNP Q6V2E7
A	516	ILE	-	expression tag	UNP Q6V2E7
A	517	GLY	-	expression tag	UNP Q6V2E7
A	518	GLY	-	expression tag	UNP Q6V2E7
A	519	TYR	-	expression tag	UNP Q6V2E7
A	520	ILE	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	521	PRO	-	expression tag	UNP Q6V2E7
A	522	GLU	-	expression tag	UNP Q6V2E7
A	523	ALA	-	expression tag	UNP Q6V2E7
A	524	PRO	-	expression tag	UNP Q6V2E7
A	525	ARG	-	expression tag	UNP Q6V2E7
A	526	ASP	-	expression tag	UNP Q6V2E7
A	527	GLY	-	expression tag	UNP Q6V2E7
A	528	GLN	-	expression tag	UNP Q6V2E7
A	529	ALA	-	expression tag	UNP Q6V2E7
A	530	TYR	-	expression tag	UNP Q6V2E7
A	531	VAL	-	expression tag	UNP Q6V2E7
A	532	ARG	-	expression tag	UNP Q6V2E7
A	533	LYS	-	expression tag	UNP Q6V2E7
A	534	ASP	-	expression tag	UNP Q6V2E7
A	535	GLY	-	expression tag	UNP Q6V2E7
A	536	GLU	-	expression tag	UNP Q6V2E7
A	537	TRP	-	expression tag	UNP Q6V2E7
A	538	VAL	-	expression tag	UNP Q6V2E7
A	539	LEU	-	expression tag	UNP Q6V2E7
A	540	LEU	-	expression tag	UNP Q6V2E7
A	541	SER	-	expression tag	UNP Q6V2E7
A	542	THR	-	expression tag	UNP Q6V2E7
A	543	PHE	-	expression tag	UNP Q6V2E7
A	544	LEU	-	expression tag	UNP Q6V2E7
A	545	GLY	-	expression tag	UNP Q6V2E7
A	546	GLY	-	expression tag	UNP Q6V2E7
A	547	LEU	-	expression tag	UNP Q6V2E7
A	548	VAL	-	expression tag	UNP Q6V2E7
A	549	PRO	-	expression tag	UNP Q6V2E7
A	550	ARG	-	expression tag	UNP Q6V2E7
A	551	GLY	-	expression tag	UNP Q6V2E7
A	552	SER	-	expression tag	UNP Q6V2E7
A	553	HIS	-	expression tag	UNP Q6V2E7
A	554	HIS	-	expression tag	UNP Q6V2E7
A	555	HIS	-	expression tag	UNP Q6V2E7
A	556	HIS	-	expression tag	UNP Q6V2E7
A	557	HIS	-	expression tag	UNP Q6V2E7
A	558	HIS	-	expression tag	UNP Q6V2E7
A	559	SER	-	expression tag	UNP Q6V2E7
A	560	ALA	-	expression tag	UNP Q6V2E7
A	561	TRP	-	expression tag	UNP Q6V2E7
A	562	SER	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	563	HIS	-	expression tag	UNP Q6V2E7
A	564	PRO	-	expression tag	UNP Q6V2E7
A	565	GLN	-	expression tag	UNP Q6V2E7
A	566	PHE	-	expression tag	UNP Q6V2E7
A	567	GLU	-	expression tag	UNP Q6V2E7
A	568	LYS	-	expression tag	UNP Q6V2E7
B	155	CYS	SER	engineered mutation	UNP Q6V2E7
B	190	PHE	SER	engineered mutation	UNP Q6V2E7
B	207	LEU	VAL	engineered mutation	UNP Q6V2E7
B	290	CYS	SER	engineered mutation	UNP Q6V2E7
B	514	SER	-	expression tag	UNP Q6V2E7
B	515	ALA	-	expression tag	UNP Q6V2E7
B	516	ILE	-	expression tag	UNP Q6V2E7
B	517	GLY	-	expression tag	UNP Q6V2E7
B	518	GLY	-	expression tag	UNP Q6V2E7
B	519	TYR	-	expression tag	UNP Q6V2E7
B	520	ILE	-	expression tag	UNP Q6V2E7
B	521	PRO	-	expression tag	UNP Q6V2E7
B	522	GLU	-	expression tag	UNP Q6V2E7
B	523	ALA	-	expression tag	UNP Q6V2E7
B	524	PRO	-	expression tag	UNP Q6V2E7
B	525	ARG	-	expression tag	UNP Q6V2E7
B	526	ASP	-	expression tag	UNP Q6V2E7
B	527	GLY	-	expression tag	UNP Q6V2E7
B	528	GLN	-	expression tag	UNP Q6V2E7
B	529	ALA	-	expression tag	UNP Q6V2E7
B	530	TYR	-	expression tag	UNP Q6V2E7
B	531	VAL	-	expression tag	UNP Q6V2E7
B	532	ARG	-	expression tag	UNP Q6V2E7
B	533	LYS	-	expression tag	UNP Q6V2E7
B	534	ASP	-	expression tag	UNP Q6V2E7
B	535	GLY	-	expression tag	UNP Q6V2E7
B	536	GLU	-	expression tag	UNP Q6V2E7
B	537	TRP	-	expression tag	UNP Q6V2E7
B	538	VAL	-	expression tag	UNP Q6V2E7
B	539	LEU	-	expression tag	UNP Q6V2E7
B	540	LEU	-	expression tag	UNP Q6V2E7
B	541	SER	-	expression tag	UNP Q6V2E7
B	542	THR	-	expression tag	UNP Q6V2E7
B	543	PHE	-	expression tag	UNP Q6V2E7
B	544	LEU	-	expression tag	UNP Q6V2E7
B	545	GLY	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	546	GLY	-	expression tag	UNP Q6V2E7
B	547	LEU	-	expression tag	UNP Q6V2E7
B	548	VAL	-	expression tag	UNP Q6V2E7
B	549	PRO	-	expression tag	UNP Q6V2E7
B	550	ARG	-	expression tag	UNP Q6V2E7
B	551	GLY	-	expression tag	UNP Q6V2E7
B	552	SER	-	expression tag	UNP Q6V2E7
B	553	HIS	-	expression tag	UNP Q6V2E7
B	554	HIS	-	expression tag	UNP Q6V2E7
B	555	HIS	-	expression tag	UNP Q6V2E7
B	556	HIS	-	expression tag	UNP Q6V2E7
B	557	HIS	-	expression tag	UNP Q6V2E7
B	558	HIS	-	expression tag	UNP Q6V2E7
B	559	SER	-	expression tag	UNP Q6V2E7
B	560	ALA	-	expression tag	UNP Q6V2E7
B	561	TRP	-	expression tag	UNP Q6V2E7
B	562	SER	-	expression tag	UNP Q6V2E7
B	563	HIS	-	expression tag	UNP Q6V2E7
B	564	PRO	-	expression tag	UNP Q6V2E7
B	565	GLN	-	expression tag	UNP Q6V2E7
B	566	PHE	-	expression tag	UNP Q6V2E7
B	567	GLU	-	expression tag	UNP Q6V2E7
B	568	LYS	-	expression tag	UNP Q6V2E7
C	155	CYS	SER	engineered mutation	UNP Q6V2E7
C	190	PHE	SER	engineered mutation	UNP Q6V2E7
C	207	LEU	VAL	engineered mutation	UNP Q6V2E7
C	290	CYS	SER	engineered mutation	UNP Q6V2E7
C	514	SER	-	expression tag	UNP Q6V2E7
C	515	ALA	-	expression tag	UNP Q6V2E7
C	516	ILE	-	expression tag	UNP Q6V2E7
C	517	GLY	-	expression tag	UNP Q6V2E7
C	518	GLY	-	expression tag	UNP Q6V2E7
C	519	TYR	-	expression tag	UNP Q6V2E7
C	520	ILE	-	expression tag	UNP Q6V2E7
C	521	PRO	-	expression tag	UNP Q6V2E7
C	522	GLU	-	expression tag	UNP Q6V2E7
C	523	ALA	-	expression tag	UNP Q6V2E7
C	524	PRO	-	expression tag	UNP Q6V2E7
C	525	ARG	-	expression tag	UNP Q6V2E7
C	526	ASP	-	expression tag	UNP Q6V2E7
C	527	GLY	-	expression tag	UNP Q6V2E7
C	528	GLN	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	529	ALA	-	expression tag	UNP Q6V2E7
C	530	TYR	-	expression tag	UNP Q6V2E7
C	531	VAL	-	expression tag	UNP Q6V2E7
C	532	ARG	-	expression tag	UNP Q6V2E7
C	533	LYS	-	expression tag	UNP Q6V2E7
C	534	ASP	-	expression tag	UNP Q6V2E7
C	535	GLY	-	expression tag	UNP Q6V2E7
C	536	GLU	-	expression tag	UNP Q6V2E7
C	537	TRP	-	expression tag	UNP Q6V2E7
C	538	VAL	-	expression tag	UNP Q6V2E7
C	539	LEU	-	expression tag	UNP Q6V2E7
C	540	LEU	-	expression tag	UNP Q6V2E7
C	541	SER	-	expression tag	UNP Q6V2E7
C	542	THR	-	expression tag	UNP Q6V2E7
C	543	PHE	-	expression tag	UNP Q6V2E7
C	544	LEU	-	expression tag	UNP Q6V2E7
C	545	GLY	-	expression tag	UNP Q6V2E7
C	546	GLY	-	expression tag	UNP Q6V2E7
C	547	LEU	-	expression tag	UNP Q6V2E7
C	548	VAL	-	expression tag	UNP Q6V2E7
C	549	PRO	-	expression tag	UNP Q6V2E7
C	550	ARG	-	expression tag	UNP Q6V2E7
C	551	GLY	-	expression tag	UNP Q6V2E7
C	552	SER	-	expression tag	UNP Q6V2E7
C	553	HIS	-	expression tag	UNP Q6V2E7
C	554	HIS	-	expression tag	UNP Q6V2E7
C	555	HIS	-	expression tag	UNP Q6V2E7
C	556	HIS	-	expression tag	UNP Q6V2E7
C	557	HIS	-	expression tag	UNP Q6V2E7
C	558	HIS	-	expression tag	UNP Q6V2E7
C	559	SER	-	expression tag	UNP Q6V2E7
C	560	ALA	-	expression tag	UNP Q6V2E7
C	561	TRP	-	expression tag	UNP Q6V2E7
C	562	SER	-	expression tag	UNP Q6V2E7
C	563	HIS	-	expression tag	UNP Q6V2E7
C	564	PRO	-	expression tag	UNP Q6V2E7
C	565	GLN	-	expression tag	UNP Q6V2E7
C	566	PHE	-	expression tag	UNP Q6V2E7
C	567	GLU	-	expression tag	UNP Q6V2E7
C	568	LYS	-	expression tag	UNP Q6V2E7
D	155	CYS	SER	engineered mutation	UNP Q6V2E7
D	190	PHE	SER	engineered mutation	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	207	LEU	VAL	engineered mutation	UNP Q6V2E7
D	290	CYS	SER	engineered mutation	UNP Q6V2E7
D	514	SER	-	expression tag	UNP Q6V2E7
D	515	ALA	-	expression tag	UNP Q6V2E7
D	516	ILE	-	expression tag	UNP Q6V2E7
D	517	GLY	-	expression tag	UNP Q6V2E7
D	518	GLY	-	expression tag	UNP Q6V2E7
D	519	TYR	-	expression tag	UNP Q6V2E7
D	520	ILE	-	expression tag	UNP Q6V2E7
D	521	PRO	-	expression tag	UNP Q6V2E7
D	522	GLU	-	expression tag	UNP Q6V2E7
D	523	ALA	-	expression tag	UNP Q6V2E7
D	524	PRO	-	expression tag	UNP Q6V2E7
D	525	ARG	-	expression tag	UNP Q6V2E7
D	526	ASP	-	expression tag	UNP Q6V2E7
D	527	GLY	-	expression tag	UNP Q6V2E7
D	528	GLN	-	expression tag	UNP Q6V2E7
D	529	ALA	-	expression tag	UNP Q6V2E7
D	530	TYR	-	expression tag	UNP Q6V2E7
D	531	VAL	-	expression tag	UNP Q6V2E7
D	532	ARG	-	expression tag	UNP Q6V2E7
D	533	LYS	-	expression tag	UNP Q6V2E7
D	534	ASP	-	expression tag	UNP Q6V2E7
D	535	GLY	-	expression tag	UNP Q6V2E7
D	536	GLU	-	expression tag	UNP Q6V2E7
D	537	TRP	-	expression tag	UNP Q6V2E7
D	538	VAL	-	expression tag	UNP Q6V2E7
D	539	LEU	-	expression tag	UNP Q6V2E7
D	540	LEU	-	expression tag	UNP Q6V2E7
D	541	SER	-	expression tag	UNP Q6V2E7
D	542	THR	-	expression tag	UNP Q6V2E7
D	543	PHE	-	expression tag	UNP Q6V2E7
D	544	LEU	-	expression tag	UNP Q6V2E7
D	545	GLY	-	expression tag	UNP Q6V2E7
D	546	GLY	-	expression tag	UNP Q6V2E7
D	547	LEU	-	expression tag	UNP Q6V2E7
D	548	VAL	-	expression tag	UNP Q6V2E7
D	549	PRO	-	expression tag	UNP Q6V2E7
D	550	ARG	-	expression tag	UNP Q6V2E7
D	551	GLY	-	expression tag	UNP Q6V2E7
D	552	SER	-	expression tag	UNP Q6V2E7
D	553	HIS	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	554	HIS	-	expression tag	UNP Q6V2E7
D	555	HIS	-	expression tag	UNP Q6V2E7
D	556	HIS	-	expression tag	UNP Q6V2E7
D	557	HIS	-	expression tag	UNP Q6V2E7
D	558	HIS	-	expression tag	UNP Q6V2E7
D	559	SER	-	expression tag	UNP Q6V2E7
D	560	ALA	-	expression tag	UNP Q6V2E7
D	561	TRP	-	expression tag	UNP Q6V2E7
D	562	SER	-	expression tag	UNP Q6V2E7
D	563	HIS	-	expression tag	UNP Q6V2E7
D	564	PRO	-	expression tag	UNP Q6V2E7
D	565	GLN	-	expression tag	UNP Q6V2E7
D	566	PHE	-	expression tag	UNP Q6V2E7
D	567	GLU	-	expression tag	UNP Q6V2E7
D	568	LYS	-	expression tag	UNP Q6V2E7
E	155	CYS	SER	engineered mutation	UNP Q6V2E7
E	190	PHE	SER	engineered mutation	UNP Q6V2E7
E	207	LEU	VAL	engineered mutation	UNP Q6V2E7
E	290	CYS	SER	engineered mutation	UNP Q6V2E7
E	514	SER	-	expression tag	UNP Q6V2E7
E	515	ALA	-	expression tag	UNP Q6V2E7
E	516	ILE	-	expression tag	UNP Q6V2E7
E	517	GLY	-	expression tag	UNP Q6V2E7
E	518	GLY	-	expression tag	UNP Q6V2E7
E	519	TYR	-	expression tag	UNP Q6V2E7
E	520	ILE	-	expression tag	UNP Q6V2E7
E	521	PRO	-	expression tag	UNP Q6V2E7
E	522	GLU	-	expression tag	UNP Q6V2E7
E	523	ALA	-	expression tag	UNP Q6V2E7
E	524	PRO	-	expression tag	UNP Q6V2E7
E	525	ARG	-	expression tag	UNP Q6V2E7
E	526	ASP	-	expression tag	UNP Q6V2E7
E	527	GLY	-	expression tag	UNP Q6V2E7
E	528	GLN	-	expression tag	UNP Q6V2E7
E	529	ALA	-	expression tag	UNP Q6V2E7
E	530	TYR	-	expression tag	UNP Q6V2E7
E	531	VAL	-	expression tag	UNP Q6V2E7
E	532	ARG	-	expression tag	UNP Q6V2E7
E	533	LYS	-	expression tag	UNP Q6V2E7
E	534	ASP	-	expression tag	UNP Q6V2E7
E	535	GLY	-	expression tag	UNP Q6V2E7
E	536	GLU	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	537	TRP	-	expression tag	UNP Q6V2E7
E	538	VAL	-	expression tag	UNP Q6V2E7
E	539	LEU	-	expression tag	UNP Q6V2E7
E	540	LEU	-	expression tag	UNP Q6V2E7
E	541	SER	-	expression tag	UNP Q6V2E7
E	542	THR	-	expression tag	UNP Q6V2E7
E	543	PHE	-	expression tag	UNP Q6V2E7
E	544	LEU	-	expression tag	UNP Q6V2E7
E	545	GLY	-	expression tag	UNP Q6V2E7
E	546	GLY	-	expression tag	UNP Q6V2E7
E	547	LEU	-	expression tag	UNP Q6V2E7
E	548	VAL	-	expression tag	UNP Q6V2E7
E	549	PRO	-	expression tag	UNP Q6V2E7
E	550	ARG	-	expression tag	UNP Q6V2E7
E	551	GLY	-	expression tag	UNP Q6V2E7
E	552	SER	-	expression tag	UNP Q6V2E7
E	553	HIS	-	expression tag	UNP Q6V2E7
E	554	HIS	-	expression tag	UNP Q6V2E7
E	555	HIS	-	expression tag	UNP Q6V2E7
E	556	HIS	-	expression tag	UNP Q6V2E7
E	557	HIS	-	expression tag	UNP Q6V2E7
E	558	HIS	-	expression tag	UNP Q6V2E7
E	559	SER	-	expression tag	UNP Q6V2E7
E	560	ALA	-	expression tag	UNP Q6V2E7
E	561	TRP	-	expression tag	UNP Q6V2E7
E	562	SER	-	expression tag	UNP Q6V2E7
E	563	HIS	-	expression tag	UNP Q6V2E7
E	564	PRO	-	expression tag	UNP Q6V2E7
E	565	GLN	-	expression tag	UNP Q6V2E7
E	566	PHE	-	expression tag	UNP Q6V2E7
E	567	GLU	-	expression tag	UNP Q6V2E7
E	568	LYS	-	expression tag	UNP Q6V2E7
F	155	CYS	SER	engineered mutation	UNP Q6V2E7
F	190	PHE	SER	engineered mutation	UNP Q6V2E7
F	207	LEU	VAL	engineered mutation	UNP Q6V2E7
F	290	CYS	SER	engineered mutation	UNP Q6V2E7
F	514	SER	-	expression tag	UNP Q6V2E7
F	515	ALA	-	expression tag	UNP Q6V2E7
F	516	ILE	-	expression tag	UNP Q6V2E7
F	517	GLY	-	expression tag	UNP Q6V2E7
F	518	GLY	-	expression tag	UNP Q6V2E7
F	519	TYR	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	520	ILE	-	expression tag	UNP Q6V2E7
F	521	PRO	-	expression tag	UNP Q6V2E7
F	522	GLU	-	expression tag	UNP Q6V2E7
F	523	ALA	-	expression tag	UNP Q6V2E7
F	524	PRO	-	expression tag	UNP Q6V2E7
F	525	ARG	-	expression tag	UNP Q6V2E7
F	526	ASP	-	expression tag	UNP Q6V2E7
F	527	GLY	-	expression tag	UNP Q6V2E7
F	528	GLN	-	expression tag	UNP Q6V2E7
F	529	ALA	-	expression tag	UNP Q6V2E7
F	530	TYR	-	expression tag	UNP Q6V2E7
F	531	VAL	-	expression tag	UNP Q6V2E7
F	532	ARG	-	expression tag	UNP Q6V2E7
F	533	LYS	-	expression tag	UNP Q6V2E7
F	534	ASP	-	expression tag	UNP Q6V2E7
F	535	GLY	-	expression tag	UNP Q6V2E7
F	536	GLU	-	expression tag	UNP Q6V2E7
F	537	TRP	-	expression tag	UNP Q6V2E7
F	538	VAL	-	expression tag	UNP Q6V2E7
F	539	LEU	-	expression tag	UNP Q6V2E7
F	540	LEU	-	expression tag	UNP Q6V2E7
F	541	SER	-	expression tag	UNP Q6V2E7
F	542	THR	-	expression tag	UNP Q6V2E7
F	543	PHE	-	expression tag	UNP Q6V2E7
F	544	LEU	-	expression tag	UNP Q6V2E7
F	545	GLY	-	expression tag	UNP Q6V2E7
F	546	GLY	-	expression tag	UNP Q6V2E7
F	547	LEU	-	expression tag	UNP Q6V2E7
F	548	VAL	-	expression tag	UNP Q6V2E7
F	549	PRO	-	expression tag	UNP Q6V2E7
F	550	ARG	-	expression tag	UNP Q6V2E7
F	551	GLY	-	expression tag	UNP Q6V2E7
F	552	SER	-	expression tag	UNP Q6V2E7
F	553	HIS	-	expression tag	UNP Q6V2E7
F	554	HIS	-	expression tag	UNP Q6V2E7
F	555	HIS	-	expression tag	UNP Q6V2E7
F	556	HIS	-	expression tag	UNP Q6V2E7
F	557	HIS	-	expression tag	UNP Q6V2E7
F	558	HIS	-	expression tag	UNP Q6V2E7
F	559	SER	-	expression tag	UNP Q6V2E7
F	560	ALA	-	expression tag	UNP Q6V2E7
F	561	TRP	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	562	SER	-	expression tag	UNP Q6V2E7
F	563	HIS	-	expression tag	UNP Q6V2E7
F	564	PRO	-	expression tag	UNP Q6V2E7
F	565	GLN	-	expression tag	UNP Q6V2E7
F	566	PHE	-	expression tag	UNP Q6V2E7
F	567	GLU	-	expression tag	UNP Q6V2E7
F	568	LYS	-	expression tag	UNP Q6V2E7
G	155	CYS	SER	engineered mutation	UNP Q6V2E7
G	190	PHE	SER	engineered mutation	UNP Q6V2E7
G	207	LEU	VAL	engineered mutation	UNP Q6V2E7
G	290	CYS	SER	engineered mutation	UNP Q6V2E7
G	514	SER	-	expression tag	UNP Q6V2E7
G	515	ALA	-	expression tag	UNP Q6V2E7
G	516	ILE	-	expression tag	UNP Q6V2E7
G	517	GLY	-	expression tag	UNP Q6V2E7
G	518	GLY	-	expression tag	UNP Q6V2E7
G	519	TYR	-	expression tag	UNP Q6V2E7
G	520	ILE	-	expression tag	UNP Q6V2E7
G	521	PRO	-	expression tag	UNP Q6V2E7
G	522	GLU	-	expression tag	UNP Q6V2E7
G	523	ALA	-	expression tag	UNP Q6V2E7
G	524	PRO	-	expression tag	UNP Q6V2E7
G	525	ARG	-	expression tag	UNP Q6V2E7
G	526	ASP	-	expression tag	UNP Q6V2E7
G	527	GLY	-	expression tag	UNP Q6V2E7
G	528	GLN	-	expression tag	UNP Q6V2E7
G	529	ALA	-	expression tag	UNP Q6V2E7
G	530	TYR	-	expression tag	UNP Q6V2E7
G	531	VAL	-	expression tag	UNP Q6V2E7
G	532	ARG	-	expression tag	UNP Q6V2E7
G	533	LYS	-	expression tag	UNP Q6V2E7
G	534	ASP	-	expression tag	UNP Q6V2E7
G	535	GLY	-	expression tag	UNP Q6V2E7
G	536	GLU	-	expression tag	UNP Q6V2E7
G	537	TRP	-	expression tag	UNP Q6V2E7
G	538	VAL	-	expression tag	UNP Q6V2E7
G	539	LEU	-	expression tag	UNP Q6V2E7
G	540	LEU	-	expression tag	UNP Q6V2E7
G	541	SER	-	expression tag	UNP Q6V2E7
G	542	THR	-	expression tag	UNP Q6V2E7
G	543	PHE	-	expression tag	UNP Q6V2E7
G	544	LEU	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
G	545	GLY	-	expression tag	UNP Q6V2E7
G	546	GLY	-	expression tag	UNP Q6V2E7
G	547	LEU	-	expression tag	UNP Q6V2E7
G	548	VAL	-	expression tag	UNP Q6V2E7
G	549	PRO	-	expression tag	UNP Q6V2E7
G	550	ARG	-	expression tag	UNP Q6V2E7
G	551	GLY	-	expression tag	UNP Q6V2E7
G	552	SER	-	expression tag	UNP Q6V2E7
G	553	HIS	-	expression tag	UNP Q6V2E7
G	554	HIS	-	expression tag	UNP Q6V2E7
G	555	HIS	-	expression tag	UNP Q6V2E7
G	556	HIS	-	expression tag	UNP Q6V2E7
G	557	HIS	-	expression tag	UNP Q6V2E7
G	558	HIS	-	expression tag	UNP Q6V2E7
G	559	SER	-	expression tag	UNP Q6V2E7
G	560	ALA	-	expression tag	UNP Q6V2E7
G	561	TRP	-	expression tag	UNP Q6V2E7
G	562	SER	-	expression tag	UNP Q6V2E7
G	563	HIS	-	expression tag	UNP Q6V2E7
G	564	PRO	-	expression tag	UNP Q6V2E7
G	565	GLN	-	expression tag	UNP Q6V2E7
G	566	PHE	-	expression tag	UNP Q6V2E7
G	567	GLU	-	expression tag	UNP Q6V2E7
G	568	LYS	-	expression tag	UNP Q6V2E7
H	155	CYS	SER	engineered mutation	UNP Q6V2E7
H	190	PHE	SER	engineered mutation	UNP Q6V2E7
H	207	LEU	VAL	engineered mutation	UNP Q6V2E7
H	290	CYS	SER	engineered mutation	UNP Q6V2E7
H	514	SER	-	expression tag	UNP Q6V2E7
H	515	ALA	-	expression tag	UNP Q6V2E7
H	516	ILE	-	expression tag	UNP Q6V2E7
H	517	GLY	-	expression tag	UNP Q6V2E7
H	518	GLY	-	expression tag	UNP Q6V2E7
H	519	TYR	-	expression tag	UNP Q6V2E7
H	520	ILE	-	expression tag	UNP Q6V2E7
H	521	PRO	-	expression tag	UNP Q6V2E7
H	522	GLU	-	expression tag	UNP Q6V2E7
H	523	ALA	-	expression tag	UNP Q6V2E7
H	524	PRO	-	expression tag	UNP Q6V2E7
H	525	ARG	-	expression tag	UNP Q6V2E7
H	526	ASP	-	expression tag	UNP Q6V2E7
H	527	GLY	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
H	528	GLN	-	expression tag	UNP Q6V2E7
H	529	ALA	-	expression tag	UNP Q6V2E7
H	530	TYR	-	expression tag	UNP Q6V2E7
H	531	VAL	-	expression tag	UNP Q6V2E7
H	532	ARG	-	expression tag	UNP Q6V2E7
H	533	LYS	-	expression tag	UNP Q6V2E7
H	534	ASP	-	expression tag	UNP Q6V2E7
H	535	GLY	-	expression tag	UNP Q6V2E7
H	536	GLU	-	expression tag	UNP Q6V2E7
H	537	TRP	-	expression tag	UNP Q6V2E7
H	538	VAL	-	expression tag	UNP Q6V2E7
H	539	LEU	-	expression tag	UNP Q6V2E7
H	540	LEU	-	expression tag	UNP Q6V2E7
H	541	SER	-	expression tag	UNP Q6V2E7
H	542	THR	-	expression tag	UNP Q6V2E7
H	543	PHE	-	expression tag	UNP Q6V2E7
H	544	LEU	-	expression tag	UNP Q6V2E7
H	545	GLY	-	expression tag	UNP Q6V2E7
H	546	GLY	-	expression tag	UNP Q6V2E7
H	547	LEU	-	expression tag	UNP Q6V2E7
H	548	VAL	-	expression tag	UNP Q6V2E7
H	549	PRO	-	expression tag	UNP Q6V2E7
H	550	ARG	-	expression tag	UNP Q6V2E7
H	551	GLY	-	expression tag	UNP Q6V2E7
H	552	SER	-	expression tag	UNP Q6V2E7
H	553	HIS	-	expression tag	UNP Q6V2E7
H	554	HIS	-	expression tag	UNP Q6V2E7
H	555	HIS	-	expression tag	UNP Q6V2E7
H	556	HIS	-	expression tag	UNP Q6V2E7
H	557	HIS	-	expression tag	UNP Q6V2E7
H	558	HIS	-	expression tag	UNP Q6V2E7
H	559	SER	-	expression tag	UNP Q6V2E7
H	560	ALA	-	expression tag	UNP Q6V2E7
H	561	TRP	-	expression tag	UNP Q6V2E7
H	562	SER	-	expression tag	UNP Q6V2E7
H	563	HIS	-	expression tag	UNP Q6V2E7
H	564	PRO	-	expression tag	UNP Q6V2E7
H	565	GLN	-	expression tag	UNP Q6V2E7
H	566	PHE	-	expression tag	UNP Q6V2E7
H	567	GLU	-	expression tag	UNP Q6V2E7
H	568	LYS	-	expression tag	UNP Q6V2E7
I	155	CYS	SER	engineered mutation	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
I	190	PHE	SER	engineered mutation	UNP Q6V2E7
I	207	LEU	VAL	engineered mutation	UNP Q6V2E7
I	290	CYS	SER	engineered mutation	UNP Q6V2E7
I	514	SER	-	expression tag	UNP Q6V2E7
I	515	ALA	-	expression tag	UNP Q6V2E7
I	516	ILE	-	expression tag	UNP Q6V2E7
I	517	GLY	-	expression tag	UNP Q6V2E7
I	518	GLY	-	expression tag	UNP Q6V2E7
I	519	TYR	-	expression tag	UNP Q6V2E7
I	520	ILE	-	expression tag	UNP Q6V2E7
I	521	PRO	-	expression tag	UNP Q6V2E7
I	522	GLU	-	expression tag	UNP Q6V2E7
I	523	ALA	-	expression tag	UNP Q6V2E7
I	524	PRO	-	expression tag	UNP Q6V2E7
I	525	ARG	-	expression tag	UNP Q6V2E7
I	526	ASP	-	expression tag	UNP Q6V2E7
I	527	GLY	-	expression tag	UNP Q6V2E7
I	528	GLN	-	expression tag	UNP Q6V2E7
I	529	ALA	-	expression tag	UNP Q6V2E7
I	530	TYR	-	expression tag	UNP Q6V2E7
I	531	VAL	-	expression tag	UNP Q6V2E7
I	532	ARG	-	expression tag	UNP Q6V2E7
I	533	LYS	-	expression tag	UNP Q6V2E7
I	534	ASP	-	expression tag	UNP Q6V2E7
I	535	GLY	-	expression tag	UNP Q6V2E7
I	536	GLU	-	expression tag	UNP Q6V2E7
I	537	TRP	-	expression tag	UNP Q6V2E7
I	538	VAL	-	expression tag	UNP Q6V2E7
I	539	LEU	-	expression tag	UNP Q6V2E7
I	540	LEU	-	expression tag	UNP Q6V2E7
I	541	SER	-	expression tag	UNP Q6V2E7
I	542	THR	-	expression tag	UNP Q6V2E7
I	543	PHE	-	expression tag	UNP Q6V2E7
I	544	LEU	-	expression tag	UNP Q6V2E7
I	545	GLY	-	expression tag	UNP Q6V2E7
I	546	GLY	-	expression tag	UNP Q6V2E7
I	547	LEU	-	expression tag	UNP Q6V2E7
I	548	VAL	-	expression tag	UNP Q6V2E7
I	549	PRO	-	expression tag	UNP Q6V2E7
I	550	ARG	-	expression tag	UNP Q6V2E7
I	551	GLY	-	expression tag	UNP Q6V2E7
I	552	SER	-	expression tag	UNP Q6V2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
I	553	HIS	-	expression tag	UNP Q6V2E7
I	554	HIS	-	expression tag	UNP Q6V2E7
I	555	HIS	-	expression tag	UNP Q6V2E7
I	556	HIS	-	expression tag	UNP Q6V2E7
I	557	HIS	-	expression tag	UNP Q6V2E7
I	558	HIS	-	expression tag	UNP Q6V2E7
I	559	SER	-	expression tag	UNP Q6V2E7
I	560	ALA	-	expression tag	UNP Q6V2E7
I	561	TRP	-	expression tag	UNP Q6V2E7
I	562	SER	-	expression tag	UNP Q6V2E7
I	563	HIS	-	expression tag	UNP Q6V2E7
I	564	PRO	-	expression tag	UNP Q6V2E7
I	565	GLN	-	expression tag	UNP Q6V2E7
I	566	PHE	-	expression tag	UNP Q6V2E7
I	567	GLU	-	expression tag	UNP Q6V2E7
I	568	LYS	-	expression tag	UNP Q6V2E7

- Molecule 2 is a protein called MEDI8897 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	J	224	Total	C	N	O	S	0	0	0
			1668	1054	273	333	8			
2	K	220	Total	C	N	O	S	0	0	0
			1643	1040	268	327	8			
2	L	221	Total	C	N	O	S	0	0	0
			1649	1043	269	329	8			
2	M	221	Total	C	N	O	S	0	0	0
			1649	1043	269	329	8			
2	N	221	Total	C	N	O	S	0	0	0
			1649	1043	269	329	8			
2	O	216	Total	C	N	O	S	0	0	0
			1622	1029	264	321	8			

- Molecule 3 is a protein called MEDI8897 Fab Light Chain.

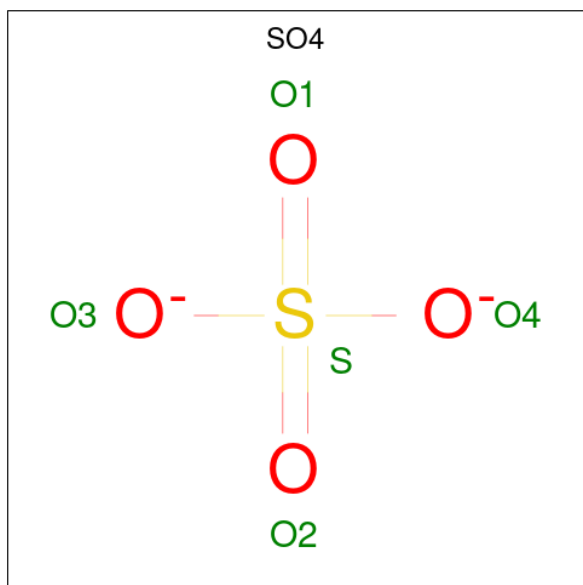
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	212	Total	C	N	O	S	0	0	0
			1623	1016	270	332	5			
3	Q	211	Total	C	N	O	S	0	0	0
			1619	1014	269	331	5			
3	R	211	Total	C	N	O	S	0	0	0
			1619	1014	269	331	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	S	211	Total	C	N	O	S	0	0	0
			1619	1014	269	331	5			
3	T	211	Total	C	N	O	S	0	0	0
			1619	1014	269	331	5			
3	U	208	Total	C	N	O	S	0	0	0
			1594	999	263	327	5			

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		

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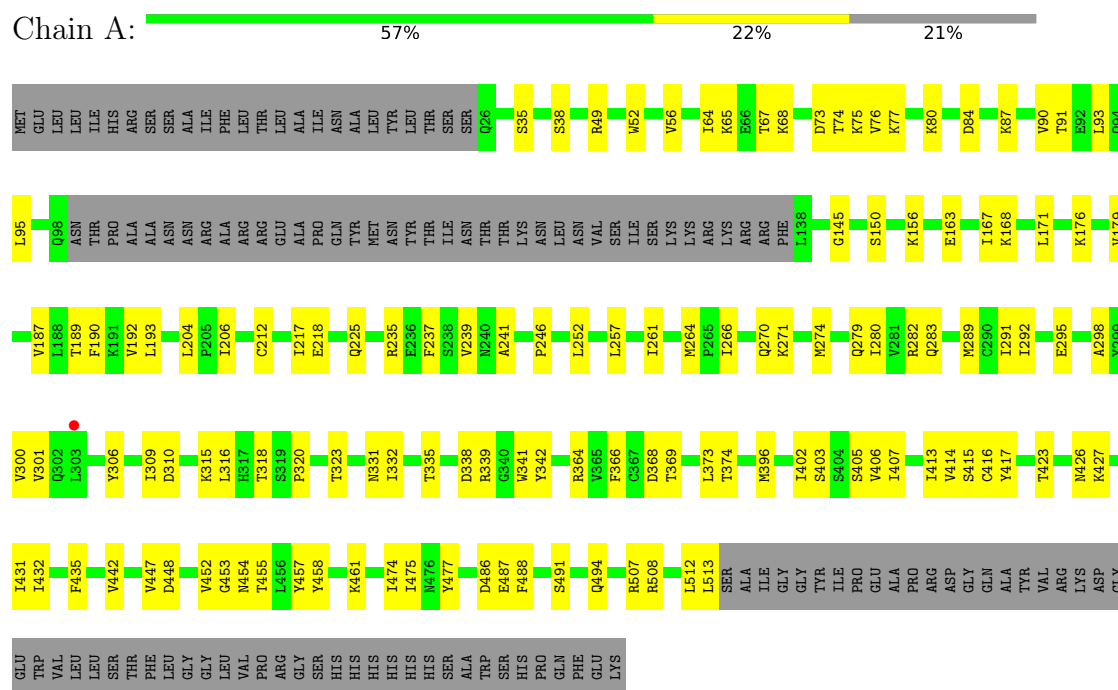
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	O	S	0	0
			5	4	1		
4	G	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	I	1	Total	O	S	0	0
			5	4	1		
4	J	1	Total	O	S	0	0
			5	4	1		
4	L	1	Total	O	S	0	0
			5	4	1		

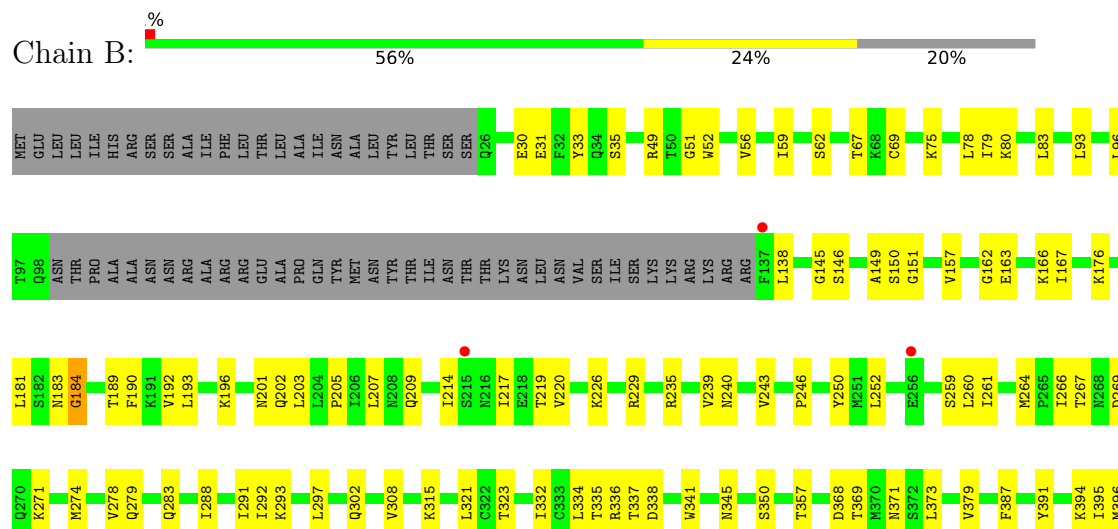
3 Residue-property plots

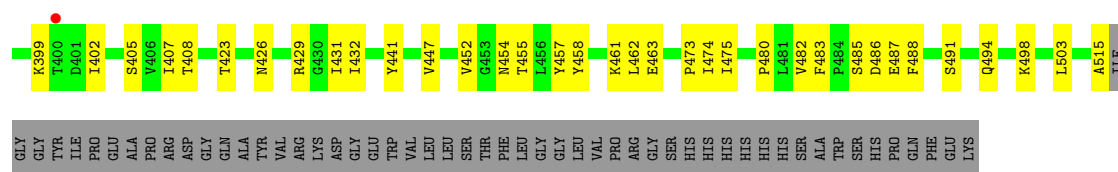
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Fusion glycoprotein F0

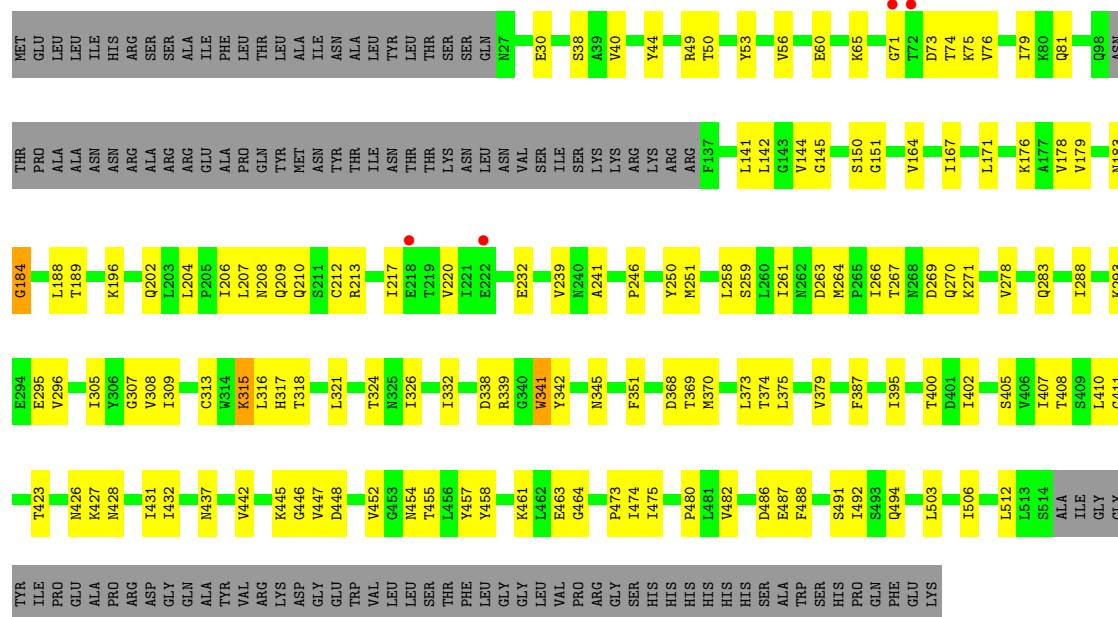


• Molecule 1: Fusion glycoprotein F0

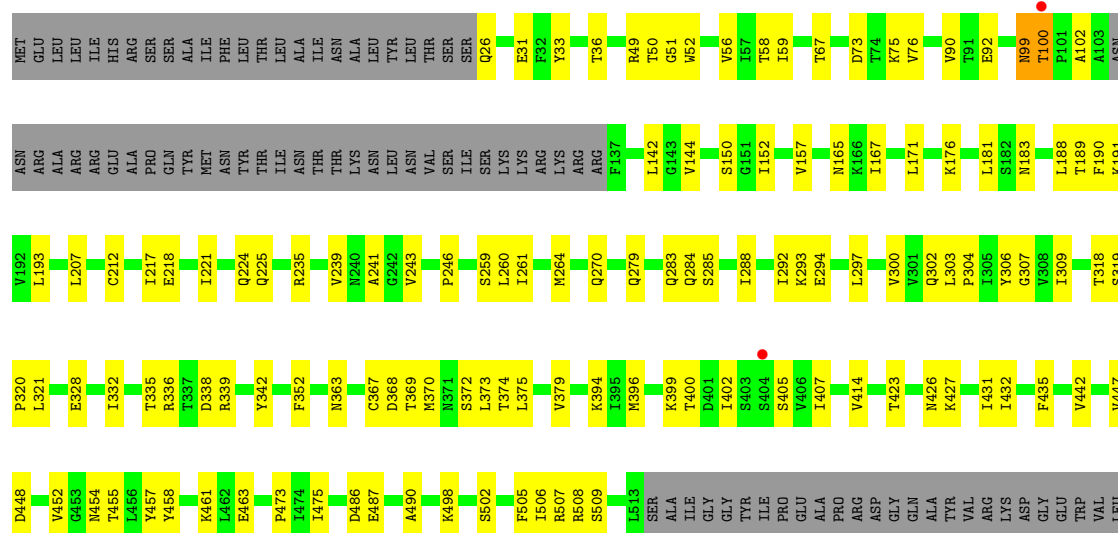




• Molecule 1: Fusion glycoprotein F0

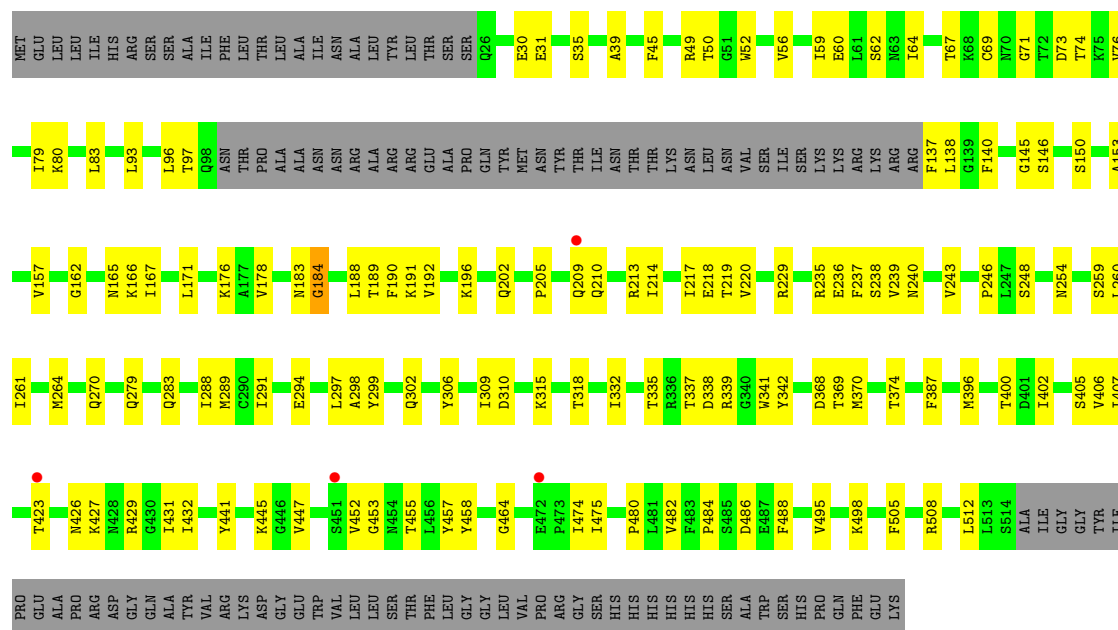


• Molecule 1: Fusion glycoprotein F0

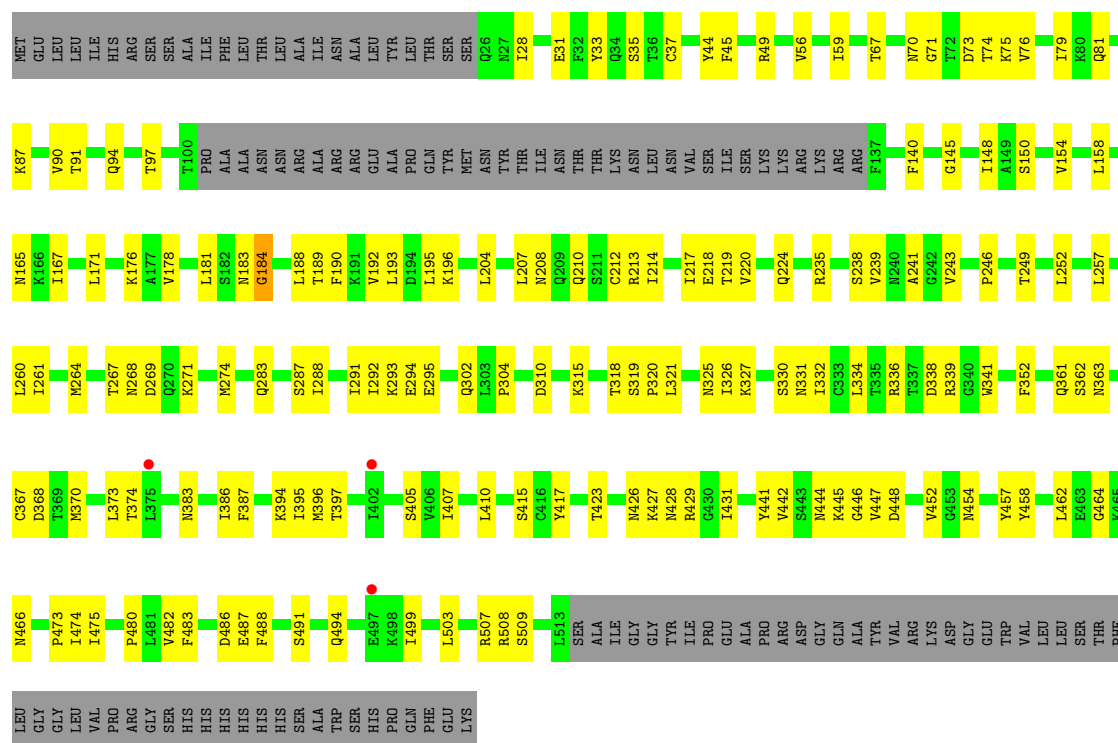


LEU SER THR LEU LEU GLY GLY LEU LEU PRO ARG GLY SER HIS HIS HIS HIS SER ALA TRP SER HIS PRO GLN PHE GLU LYS

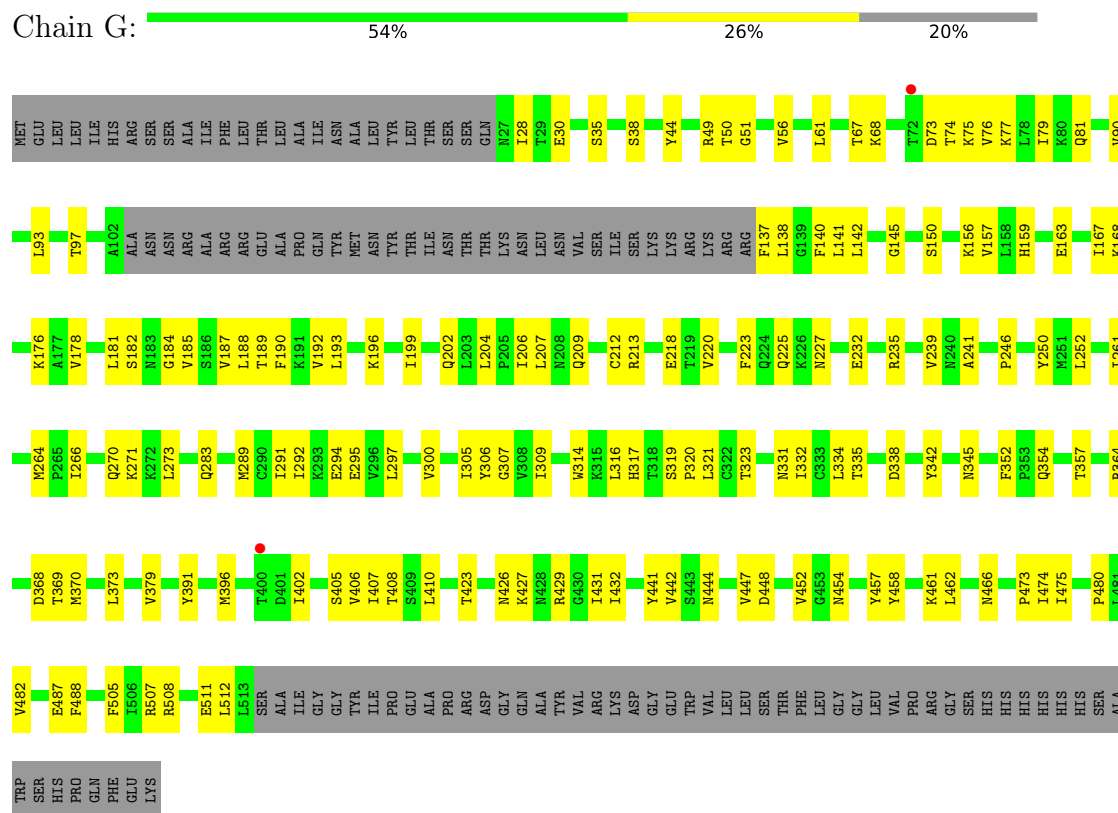
● Molecule 1: Fusion glycoprotein F0



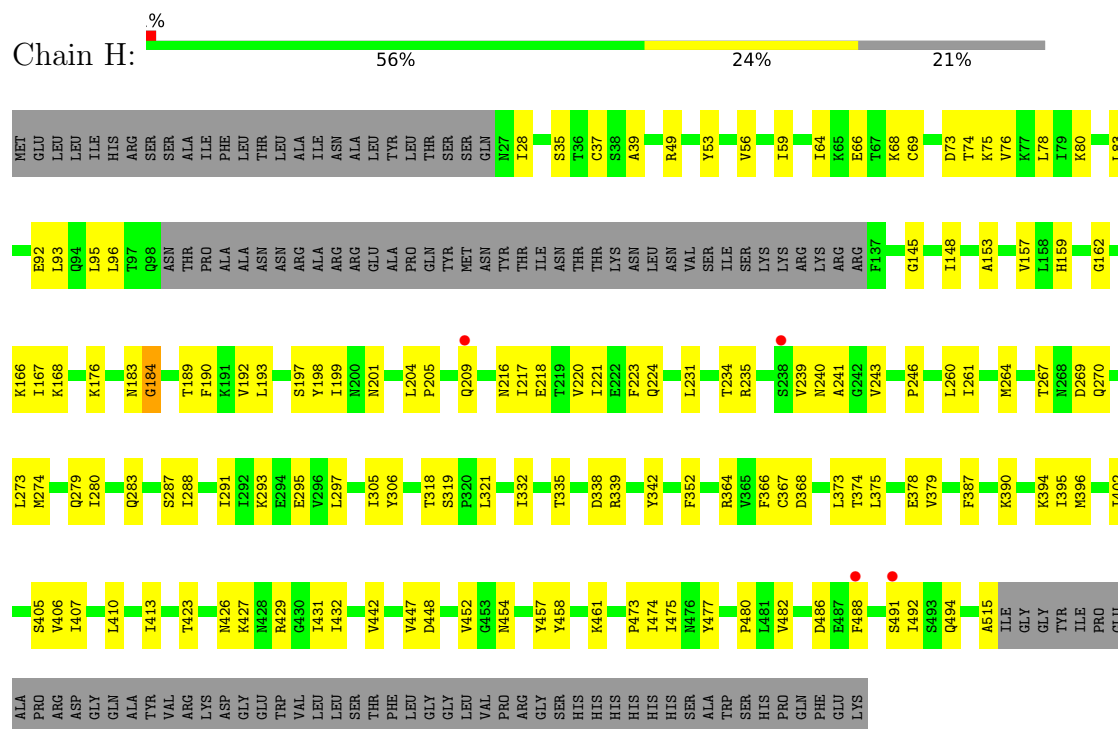
● Molecule 1: Fusion glycoprotein F0



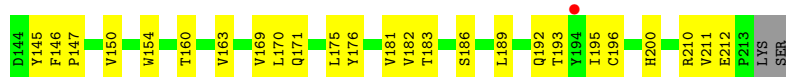
- Molecule 1: Fusion glycoprotein F0



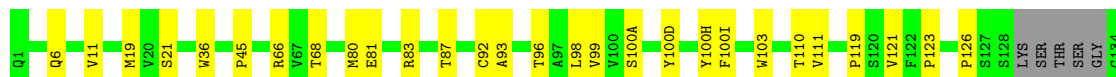
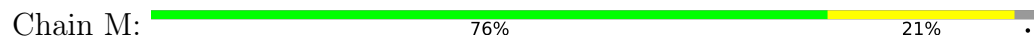
- Molecule 1: Fusion glycoprotein F0



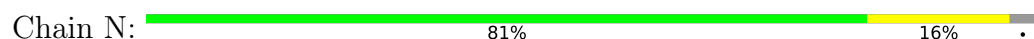
- Molecule 1: Fusion glycoprotein F0



• Molecule 2: MEDI8897 Fab Heavy Chain



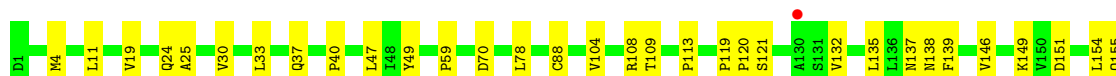
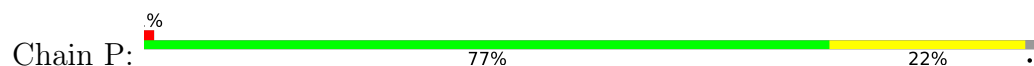
• Molecule 2: MEDI8897 Fab Heavy Chain



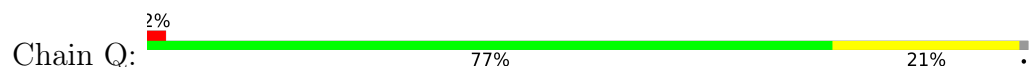
• Molecule 2: MEDI8897 Fab Heavy Chain

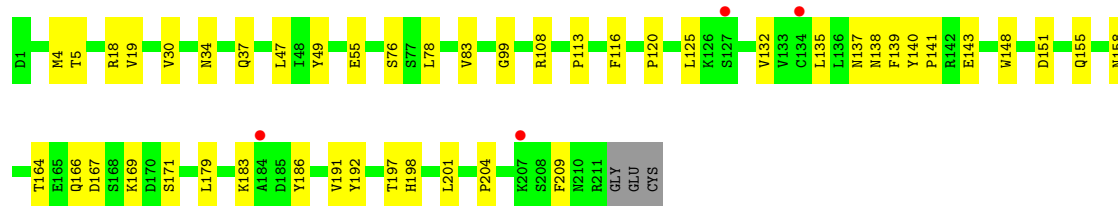


• Molecule 3: MEDI8897 Fab Light Chain



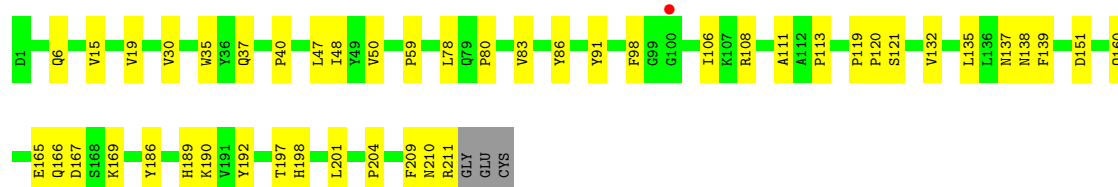
• Molecule 3: MEDI8897 Fab Light Chain





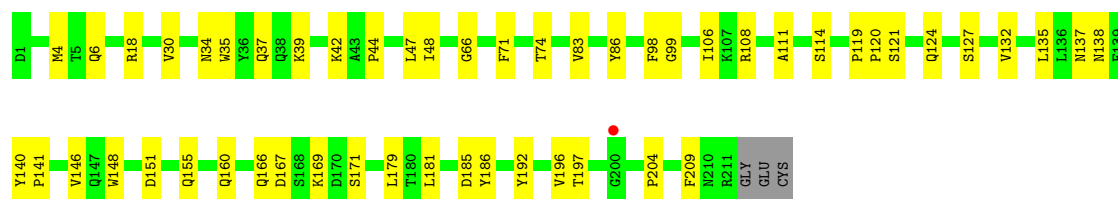
• Molecule 3: MEDI8897 Fab Light Chain

Chain R: 77% 21% .



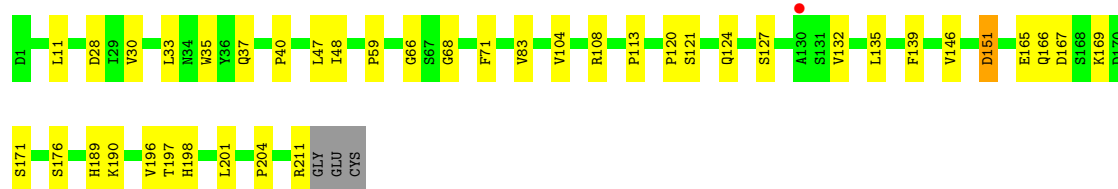
• Molecule 3: MEDI8897 Fab Light Chain

Chain S: 74% 24% .



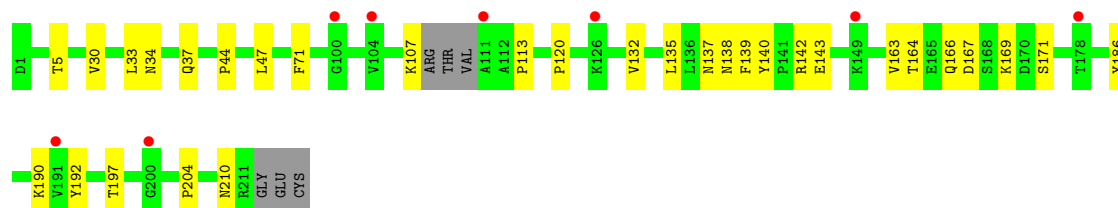
• Molecule 3: MEDI8897 Fab Light Chain

Chain T: 80% 18% .



• Molecule 3: MEDI8897 Fab Light Chain

Chain U: 4% 83% 14% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	229.02Å 229.02Å 343.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.31 – 4.30 46.31 – 4.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.31-4.30) 99.8 (46.31-4.30)	Depositor EDS
R_{merge}	0.57	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 4.28Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.236 , 0.294 0.241 , 0.296	Depositor DCC
R_{free} test set	3466 reflections (1.67%)	wwPDB-VP
Wilson B-factor (Å ²)	82.9	Xtriage
Anisotropy	0.305	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 118.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	51201	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.54% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.22	0/3538	0.48	0/4794
1	B	0.23	0/3561	0.46	0/4825
1	C	1.02	7/3547 (0.2%)	0.50	1/4806 (0.0%)
1	D	0.21	0/3583	0.47	2/4857 (0.0%)
1	E	0.21	0/3556	0.48	0/4818
1	F	0.21	0/3565	0.47	0/4831
1	G	0.23	0/3569	0.49	0/4838
1	H	0.21	0/3552	0.48	0/4813
1	I	0.21	0/3533	0.47	0/4787
2	J	0.18	0/1708	0.40	0/2334
2	K	0.17	0/1683	0.40	0/2302
2	L	0.18	0/1689	0.40	0/2310
2	M	0.18	0/1689	0.40	0/2310
2	N	0.19	0/1689	0.40	0/2310
2	O	0.17	0/1661	0.38	0/2271
3	P	0.17	0/1656	0.39	0/2252
3	Q	0.16	0/1652	0.39	0/2247
3	R	0.16	0/1652	0.39	0/2247
3	S	0.17	0/1652	0.42	0/2247
3	T	0.16	0/1652	0.40	0/2247
3	U	0.17	0/1626	0.40	0/2210
All	All	0.33	7/52013 (0.0%)	0.45	3/70656 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	315	LYS	CE-NZ	48.34	2.94	1.49
1	C	341	TRP	CE3-CZ3	18.48	1.94	1.38
1	C	341	TRP	CE2-CZ2	15.64	1.72	1.39
1	C	341	TRP	CZ3-CH2	14.21	1.75	1.40
1	C	341	TRP	CD2-CE2	12.11	1.61	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	341	TRP	CZ2-CH2	11.83	1.59	1.37
1	C	341	TRP	CD2-CE3	10.89	1.57	1.40

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	315	LYS	CD-CE-NZ	7.05	134.48	111.90
1	D	99	ASN	CA-C-N	5.35	134.86	121.80
1	D	99	ASN	C-N-CA	5.35	134.86	121.80

There are no chirality outliers.

There are no planarity outliers.

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	3489	0	3527	110	0
1	B	3511	0	3546	116	0
1	C	3497	0	3533	147	0
1	D	3532	0	3566	109	0
1	E	3506	0	3541	110	0
1	F	3515	0	3549	133	0
1	G	3518	0	3553	125	0
1	H	3502	0	3538	110	0
1	I	3483	0	3517	122	0
2	J	1668	0	1630	39	1
2	K	1643	0	1602	34	1
2	L	1649	0	1609	40	0
2	M	1649	0	1609	32	0
2	N	1649	0	1609	25	0
2	O	1622	0	1585	39	0
3	P	1623	0	1582	28	0
3	Q	1619	0	1579	30	1
3	R	1619	0	1579	27	0
3	S	1619	0	1579	31	0
3	T	1619	0	1579	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	U	1594	0	1549	18	1
4	A	5	0	0	0	0
4	B	20	0	0	0	0
4	C	10	0	0	0	0
4	D	5	0	0	0	0
4	E	5	0	0	0	0
4	G	5	0	0	0	0
4	H	10	0	0	0	0
4	I	5	0	0	0	0
4	J	5	0	0	0	0
4	L	5	0	0	0	0
All	All	51201	0	50961	1251	2

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 12.

All (1251) 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:341:TRP:CH2	1:C:341:TRP:CZ3	1.76	1.66
1:C:341:TRP:CZ3	1:C:341:TRP:CE3	1.94	1.51
1:C:315:LYS:NZ	1:C:341:TRP:CE2	1.98	1.31
1:C:315:LYS:NZ	1:C:341:TRP:CD2	2.01	1.27
1:C:315:LYS:NZ	1:C:341:TRP:CE3	2.01	1.27
1:C:315:LYS:NZ	1:C:341:TRP:CZ3	2.02	1.27
1:C:315:LYS:NZ	1:C:341:TRP:CZ2	2.08	1.21
1:C:315:LYS:NZ	1:C:341:TRP:CH2	2.09	1.20
1:E:69:CYS:SG	1:E:80:LYS:NZ	2.28	1.07
1:A:448:ASP:OD1	1:A:461:LYS:NZ	1.93	1.01
1:C:315:LYS:CE	1:C:341:TRP:CE2	2.46	0.98
1:C:315:LYS:CE	1:C:341:TRP:CZ3	2.48	0.96
1:H:407:ILE:HD11	1:H:457:TYR:HB3	1.47	0.95
1:C:315:LYS:CE	1:C:341:TRP:CE3	2.49	0.95
1:C:315:LYS:CE	1:C:341:TRP:CD2	2.51	0.94
1:C:246:PRO:HB3	1:C:283:GLN:HA	1.50	0.93
1:A:246:PRO:HB3	1:A:283:GLN:HA	1.52	0.92
1:G:407:ILE:HD11	1:G:457:TYR:HB3	1.51	0.92
1:B:201:ASN:HB2	1:F:429:ARG:HH21	1.34	0.92
1:C:315:LYS:CE	1:C:341:TRP:CZ2	2.52	0.92
1:A:291:ILE:HD12	1:A:291:ILE:O	1.70	0.91
1:A:374:THR:HG21	1:B:454:ASN:H	1.32	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:315:LYS:CE	1:C:341:TRP:CH2	2.53	0.91
1:G:168:LYS:NZ	1:G:295:GLU:OE2	2.03	0.90
1:I:246:PRO:HB3	1:I:283:GLN:HA	1.53	0.90
1:D:407:ILE:HD11	1:D:457:TYR:HB3	1.54	0.89
1:B:176:LYS:NZ	1:B:259:SER:OG	2.04	0.89
1:F:214:ILE:HD11	1:F:219:THR:HB	1.54	0.88
1:D:448:ASP:OD1	1:D:461:LYS:NZ	2.08	0.86
1:E:432:ILE:HD11	1:E:447:VAL:HG22	1.57	0.86
1:G:261:ILE:HA	1:G:264:MET:HE2	1.58	0.86
1:H:246:PRO:HB3	1:H:283:GLN:HA	1.56	0.85
1:B:205:PRO:HB3	1:F:446:GLY:HA3	1.58	0.85
3:Q:158:ASN:HD22	3:Q:179:LEU:CD1	1.88	0.85
1:E:246:PRO:HB3	1:E:283:GLN:HA	1.58	0.85
1:F:246:PRO:HB3	1:F:283:GLN:HA	1.58	0.85
1:G:332:ILE:HG22	1:G:475:ILE:HD11	1.57	0.85
1:H:374:THR:HG21	1:I:454:ASN:H	1.42	0.85
1:I:332:ILE:HG22	1:I:475:ILE:HD11	1.58	0.85
1:A:407:ILE:HD11	1:A:457:TYR:HB3	1.58	0.84
1:G:225:GLN:OE1	1:I:81:GLN:NE2	2.10	0.84
1:B:246:PRO:HB3	1:B:283:GLN:HA	1.58	0.84
1:I:176:LYS:NZ	1:I:259:SER:OG	2.10	0.83
1:H:426:ASN:HB3	1:H:429:ARG:HB2	1.61	0.83
1:H:332:ILE:HG22	1:H:475:ILE:HD11	1.58	0.83
1:B:214:ILE:HD11	1:B:219:THR:HB	1.59	0.82
1:I:261:ILE:HA	1:I:264:MET:HE2	1.62	0.82
1:E:205:PRO:HB3	1:I:446:GLY:HA3	1.61	0.81
1:H:168:LYS:NZ	1:H:295:GLU:HB2	1.95	0.81
1:E:407:ILE:HD11	1:E:457:TYR:HB3	1.62	0.81
1:H:273:LEU:HD13	1:H:364:ARG:NH1	1.96	0.81
1:F:67:THR:HA	2:M:99:VAL:HG22	1.63	0.80
1:C:332:ILE:HG22	1:C:475:ILE:HD11	1.62	0.80
1:G:157:VAL:HG11	1:G:181:LEU:HB3	1.63	0.80
1:I:150:SER:OG	1:I:302:GLN:NE2	2.14	0.80
2:O:125:ALA:HB1	2:O:213:PRO:HA	1.63	0.80
1:G:218:GLU:OE1	1:I:75:LYS:NZ	2.14	0.80
1:A:291:ILE:HD11	1:A:298:ALA:HB3	1.63	0.80
1:H:261:ILE:HA	1:H:264:MET:HE2	1.65	0.79
1:F:73:ASP:OD2	1:F:213:ARG:NH2	2.16	0.79
2:O:11:VAL:HB	2:O:147:PRO:HG3	1.65	0.79
1:C:53:TYR:HB2	1:C:305:ILE:HD11	1.65	0.79
1:A:270:GLN:HG2	1:A:309:ILE:HD12	1.63	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:GLN:OE1	1:C:81:GLN:NE2	2.16	0.78
1:B:407:ILE:HD11	1:B:457:TYR:HB3	1.65	0.78
3:P:120:PRO:HD3	3:P:132:VAL:HG22	1.65	0.78
3:Q:120:PRO:HD3	3:Q:132:VAL:HG22	1.67	0.77
1:D:246:PRO:HB3	1:D:283:GLN:HA	1.66	0.77
3:Q:158:ASN:ND2	3:Q:179:LEU:CD1	2.47	0.77
1:E:374:THR:HG21	1:F:454:ASN:H	1.50	0.77
1:G:454:ASN:H	1:I:374:THR:HG21	1.50	0.77
1:C:407:ILE:HD11	1:C:457:TYR:HB3	1.67	0.76
1:C:446:GLY:HA3	1:H:205:PRO:HB3	1.67	0.76
2:O:12:LYS:HE3	2:O:17:SER:O	1.86	0.76
1:F:79:ILE:HD12	1:F:207:LEU:HD11	1.67	0.76
1:B:332:ILE:HG22	1:B:475:ILE:HD11	1.66	0.76
1:B:426:ASN:HB3	1:B:429:ARG:HB2	1.67	0.76
1:F:76:VAL:HG13	1:F:212:CYS:HB3	1.66	0.75
1:A:453:GLY:HA3	1:C:374:THR:HG21	1.67	0.75
2:O:119:PRO:HB3	2:O:145:TYR:HB3	1.67	0.75
1:A:332:ILE:HG22	1:A:475:ILE:HD11	1.67	0.75
1:E:176:LYS:NZ	1:E:259:SER:OG	2.18	0.75
1:A:488:PHE:HB3	1:B:488:PHE:CZ	2.22	0.75
1:E:332:ILE:HG22	1:E:475:ILE:HD11	1.67	0.74
1:D:270:GLN:NE2	1:D:306:TYR:O	2.19	0.74
1:C:315:LYS:HE2	1:C:341:TRP:CZ3	2.19	0.74
1:E:426:ASN:HB3	1:E:429:ARG:HB2	1.70	0.74
1:F:423:THR:HG21	1:F:431:ILE:HG12	1.67	0.74
1:B:426:ASN:HD22	1:B:429:ARG:HD2	1.53	0.74
1:A:402:ILE:HG21	1:C:373:LEU:HD13	1.69	0.73
1:E:261:ILE:HA	1:E:264:MET:HE2	1.70	0.73
1:G:75:LYS:HE3	1:G:213:ARG:HH21	1.52	0.73
2:N:119:PRO:HB3	2:N:145:TYR:HB3	1.69	0.73
1:G:79:ILE:HD13	1:G:207:LEU:HD11	1.71	0.73
2:J:123:PRO:O	3:P:121:SER:OG	2.07	0.73
1:D:407:ILE:HD12	1:F:145:GLY:HA2	1.69	0.73
1:C:315:LYS:HE3	1:C:341:TRP:CZ2	2.23	0.73
1:C:315:LYS:HG2	1:C:317:HIS:HE1	1.53	0.72
1:D:261:ILE:HA	1:D:264:MET:HE2	1.71	0.72
1:D:454:ASN:H	1:F:374:THR:HG21	1.53	0.72
1:E:171:LEU:O	1:E:191:LYS:NZ	2.19	0.72
1:I:336:ARG:NH1	1:I:382:CYS:O	2.22	0.72
1:E:498:LYS:NZ	1:F:486:ASP:HB2	2.04	0.72
2:O:123:PRO:HB3	2:O:211:VAL:HG12	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:167:ILE:HD12	1:H:189:THR:HG21	1.72	0.72
2:L:143:LYS:NZ	2:L:171:GLN:OE1	2.22	0.72
1:G:270:GLN:HG2	1:G:309:ILE:HD12	1.72	0.72
1:B:69:CYS:HB2	1:B:80:LYS:HE3	1.72	0.72
2:K:68:THR:HB	2:K:81:GLU:HB3	1.72	0.72
1:A:323:THR:OG1	1:A:331:ASN:OD1	2.08	0.71
1:B:56:VAL:HB	1:B:189:THR:HG22	1.72	0.71
1:C:261:ILE:HA	1:C:264:MET:HE2	1.70	0.71
1:D:332:ILE:HG22	1:D:475:ILE:HD11	1.71	0.71
1:C:326:ILE:HD12	3:T:59:PRO:HA	1.72	0.71
1:G:321:LEU:HD11	1:G:473:PRO:HB3	1.72	0.71
2:O:143:LYS:NZ	2:O:171:GLN:OE1	2.24	0.71
1:F:165:ASN:ND2	1:F:294:GLU:OE2	2.23	0.71
1:G:488:PHE:HB2	1:H:488:PHE:CZ	2.25	0.71
1:D:56:VAL:HB	1:D:189:THR:HG22	1.72	0.71
1:I:427:LYS:HG2	1:I:448:ASP:OD2	1.90	0.71
3:T:120:PRO:HD3	3:T:132:VAL:HG22	1.73	0.71
1:I:396:MET:HG3	1:I:488:PHE:HA	1.73	0.70
1:F:325:ASN:ND2	1:F:331:ASN:OD1	2.25	0.70
1:B:31:GLU:OE1	1:B:33:TYR:OH	2.08	0.70
1:G:323:THR:OG1	1:G:331:ASN:OD1	2.07	0.70
1:A:318:THR:O	1:A:339:ARG:NH2	2.25	0.70
2:N:82(B):SER:O	2:N:83:ARG:NH2	2.24	0.70
1:F:407:ILE:HD11	1:F:457:TYR:HB3	1.73	0.70
2:O:23:GLN:OE1	2:O:77:THR:OG1	2.08	0.69
1:A:407:ILE:HD12	1:C:145:GLY:HA2	1.74	0.69
3:U:113:PRO:HB3	3:U:139:PHE:HB3	1.73	0.69
1:E:498:LYS:HZ1	1:F:486:ASP:HB2	1.58	0.69
3:U:186:TYR:O	3:U:192:TYR:OH	2.10	0.69
1:I:75:LYS:HB3	1:I:214:ILE:HG22	1.74	0.69
2:N:181:VAL:HG11	3:T:135:LEU:HD22	1.75	0.69
1:B:59:ILE:HB	1:B:297:LEU:HD21	1.75	0.69
1:B:167:ILE:HD12	1:B:189:THR:HG21	1.74	0.69
1:B:183:ASN:OD1	1:B:184:GLY:N	2.25	0.68
2:M:119:PRO:HB3	2:M:145:TYR:HB3	1.74	0.68
3:S:197:THR:HG22	3:S:204:PRO:HB3	1.75	0.68
2:L:142:VAL:HG11	2:L:150:VAL:HG11	1.75	0.68
3:U:120:PRO:HD3	3:U:132:VAL:HG22	1.74	0.68
1:B:145:GLY:HA2	1:C:407:ILE:HD12	1.74	0.68
2:K:33:ILE:HB	2:K:95:GLU:HB3	1.76	0.68
1:E:79:ILE:HG23	1:E:220:VAL:HG23	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:GLN:NE2	1:A:306:TYR:O	2.27	0.68
2:J:82(B):SER:O	2:J:83:ARG:NH2	2.27	0.67
1:E:30:GLU:OE1	1:E:441:TYR:OH	2.09	0.67
1:G:196:LYS:NZ	1:G:295:GLU:OE1	2.25	0.67
3:T:151:ASP:OD1	3:T:189:HIS:ND1	2.26	0.67
1:E:445:LYS:HZ1	1:E:464:GLY:H	1.43	0.67
1:H:92:GLU:HG2	1:I:254:ASN:HD22	1.59	0.67
1:H:64:ILE:HD11	1:H:199:ILE:HG21	1.76	0.67
1:D:56:VAL:HG22	1:D:300:VAL:HG22	1.77	0.67
1:B:405:SER:HB2	1:B:452:VAL:HG21	1.77	0.67
3:Q:83:VAL:HG11	3:Q:166:GLN:HB3	1.77	0.67
3:S:120:PRO:HD3	3:S:132:VAL:HG22	1.77	0.67
3:S:181:LEU:HD22	3:S:185:ASP:OD2	1.95	0.67
1:G:206:ILE:O	1:G:209:GLN:NE2	2.24	0.67
2:M:93:ALA:HB1	2:M:100(I):PHE:HB3	1.76	0.67
1:C:315:LYS:HG2	1:C:317:HIS:CE1	2.31	0.66
1:I:79:ILE:HD13	1:I:207:LEU:HD11	1.75	0.66
3:R:113:PRO:HB3	3:R:139:PHE:HB3	1.77	0.66
1:I:491:SER:HB2	1:I:494:GLN:HG3	1.78	0.66
1:H:291:ILE:HD11	1:H:293:LYS:HB2	1.77	0.66
1:D:73:ASP:OD1	1:I:434:THR:OG1	2.09	0.66
1:E:405:SER:HB3	1:E:457:TYR:CE2	2.30	0.66
2:L:181:VAL:HG11	3:R:135:LEU:HD22	1.77	0.66
1:E:405:SER:HB3	1:E:457:TYR:HE2	1.60	0.66
1:H:64:ILE:HG12	1:H:83:LEU:HD21	1.76	0.66
2:J:143:LYS:NZ	2:J:171:GLN:OE1	2.27	0.66
2:K:139:GLY:HA2	2:K:154:TRP:HH2	1.60	0.66
1:G:241:ALA:HA	1:H:279:GLN:HG2	1.77	0.66
2:J:83:ARG:O	2:J:111:VAL:HG11	1.96	0.66
1:H:168:LYS:HZ1	1:H:295:GLU:HB2	1.60	0.66
1:I:29:THR:HG23	1:I:42:ARG:HB2	1.77	0.66
1:F:150:SER:OG	1:F:302:GLN:OE1	2.13	0.65
1:F:261:ILE:HA	1:F:264:MET:HE2	1.79	0.65
2:J:195:ILE:HD12	2:J:210:ARG:HG2	1.78	0.65
1:B:229:ARG:NE	1:B:250:TYR:O	2.28	0.65
2:L:68:THR:HB	2:L:81:GLU:HB3	1.79	0.65
1:D:90:VAL:HG13	1:D:292:ILE:HD11	1.77	0.65
1:C:423:THR:HG21	1:C:431:ILE:HG13	1.78	0.65
1:D:335:THR:HB	1:D:396:MET:HG2	1.77	0.65
1:G:246:PRO:HB3	1:G:283:GLN:HA	1.79	0.65
3:S:146:VAL:HG22	3:S:196:VAL:HG22	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:ILE:HD11	1:B:293:LYS:HB3	1.79	0.65
1:F:148:ILE:HA	1:F:302:GLN:HE22	1.61	0.65
1:F:332:ILE:HG23	1:F:475:ILE:HD11	1.79	0.65
1:G:423:THR:HG21	1:G:431:ILE:HG12	1.79	0.65
1:F:73:ASP:HB3	1:F:76:VAL:HG23	1.79	0.65
1:F:196:LYS:NZ	1:F:295:GLU:HG3	2.12	0.65
2:K:126:PRO:HG2	2:K:213:PRO:HG3	1.79	0.65
2:L:123:PRO:HB3	2:L:211:VAL:HG12	1.77	0.65
1:D:270:GLN:HG2	1:D:309:ILE:HD12	1.79	0.65
1:G:458:TYR:CD2	1:I:150:SER:HB3	2.32	0.65
1:B:350:SER:OG	1:C:454:ASN:ND2	2.30	0.64
1:G:488:PHE:CZ	1:I:488:PHE:HB2	2.32	0.64
1:G:442:VAL:HG11	1:G:447:VAL:HG21	1.79	0.64
1:B:488:PHE:HB2	1:C:488:PHE:CZ	2.32	0.64
1:F:243:VAL:HG22	1:F:288:ILE:HG23	1.79	0.64
1:H:168:LYS:HZ2	1:H:295:GLU:HB2	1.62	0.64
2:J:181:VAL:HG11	3:P:135:LEU:HD22	1.79	0.64
2:L:119:PRO:HB3	2:L:145:TYR:HB3	1.79	0.64
2:K:30:GLU:HB2	2:K:73:GLU:OE2	1.98	0.64
2:K:30:GLU:HG3	2:K:53:VAL:HG22	1.80	0.64
1:H:145:GLY:HA2	1:I:407:ILE:HD12	1.80	0.64
3:P:151:ASP:HA	3:P:191:VAL:HG13	1.79	0.64
3:Q:148:TRP:HB2	3:Q:155:GLN:HB2	1.79	0.64
2:N:143:LYS:NZ	2:N:171:GLN:OE1	2.30	0.64
1:D:452:VAL:O	1:D:455:THR:OG1	2.16	0.63
2:O:53:VAL:HG13	2:O:54:LEU:HD22	1.80	0.63
1:H:423:THR:HG21	1:H:431:ILE:HG12	1.80	0.63
1:G:159:HIS:NE2	1:G:291:ILE:HD13	2.14	0.63
1:G:292:ILE:HD12	1:G:297:LEU:HD12	1.80	0.63
2:K:93:ALA:HB1	2:K:100(I):PHE:HB3	1.81	0.63
1:D:402:ILE:HG21	1:F:373:LEU:HD13	1.81	0.63
3:P:167:ASP:OD1	3:P:169:LYS:HG2	1.99	0.62
2:K:123:PRO:HB3	2:K:211:VAL:HG12	1.82	0.62
1:C:318:THR:O	1:C:339:ARG:NH2	2.33	0.62
2:J:123:PRO:HD3	2:J:209:LYS:HE2	1.82	0.62
3:Q:197:THR:HG22	3:Q:204:PRO:HB3	1.81	0.62
1:A:373:LEU:HD13	1:B:402:ILE:HG21	1.81	0.62
1:D:423:THR:HG21	1:D:431:ILE:HG12	1.82	0.62
3:Q:158:ASN:ND2	3:Q:179:LEU:HD13	2.14	0.62
1:B:209:GLN:NE2	1:F:441:TYR:O	2.33	0.62
1:H:494:GLN:NE2	1:I:399:LYS:HB3	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:405:SER:HB2	1:H:452:VAL:HG21	1.81	0.62
3:U:190:LYS:HZ3	3:U:210:ASN:HB3	1.64	0.62
1:G:73:ASP:HB3	1:G:76:VAL:HG23	1.82	0.62
1:B:150:SER:HB3	1:C:458:TYR:CD2	2.35	0.62
1:C:56:VAL:HB	1:C:189:THR:HG22	1.81	0.62
2:J:119:PRO:HB3	2:J:145:TYR:HB3	1.82	0.62
1:G:488:PHE:HZ	1:I:488:PHE:HB2	1.64	0.61
3:R:35:TRP:HB2	3:R:48:ILE:HB	1.81	0.61
1:C:183:ASN:OD1	1:C:184:GLY:N	2.33	0.61
1:E:488:PHE:HB3	1:F:488:PHE:CZ	2.34	0.61
1:C:315:LYS:HE3	1:C:341:TRP:CH2	2.34	0.61
1:F:183:ASN:OD1	1:F:184:GLY:N	2.33	0.61
1:C:60:GLU:HG2	1:C:296:VAL:HG22	1.82	0.61
1:A:56:VAL:HB	1:A:189:THR:HG22	1.82	0.61
1:E:214:ILE:HD11	1:E:219:THR:HB	1.82	0.61
1:I:49:ARG:HE	1:I:368:ASP:CG	2.08	0.61
3:Q:137:ASN:OD1	3:Q:138:ASN:ND2	2.34	0.61
1:C:267:THR:HG22	1:C:269:ASP:H	1.66	0.61
1:B:432:ILE:HD11	1:B:447:VAL:HG22	1.83	0.61
1:D:374:THR:HG21	1:E:453:GLY:HA3	1.81	0.61
1:G:185:VAL:HG13	1:H:427:LYS:HZ3	1.66	0.61
1:G:402:ILE:HG21	1:I:373:LEU:HD13	1.82	0.61
3:S:186:TYR:O	3:S:192:TYR:OH	2.18	0.61
1:I:33:TYR:HE2	1:I:383:ASN:HB3	1.65	0.60
1:B:261:ILE:HA	1:B:264:MET:HE2	1.83	0.60
1:D:49:ARG:NH1	1:D:51:GLY:O	2.34	0.60
3:U:37:GLN:HB2	3:U:47:LEU:HD11	1.82	0.60
1:H:335:THR:HB	1:H:396:MET:HG2	1.84	0.60
1:B:201:ASN:HB2	1:F:429:ARG:NH2	2.13	0.60
3:R:40:PRO:HB3	3:R:165:GLU:HG3	1.82	0.60
3:T:190:LYS:HD2	3:T:211:ARG:HB3	1.83	0.60
1:D:157:VAL:HG11	1:D:181:LEU:HB3	1.83	0.60
1:F:445:LYS:HZ1	1:F:464:GLY:H	1.50	0.60
1:G:407:ILE:HD12	1:I:145:GLY:HA2	1.84	0.60
2:N:11:VAL:HB	2:N:147:PRO:HG3	1.84	0.60
1:B:394:LYS:HZ2	1:C:402:ILE:HD11	1.66	0.59
1:C:232:GLU:HG2	1:C:250:TYR:CD2	2.36	0.59
1:G:505:PHE:HE2	1:I:505:PHE:HB3	1.66	0.59
1:F:196:LYS:HZ3	1:F:295:GLU:HG3	1.67	0.59
3:R:120:PRO:HD3	3:R:132:VAL:HG22	1.83	0.59
1:E:289:MET:HG2	1:E:299:TYR:HB3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:498:LYS:NZ	1:C:486:ASP:HB3	2.17	0.59
1:G:56:VAL:HB	1:G:189:THR:HG22	1.85	0.59
3:T:37:GLN:HB2	3:T:47:LEU:HD11	1.84	0.59
1:G:273:LEU:HD13	1:G:364:ARG:NH1	2.17	0.59
2:M:11:VAL:HB	2:M:147:PRO:HG3	1.85	0.59
3:P:108:ARG:NH1	3:P:109:THR:O	2.31	0.59
1:A:279:GLN:HG2	1:C:241:ALA:HA	1.84	0.59
1:A:452:VAL:O	1:A:455:THR:OG1	2.20	0.59
1:G:448:ASP:OD1	1:G:461:LYS:NZ	2.33	0.58
1:I:183:ASN:OD1	1:I:184:GLY:N	2.36	0.58
2:O:93:ALA:HB1	2:O:100(I):PHE:HB3	1.84	0.58
1:B:491:SER:HB2	1:B:494:GLN:HG3	1.84	0.58
1:D:167:ILE:HD12	1:D:189:THR:HG21	1.85	0.58
1:B:308:VAL:HG21	1:B:345:ASN:ND2	2.18	0.58
1:H:183:ASN:OD1	1:H:184:GLY:N	2.34	0.58
1:I:326:ILE:HG21	3:R:59:PRO:HA	1.85	0.58
1:G:167:ILE:HD12	1:G:189:THR:HG21	1.83	0.58
2:N:93:ALA:HB1	2:N:100(I):PHE:HB3	1.84	0.58
1:H:273:LEU:HD13	1:H:364:ARG:HH11	1.69	0.58
2:K:119:PRO:HB3	2:K:145:TYR:HB3	1.84	0.58
2:N:160:THR:O	2:N:163:VAL:HG22	2.03	0.58
1:B:176:LYS:HG2	1:B:190:PHE:CE1	2.38	0.58
1:C:79:ILE:HD12	1:C:207:LEU:HD11	1.85	0.58
1:E:423:THR:HG23	1:E:431:ILE:HG23	1.84	0.58
1:F:208:ASN:ND2	2:M:96:THR:O	2.35	0.58
1:G:505:PHE:CE2	1:I:505:PHE:HB3	2.38	0.58
1:I:336:ARG:HH12	1:I:382:CYS:C	2.10	0.58
3:T:66:GLY:HA3	3:T:71:PHE:HA	1.85	0.58
1:D:31:GLU:OE1	1:D:33:TYR:OH	2.19	0.58
1:G:335:THR:HB	1:G:396:MET:HG2	1.86	0.58
1:G:426:ASN:HB3	1:G:429:ARG:HB2	1.85	0.58
3:U:137:ASN:OD1	3:U:138:ASN:ND2	2.36	0.58
1:A:93:LEU:HD22	1:A:289:MET:HE2	1.85	0.58
2:M:36:TRP:CE2	2:M:80:MET:HB2	2.39	0.58
1:B:150:SER:OG	1:B:302:GLN:NE2	2.37	0.57
1:G:73:ASP:OD1	1:G:74:THR:N	2.37	0.57
1:F:429:ARG:HG3	1:F:429:ARG:NH1	2.19	0.57
3:Q:186:TYR:O	3:Q:192:TYR:OH	2.22	0.57
1:B:463:GLU:OE1	1:B:463:GLU:N	2.31	0.57
1:F:56:VAL:HB	1:F:189:THR:HG22	1.85	0.57
3:R:167:ASP:OD1	3:R:169:LYS:HG2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:317:HIS:HD2	1:C:408:THR:HG22	1.69	0.57
1:A:67:THR:HA	2:J:99:VAL:HG13	1.86	0.57
1:C:463:GLU:OE1	1:C:463:GLU:N	2.26	0.57
1:C:49:ARG:HE	1:C:368:ASP:CG	2.12	0.57
1:D:165:ASN:ND2	1:D:294:GLU:OE2	2.32	0.57
1:A:423:THR:HG21	1:A:431:ILE:HG12	1.85	0.57
1:C:405:SER:HB3	1:C:457:TYR:CE2	2.40	0.57
1:D:157:VAL:HG21	1:D:183:ASN:HB2	1.87	0.57
1:I:407:ILE:HD11	1:I:457:TYR:HB3	1.86	0.57
3:S:6:GLN:NE2	3:S:86:TYR:O	2.34	0.57
1:A:427:LYS:HG2	1:A:448:ASP:OD2	2.05	0.57
1:B:192:VAL:HG11	1:B:229:ARG:HH22	1.69	0.57
1:C:40:VAL:HA	1:C:315:LYS:O	2.04	0.57
1:E:423:THR:HG21	1:E:431:ILE:HG12	1.86	0.57
1:I:336:ARG:NH2	1:I:383:ASN:OD1	2.37	0.57
2:M:66:ARG:CZ	2:M:83:ARG:HH12	2.18	0.57
1:B:190:PHE:HE2	1:B:260:LEU:HB2	1.69	0.57
1:A:335:THR:HB	1:A:396:MET:HG2	1.86	0.56
1:D:150:SER:OG	1:D:302:GLN:NE2	2.38	0.56
1:G:93:LEU:HD13	1:G:297:LEU:HD11	1.88	0.56
2:J:93:ALA:HB1	2:J:100(I):PHE:HB3	1.86	0.56
2:L:93:ALA:HB1	2:L:100(I):PHE:HB3	1.86	0.56
3:S:167:ASP:OD1	3:S:169:LYS:HG2	2.05	0.56
1:A:494:GLN:NE2	1:B:399:LYS:HB2	2.21	0.56
1:E:67:THR:OG1	1:E:80:LYS:HE3	2.03	0.56
1:G:56:VAL:HG22	1:G:300:VAL:HG22	1.86	0.56
1:H:176:LYS:HG2	1:H:190:PHE:CE1	2.39	0.56
1:I:214:ILE:HD11	1:I:219:THR:HB	1.86	0.56
1:I:405:SER:HB3	1:I:457:TYR:CE2	2.41	0.56
2:O:18:VAL:HB	2:O:82(C):LEU:HD11	1.86	0.56
3:P:137:ASN:OD1	3:P:138:ASN:ND2	2.38	0.56
3:U:190:LYS:NZ	3:U:210:ASN:HB3	2.20	0.56
1:E:318:THR:O	1:E:339:ARG:NH2	2.38	0.56
1:F:291:ILE:HD11	1:F:293:LYS:HG3	1.86	0.56
1:G:432:ILE:HD11	1:G:447:VAL:HG22	1.86	0.56
1:D:26:GLN:N	1:D:363:ASN:HD21	2.03	0.56
1:F:81:GLN:O	1:F:81:GLN:NE2	2.39	0.56
1:H:198:TYR:HE2	1:H:223:PHE:HD1	1.54	0.56
1:G:75:LYS:CE	1:G:213:ARG:HH21	2.19	0.56
3:P:146:VAL:HG22	3:P:196:VAL:HG22	1.88	0.56
1:B:394:LYS:NZ	1:C:400:THR:HG23	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:487:GLU:OE2	1:D:498:LYS:HD3	2.06	0.56
2:N:123:PRO:O	3:T:121:SER:OG	2.22	0.56
1:B:399:LYS:HG3	1:B:485:SER:HB2	1.88	0.55
1:C:405:SER:HB3	1:C:457:TYR:HE2	1.71	0.55
1:F:154:VAL:O	1:F:158:LEU:HD12	2.06	0.55
1:F:210:GLN:HB3	1:F:213:ARG:HG2	1.86	0.55
1:G:38:SER:HB2	1:G:316:LEU:HD11	1.86	0.55
2:M:123:PRO:O	3:S:121:SER:OG	2.24	0.55
1:A:68:LYS:H	2:J:99:VAL:HG22	1.71	0.55
1:D:442:VAL:HG11	1:D:447:VAL:HG21	1.88	0.55
1:G:49:ARG:HE	1:G:368:ASP:CG	2.13	0.55
1:H:448:ASP:OD1	1:H:461:LYS:NZ	2.37	0.55
1:H:59:ILE:HB	1:H:297:LEU:HD21	1.88	0.55
1:I:336:ARG:HH12	1:I:382:CYS:HB3	1.70	0.55
1:C:208:ASN:ND2	2:K:96:THR:O	2.38	0.55
1:D:284:GLN:OE1	1:D:306:TYR:OH	2.18	0.55
1:H:73:ASP:OD1	1:H:74:THR:N	2.40	0.55
2:J:150:VAL:HG22	2:J:200:HIS:HB2	1.87	0.55
3:P:37:GLN:HB2	3:P:47:LEU:HD11	1.87	0.55
1:B:369:THR:O	1:C:455:THR:HG22	2.05	0.55
1:F:429:ARG:HG3	1:F:429:ARG:HH11	1.71	0.55
2:L:169:VAL:HG21	3:R:160:GLN:HB3	1.89	0.55
1:A:512:LEU:HD11	1:B:515:ALA:HB3	1.89	0.55
1:G:163:GLU:OE2	1:G:182:SER:N	2.37	0.55
1:D:321:LEU:HD11	1:D:473:PRO:HB3	1.89	0.55
3:T:35:TRP:HB2	3:T:48:ILE:HB	1.89	0.55
1:A:405:SER:HB3	1:A:457:TYR:CE2	2.42	0.55
1:C:73:ASP:OD1	1:C:74:THR:N	2.40	0.55
1:G:373:LEU:HD13	1:H:402:ILE:HD13	1.89	0.55
1:I:39:ALA:HB2	1:I:413:ILE:HD11	1.88	0.55
1:C:428:ASN:O	1:C:428:ASN:ND2	2.24	0.55
1:D:49:ARG:HE	1:D:368:ASP:CG	2.15	0.55
3:S:114:SER:HB2	3:S:137:ASN:HB3	1.89	0.55
3:T:197:THR:HG22	3:T:204:PRO:HB3	1.88	0.55
1:E:93:LEU:O	1:E:97:THR:HG23	2.06	0.54
1:E:387:PHE:HE2	1:E:474:ILE:HD12	1.73	0.54
1:H:162:GLY:O	1:H:166:LYS:HG3	2.07	0.54
3:T:108:ARG:HD2	3:T:171:SER:HB2	1.89	0.54
1:A:320:PRO:HG3	1:C:141:LEU:HD11	1.89	0.54
1:C:452:VAL:O	1:C:455:THR:OG1	2.25	0.54
2:N:51:ILE:HG13	2:N:57:VAL:HG22	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:463:GLU:OE1	1:D:463:GLU:N	2.33	0.54
1:D:487:GLU:CD	1:D:498:LYS:HZ3	2.16	0.54
3:Q:19:VAL:HG21	3:Q:78:LEU:HD22	1.88	0.54
1:B:49:ARG:O	1:B:369:THR:HG23	2.08	0.54
1:B:394:LYS:HZ1	1:C:400:THR:HG23	1.72	0.54
1:H:92:GLU:HG2	1:I:254:ASN:ND2	2.22	0.54
2:L:30:GLU:HG3	2:L:53:VAL:HG22	1.89	0.54
3:P:187:GLU:HA	3:P:211:ARG:HH22	1.72	0.54
3:S:39:LYS:HB2	3:S:42:LYS:HD2	1.89	0.54
2:J:142:VAL:HG11	2:J:150:VAL:HG11	1.89	0.54
2:N:83:ARG:O	2:N:111:VAL:HG11	2.07	0.54
3:R:108:ARG:HH12	3:R:111:ALA:HB2	1.71	0.54
1:I:408:THR:O	1:I:460:ASN:ND2	2.40	0.54
1:A:150:SER:HB3	1:B:458:TYR:CD2	2.42	0.54
1:B:387:PHE:HE2	1:B:474:ILE:HD12	1.72	0.54
1:D:400:THR:OG1	1:F:394:LYS:NZ	2.40	0.54
2:L:160:THR:O	2:L:163:VAL:HG22	2.07	0.54
2:N:23:GLN:NE2	2:N:24:ALA:O	2.39	0.54
3:R:151:ASP:OD1	3:R:189:HIS:ND1	2.40	0.54
3:S:148:TRP:HB2	3:S:155:GLN:HB2	1.89	0.54
1:I:162:GLY:O	1:I:166:LYS:HG3	2.07	0.54
1:A:90:VAL:HG13	1:A:292:ILE:HD11	1.89	0.53
1:F:321:LEU:HD11	1:F:473:PRO:HB3	1.89	0.53
2:K:139:GLY:HA2	2:K:154:TRP:CH2	2.43	0.53
3:R:190:LYS:HD2	3:R:211:ARG:HB3	1.89	0.53
1:A:291:ILE:O	1:A:291:ILE:CD1	2.51	0.53
1:C:442:VAL:HG11	1:C:447:VAL:HG21	1.90	0.53
1:D:458:TYR:CD2	1:F:150:SER:HB3	2.43	0.53
1:G:75:LYS:HZ2	1:H:218:GLU:CD	2.16	0.53
2:L:83:ARG:O	2:L:111:VAL:HG11	2.07	0.53
3:S:83:VAL:HG11	3:S:166:GLN:HB3	1.90	0.53
1:A:145:GLY:HA2	1:B:407:ILE:HD12	1.91	0.53
3:Q:167:ASP:OD1	3:Q:169:LYS:HG2	2.08	0.53
1:F:326:ILE:HD12	3:P:59:PRO:HA	1.90	0.53
1:G:232:GLU:HG2	1:G:250:TYR:CD2	2.44	0.53
1:I:69:CYS:HB2	1:I:80:LYS:HE3	1.89	0.53
2:J:146:PHE:HB2	2:J:175:LEU:HD22	1.89	0.53
3:P:186:TYR:O	3:P:211:ARG:NH2	2.41	0.53
1:D:218:GLU:OE1	1:F:75:LYS:HE3	2.08	0.53
1:F:76:VAL:HG22	1:F:212:CYS:O	2.08	0.53
3:R:37:GLN:HB2	3:R:47:LEU:HD11	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:49:ARG:O	1:G:369:THR:HG23	2.09	0.53
1:G:56:VAL:HG23	1:G:187:VAL:HG21	1.88	0.53
1:C:176:LYS:NZ	1:C:259:SER:OG	2.33	0.53
1:E:183:ASN:OD1	1:E:184:GLY:N	2.42	0.53
1:H:378:GLU:HG2	1:H:390:LYS:HD2	1.91	0.53
3:R:119:PRO:HB3	3:R:209:PHE:CE1	2.44	0.53
1:D:370:MET:HG3	1:E:457:TYR:HE1	1.73	0.53
3:P:19:VAL:HG21	3:P:78:LEU:HD22	1.91	0.53
1:C:427:LYS:HG2	1:C:448:ASP:OD2	2.09	0.53
1:E:209:GLN:NE2	1:I:442:VAL:HG13	2.23	0.53
1:F:73:ASP:OD1	1:F:74:THR:N	2.42	0.53
1:G:232:GLU:HG2	1:G:250:TYR:CG	2.44	0.53
1:A:455:THR:HG22	1:C:369:THR:O	2.08	0.52
1:D:73:ASP:HB3	1:D:76:VAL:HG23	1.91	0.52
1:F:176:LYS:HG2	1:F:190:PHE:CE1	2.44	0.52
1:D:279:GLN:HG2	1:F:241:ALA:HA	1.90	0.52
1:E:49:ARG:HE	1:E:368:ASP:CG	2.17	0.52
1:E:192:VAL:HG11	1:E:229:ARG:NH1	2.23	0.52
1:H:321:LEU:HD11	1:H:473:PRO:HB3	1.91	0.52
2:M:126:PRO:HG2	2:M:213:PRO:HG3	1.92	0.52
1:A:56:VAL:O	1:A:189:THR:HA	2.10	0.52
1:A:261:ILE:HA	1:A:264:MET:HE3	1.91	0.52
1:G:28:ILE:HG13	1:G:410:LEU:HD11	1.91	0.52
1:I:204:LEU:HD12	2:O:99:VAL:O	2.09	0.52
1:C:76:VAL:HG22	1:C:212:CYS:HB2	1.91	0.52
2:M:68:THR:HB	2:M:81:GLU:HB3	1.92	0.52
1:E:140:PHE:HD1	1:E:140:PHE:H	1.56	0.52
3:R:83:VAL:HG11	3:R:166:GLN:HB3	1.92	0.52
1:D:486:ASP:OD2	1:F:487:GLU:HA	2.09	0.52
1:E:338:ASP:HB2	1:E:342:TYR:OH	2.10	0.52
1:C:38:SER:HB2	1:C:316:LEU:HD11	1.92	0.52
1:I:56:VAL:HG22	1:I:300:VAL:HG22	1.92	0.52
2:O:82(B):SER:O	2:O:83:ARG:NH2	2.42	0.52
3:T:167:ASP:OD1	3:T:169:LYS:HG2	2.09	0.52
1:A:291:ILE:HD12	1:A:291:ILE:C	2.34	0.52
1:A:454:ASN:H	1:C:374:THR:HG21	1.75	0.52
1:B:52:TRP:CG	1:B:302:GLN:HE21	2.28	0.52
1:B:162:GLY:O	1:B:166:LYS:HG3	2.10	0.52
1:C:308:VAL:HG21	1:C:345:ASN:ND2	2.24	0.52
1:E:243:VAL:HG22	1:E:288:ILE:HG23	1.92	0.52
1:G:141:LEU:HD13	1:H:402:ILE:HD12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:66:GLU:HB3	1:H:68:LYS:HE2	1.92	0.52
1:C:405:SER:HB2	1:C:452:VAL:HG21	1.92	0.52
1:F:268:ASN:HA	1:F:271:LYS:HB2	1.92	0.52
1:H:35:SER:O	1:H:474:ILE:HG12	2.10	0.52
1:C:151:GLY:HA3	1:C:288:ILE:HD12	1.92	0.51
1:G:270:GLN:NE2	1:G:306:TYR:O	2.43	0.51
1:E:59:ILE:HB	1:E:297:LEU:CD2	2.41	0.51
1:E:167:ILE:HD12	1:E:189:THR:HG21	1.92	0.51
1:F:415:SER:HB3	1:F:417:TYR:CE2	2.45	0.51
1:F:444:ASN:ND2	1:F:462:LEU:O	2.36	0.51
1:I:387:PHE:CE2	1:I:474:ILE:HD12	2.45	0.51
2:M:139:GLY:HA2	2:M:154:TRP:HH2	1.76	0.51
3:R:80:PRO:HA	3:R:106:ILE:HG13	1.93	0.51
1:E:188:LEU:HD23	1:E:260:LEU:HD12	1.92	0.51
1:G:405:SER:HB3	1:G:457:TYR:CE2	2.46	0.51
3:P:197:THR:HG22	3:P:204:PRO:HB3	1.92	0.51
3:R:186:TYR:O	3:R:192:TYR:OH	2.27	0.51
3:S:106:ILE:H	3:S:166:GLN:HE22	1.58	0.51
1:B:75:LYS:HE3	1:B:217:ILE:HG13	1.92	0.51
1:B:357:THR:HG21	1:B:371:ASN:HB2	1.92	0.51
1:C:178:VAL:HG12	1:C:188:LEU:HD12	1.92	0.51
1:E:217:ILE:HD13	1:F:218:GLU:HG2	1.92	0.51
1:C:445:LYS:NZ	1:C:464:GLY:H	2.09	0.51
1:D:405:SER:HB3	1:D:457:TYR:CE2	2.46	0.51
1:H:217:ILE:O	1:H:220:VAL:HG12	2.11	0.51
2:L:45:PRO:HG2	3:R:98:PHE:CD2	2.46	0.51
1:B:79:ILE:HD11	1:B:203:LEU:HD11	1.92	0.51
1:E:59:ILE:HB	1:E:297:LEU:HD21	1.91	0.51
1:F:167:ILE:HD11	1:F:181:LEU:HD21	1.93	0.51
1:H:423:THR:HG23	1:H:431:ILE:HG23	1.92	0.51
1:I:176:LYS:HG2	1:I:190:PHE:CE1	2.46	0.51
3:P:155:GLN:HB3	3:P:158:ASN:HD21	1.76	0.51
1:B:30:GLU:OE1	1:B:441:TYR:OH	2.28	0.51
1:B:67:THR:HG21	1:B:83:LEU:HD13	1.93	0.51
1:F:499:ILE:O	1:F:503:LEU:N	2.39	0.51
1:D:405:SER:HB2	1:D:452:VAL:HG21	1.93	0.50
1:F:267:THR:HG22	1:F:269:ASP:H	1.76	0.50
1:H:491:SER:HB2	1:H:494:GLN:HG3	1.93	0.50
2:K:94:THR:OG1	2:K:102:ASN:HB3	2.11	0.50
1:B:423:THR:HG23	1:B:431:ILE:HG23	1.92	0.50
2:K:121:VAL:HA	2:K:141:LEU:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:SER:O	1:A:474:ILE:HG12	2.12	0.50
1:G:68:LYS:H	2:N:99:VAL:HG22	1.77	0.50
1:I:463:GLU:OE1	1:I:463:GLU:N	2.31	0.50
2:L:117:LYS:HD3	2:L:175:LEU:HD11	1.94	0.50
2:O:126:PRO:HG2	2:O:213:PRO:HG3	1.92	0.50
2:O:181:VAL:HG11	3:U:135:LEU:HD22	1.94	0.50
1:A:454:ASN:HD22	1:C:345:ASN:CG	2.20	0.50
1:D:241:ALA:HA	1:E:279:GLN:HG2	1.93	0.50
1:F:405:SER:HB3	1:F:457:TYR:CE2	2.47	0.50
1:G:178:VAL:HG12	1:G:188:LEU:HD12	1.92	0.50
2:K:100(H):TYR:HB3	3:Q:34:ASN:ND2	2.26	0.50
1:A:266:ILE:HG13	1:A:271:LYS:HG3	1.94	0.50
1:B:62:SER:HB3	1:B:196:LYS:HG2	1.94	0.50
1:B:209:GLN:HG3	1:F:442:VAL:HG13	1.92	0.50
1:B:423:THR:HG21	1:B:431:ILE:HG12	1.94	0.50
1:D:270:GLN:HE22	1:D:307:GLY:HA2	1.77	0.50
1:H:375:LEU:HB3	1:H:379:VAL:HG21	1.94	0.50
1:I:73:ASP:OD1	1:I:74:THR:N	2.45	0.50
1:I:321:LEU:HD11	1:I:473:PRO:HB3	1.94	0.50
2:J:160:THR:O	2:J:163:VAL:HG22	2.11	0.50
2:L:154:TRP:CZ3	2:L:196:CYS:HB3	2.47	0.50
3:Q:125:LEU:HD22	3:Q:183:LYS:HG3	1.94	0.50
1:A:310:ASP:OD1	1:A:364:ARG:NH1	2.45	0.50
1:D:217:ILE:HG21	1:F:217:ILE:HG21	1.93	0.50
1:E:96:LEU:HD11	1:E:238:SER:HA	1.94	0.50
1:F:37:CYS:SG	1:F:319:SER:HB3	2.52	0.50
2:O:97:ALA:HB1	2:O:100:VAL:HG11	1.93	0.50
3:R:15:VAL:HG22	3:R:106:ILE:HD12	1.94	0.50
1:E:73:ASP:H	1:E:76:VAL:HG22	1.77	0.50
1:I:150:SER:HG	1:I:302:GLN:NE2	2.10	0.50
3:Q:151:ASP:HA	3:Q:191:VAL:HG13	1.92	0.50
1:F:321:LEU:HD21	1:F:473:PRO:HB3	1.94	0.50
1:F:397:THR:HB	1:F:483:PHE:HE2	1.75	0.50
1:F:491:SER:HB2	1:F:494:GLN:HG3	1.93	0.50
3:S:108:ARG:HD2	3:S:171:SER:HB2	1.94	0.50
1:A:338:ASP:HB2	1:A:342:TYR:OH	2.12	0.50
1:D:58:THR:O	1:D:191:LYS:HA	2.12	0.50
1:D:59:ILE:HB	1:D:297:LEU:HD21	1.94	0.50
1:G:334:LEU:HB2	1:G:475:ILE:HD13	1.94	0.50
3:R:19:VAL:HG21	3:R:78:LEU:HD22	1.92	0.50
1:C:308:VAL:HG21	1:C:345:ASN:HD21	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:414:VAL:HG21	1:D:435:PHE:CE2	2.47	0.49
1:F:190:PHE:HE2	1:F:260:LEU:HB2	1.76	0.49
1:I:386:ILE:HG21	1:I:474:ILE:HG13	1.94	0.49
2:L:137:ALA:HB2	2:L:183:THR:HG22	1.93	0.49
3:Q:158:ASN:HD22	3:Q:179:LEU:HD12	1.76	0.49
3:T:146:VAL:HG22	3:T:196:VAL:HG22	1.94	0.49
1:A:507:ARG:NH2	1:A:508:ARG:HE	2.11	0.49
1:D:235:ARG:O	1:D:239:VAL:HG23	2.11	0.49
1:A:487:GLU:HA	1:B:486:ASP:OD2	2.11	0.49
1:E:315:LYS:HD2	1:E:341:TRP:CZ2	2.47	0.49
1:F:428:ASN:HB2	1:F:429:ARG:NH2	2.27	0.49
1:H:190:PHE:HE2	1:H:260:LEU:HB2	1.77	0.49
3:Q:116:PHE:HD2	3:Q:135:LEU:HD23	1.78	0.49
3:U:142:ARG:NH2	3:U:163:VAL:HG11	2.27	0.49
1:A:241:ALA:HA	1:B:279:GLN:CG	2.43	0.49
1:A:374:THR:HG21	1:B:454:ASN:N	2.13	0.49
1:E:190:PHE:HE2	1:E:260:LEU:HD13	1.75	0.49
1:H:56:VAL:HB	1:H:189:THR:HG22	1.94	0.49
1:I:56:VAL:HB	1:I:189:THR:HG22	1.94	0.49
2:O:66:ARG:NH2	2:O:86:ASP:OD1	2.37	0.49
1:H:477:TYR:HE1	2:L:195:ILE:HD13	1.78	0.49
1:A:49:ARG:NH1	1:A:52:TRP:CE2	2.81	0.49
1:B:315:LYS:HD2	1:B:341:TRP:CZ2	2.48	0.49
1:I:270:GLN:HG2	1:I:309:ILE:HD12	1.94	0.49
1:H:28:ILE:HG13	1:H:410:LEU:HD11	1.94	0.49
2:L:139:GLY:HA2	2:L:154:TRP:CH2	2.46	0.49
1:B:59:ILE:HB	1:B:297:LEU:CD2	2.43	0.49
1:I:424:ALA:HB2	1:I:435:PHE:CZ	2.47	0.49
2:O:14:PRO:HD3	2:O:112:SER:C	2.37	0.49
1:A:405:SER:HB3	1:A:457:TYR:HE2	1.78	0.48
2:L:100(E):LEU:HB2	2:L:100(G):HIS:CE1	2.48	0.48
2:N:142:VAL:HG11	2:N:150:VAL:HG11	1.95	0.48
1:A:406:VAL:HB	1:A:413:ILE:HB	1.95	0.48
1:B:373:LEU:HD13	1:C:402:ILE:HD13	1.95	0.48
1:D:150:SER:HB3	1:E:458:TYR:CD2	2.48	0.48
1:G:185:VAL:HG13	1:H:427:LYS:NZ	2.27	0.48
1:H:64:ILE:HG21	1:H:83:LEU:HD11	1.95	0.48
1:I:31:GLU:OE1	1:I:33:TYR:OH	2.21	0.48
1:I:395:ILE:HD13	1:I:492:ILE:HD13	1.96	0.48
2:M:87:THR:OG1	2:M:111:VAL:HG12	2.13	0.48
2:M:139:GLY:HA2	2:M:154:TRP:CH2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:LEU:HD23	1:B:96:LEU:HD12	1.95	0.48
1:C:338:ASP:O	1:C:342:TYR:OH	2.27	0.48
1:G:373:LEU:HD13	1:H:402:ILE:HG21	1.95	0.48
1:H:270:GLN:NE2	1:H:306:TYR:O	2.38	0.48
3:Q:18:ARG:HG3	3:Q:76:SER:HA	1.94	0.48
1:A:56:VAL:HG23	1:A:187:VAL:HG21	1.94	0.48
1:A:95:LEU:HD22	1:B:278:VAL:HG22	1.94	0.48
1:F:35:SER:O	1:F:474:ILE:HG12	2.13	0.48
1:F:410:LEU:HB3	1:F:466:ASN:HD21	1.78	0.48
1:G:75:LYS:NZ	1:H:218:GLU:OE1	2.47	0.48
1:G:145:GLY:HA2	1:H:407:ILE:HD12	1.95	0.48
1:H:190:PHE:CE2	1:H:260:LEU:HB2	2.49	0.48
2:O:66:ARG:HH12	2:O:86:ASP:CG	2.21	0.48
3:T:124:GLN:O	3:T:127:SER:OG	2.26	0.48
1:A:206:ILE:HD13	3:P:49:TYR:CE2	2.49	0.48
1:F:79:ILE:HD12	1:F:207:LEU:CD1	2.40	0.48
1:F:178:VAL:HG12	1:F:188:LEU:HD12	1.95	0.48
1:H:75:LYS:HE3	1:I:218:GLU:OE1	2.13	0.48
1:I:59:ILE:HB	1:I:297:LEU:HD21	1.95	0.48
2:L:94:THR:OG1	2:L:102:ASN:HB3	2.13	0.48
1:B:394:LYS:NZ	1:C:402:ILE:HD11	2.29	0.48
1:F:252:LEU:HD23	1:F:257:LEU:HD13	1.96	0.48
1:G:457:TYR:CE1	1:I:370:MET:HG3	2.49	0.48
1:I:423:THR:HG21	1:I:431:ILE:HG12	1.96	0.48
3:R:6:GLN:NE2	3:R:86:TYR:O	2.44	0.48
3:U:167:ASP:OD1	3:U:169:LYS:HG2	2.13	0.48
1:A:38:SER:HB2	1:A:316:LEU:HD11	1.96	0.48
1:C:491:SER:HB2	1:C:494:GLN:HG3	1.95	0.48
1:D:142:LEU:HA	1:D:373:LEU:HD21	1.95	0.48
1:E:71:GLY:O	1:E:76:VAL:HG21	2.13	0.48
1:G:51:GLY:C	1:G:305:ILE:HG12	2.38	0.48
2:K:100(G):HIS:HB2	2:K:100(H):TYR:HD1	1.79	0.48
2:M:123:PRO:HB3	2:M:211:VAL:HG12	1.95	0.48
1:H:477:TYR:HA	2:L:192:GLN:HE22	1.79	0.48
2:O:186:SER:HA	2:O:189:LEU:HD13	1.95	0.48
3:S:37:GLN:HB2	3:S:47:LEU:HD11	1.96	0.48
1:A:405:SER:HB2	1:A:452:VAL:HG21	1.95	0.48
1:E:237:PHE:CE1	1:E:289:MET:HB2	2.49	0.48
1:G:441:TYR:OH	1:G:466:ASN:ND2	2.47	0.48
2:J:36:TRP:CE2	2:J:80:MET:HB2	2.49	0.48
2:L:36:TRP:CE2	2:L:80:MET:HB2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S:181:LEU:CD2	3:S:185:ASP:OD2	2.61	0.48
1:C:270:GLN:HG2	1:C:309:ILE:HD11	1.95	0.48
1:F:28:ILE:O	1:F:410:LEU:HD11	2.14	0.48
1:G:138:LEU:HA	1:G:140:PHE:CE1	2.49	0.48
1:G:405:SER:HB2	1:G:452:VAL:HG21	1.94	0.48
1:I:405:SER:HB3	1:I:457:TYR:HE2	1.78	0.48
3:P:24:GLN:HG2	3:P:70:ASP:OD1	2.14	0.48
3:R:137:ASN:OD1	3:R:138:ASN:ND2	2.46	0.48
1:G:35:SER:O	1:G:474:ILE:HG12	2.14	0.47
1:G:202:GLN:O	1:G:206:ILE:HG13	2.14	0.47
1:H:148:ILE:HB	1:H:288:ILE:HD11	1.96	0.47
1:A:176:LYS:HG2	1:A:190:PHE:CZ	2.49	0.47
1:B:336:ARG:HB3	1:B:338:ASP:OD1	2.15	0.47
1:D:36:THR:HB	1:D:336:ARG:HD2	1.95	0.47
1:D:352:PHE:CE2	1:D:367:CYS:HB3	2.49	0.47
1:G:444:ASN:ND2	1:G:462:LEU:O	2.35	0.47
1:B:261:ILE:HD12	1:B:274:MET:HB3	1.97	0.47
1:F:325:ASN:ND2	1:F:330:SER:O	2.47	0.47
1:G:61:LEU:HD13	1:G:90:VAL:HG22	1.96	0.47
2:K:96:THR:HG22	2:K:98:LEU:HD12	1.96	0.47
2:L:150:VAL:HG22	2:L:200:HIS:HB2	1.96	0.47
3:T:40:PRO:HB3	3:T:165:GLU:HG3	1.95	0.47
1:A:279:GLN:CG	1:C:241:ALA:HA	2.44	0.47
1:C:30:GLU:HB2	1:C:410:LEU:HD12	1.96	0.47
1:A:252:LEU:O	1:A:282:ARG:NH2	2.37	0.47
1:D:207:LEU:HD21	1:D:212:CYS:SG	2.54	0.47
1:G:273:LEU:HD13	1:G:364:ARG:HH11	1.77	0.47
1:A:76:VAL:HG22	1:A:212:CYS:O	2.15	0.47
1:A:458:TYR:CD2	1:C:150:SER:HB3	2.49	0.47
1:B:345:ASN:ND2	1:C:454:ASN:OD1	2.47	0.47
1:D:241:ALA:HA	1:E:279:GLN:CG	2.44	0.47
1:I:352:PHE:CE2	1:I:367:CYS:HB3	2.49	0.47
1:I:487:GLU:OE1	1:I:498:LYS:NZ	2.31	0.47
1:A:423:THR:CG2	1:A:431:ILE:HG12	2.45	0.47
1:A:426:ASN:HB2	1:A:432:ILE:HD11	1.96	0.47
1:B:292:ILE:HA	1:B:297:LEU:HA	1.96	0.47
1:C:142:LEU:HD23	1:C:373:LEU:HG	1.95	0.47
1:D:221:ILE:O	1:D:224:GLN:HG2	2.15	0.47
1:F:217:ILE:O	1:F:220:VAL:HG12	2.15	0.47
1:G:370:MET:HG3	1:H:457:TYR:CE1	2.50	0.47
1:H:76:VAL:HG12	1:H:80:LYS:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:216:ASN:ND2	1:H:218:GLU:OE2	2.48	0.47
2:N:184:VAL:HG21	2:N:194:TYR:CZ	2.49	0.47
2:O:33:ILE:HD11	2:O:100(D):TYR:HD2	1.79	0.47
1:A:246:PRO:HG2	1:C:239:VAL:HG12	1.96	0.47
1:B:240:ASN:HB3	1:B:243:VAL:O	2.15	0.47
1:D:432:ILE:HD11	1:D:447:VAL:HG22	1.96	0.47
1:H:78:LEU:HB3	1:H:220:VAL:HG21	1.95	0.47
2:L:1:GLN:OE1	2:L:1:GLN:N	2.42	0.47
1:D:375:LEU:HD13	1:D:379:VAL:HG21	1.97	0.47
1:E:153:ALA:O	1:E:157:VAL:HG23	2.14	0.47
1:H:74:THR:O	1:H:78:LEU:HD23	2.13	0.47
2:K:184:VAL:HG22	2:K:185:PRO:HD2	1.96	0.47
1:C:428:ASN:HD22	1:C:428:ASN:C	2.17	0.47
1:E:202:GLN:HG3	1:I:432:ILE:HG22	1.96	0.47
1:F:407:ILE:HD13	1:F:458:TYR:O	2.14	0.47
1:G:150:SER:HB3	1:H:458:TYR:CD2	2.50	0.47
1:H:221:ILE:O	1:H:224:GLN:HG2	2.15	0.47
1:I:336:ARG:NH1	1:I:382:CYS:HB3	2.29	0.47
2:L:186:SER:HA	2:L:189:LEU:HD13	1.96	0.47
3:Q:37:GLN:HB2	3:Q:47:LEU:HD11	1.96	0.47
1:A:486:ASP:OD2	1:C:487:GLU:HA	2.15	0.46
1:B:321:LEU:HD11	1:B:473:PRO:HB3	1.97	0.46
1:C:75:LYS:HE3	1:C:75:LYS:HB2	1.70	0.46
1:C:338:ASP:HB2	1:C:342:TYR:OH	2.15	0.46
1:A:80:LYS:HE3	1:A:84:ASP:OD2	2.15	0.46
1:C:204:LEU:HD23	1:C:204:LEU:HA	1.71	0.46
1:D:373:LEU:HD13	1:E:402:ILE:HD13	1.97	0.46
3:T:113:PRO:HB3	3:T:139:PHE:HB3	1.96	0.46
1:A:68:LYS:N	2:J:99:VAL:HG22	2.30	0.46
1:A:513:LEU:HD11	1:C:512:LEU:HD11	1.97	0.46
1:C:208:ASN:ND2	2:K:97:ALA:HA	2.30	0.46
1:E:35:SER:O	1:E:474:ILE:HG12	2.14	0.46
1:H:338:ASP:HB2	1:H:342:TYR:OH	2.15	0.46
1:I:387:PHE:CZ	1:I:474:ILE:HG23	2.50	0.46
2:M:103:TRP:CE3	3:S:44:PRO:HD2	2.51	0.46
2:O:33:ILE:HB	2:O:95:GLU:HB3	1.97	0.46
1:A:56:VAL:HG22	1:A:300:VAL:HG22	1.98	0.46
1:A:218:GLU:HG2	1:C:75:LYS:CG	2.45	0.46
1:B:75:LYS:HD3	1:B:214:ILE:O	2.15	0.46
1:C:426:ASN:HB2	1:C:432:ILE:HD13	1.98	0.46
1:F:445:LYS:HZ1	1:F:464:GLY:N	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:155:GLN:HB3	3:Q:158:ASN:OD1	2.15	0.46
1:B:35:SER:O	1:B:474:ILE:HG12	2.15	0.46
1:B:78:LEU:HD23	1:B:220:VAL:HG11	1.96	0.46
1:F:427:LYS:HG2	1:F:448:ASP:OD2	2.16	0.46
1:F:507:ARG:HH22	1:F:508:ARG:HH21	1.62	0.46
1:H:53:TYR:HB2	1:H:305:ILE:HD11	1.96	0.46
1:C:387:PHE:CE2	1:C:474:ILE:HD12	2.50	0.46
1:C:461:LYS:HA	1:C:461:LYS:HD2	1.67	0.46
1:D:502:SER:O	1:D:506:ILE:HD13	2.16	0.46
2:M:160:THR:O	2:M:163:VAL:HG22	2.15	0.46
2:O:160:THR:O	2:O:163:VAL:HG22	2.16	0.46
1:A:171:LEU:HD21	1:A:189:THR:OG1	2.15	0.46
1:F:70:ASN:OD1	1:F:71:GLY:N	2.49	0.46
1:I:217:ILE:O	1:I:220:VAL:HG12	2.16	0.46
2:J:121:VAL:HA	2:J:141:LEU:O	2.15	0.46
2:O:11:VAL:HB	2:O:147:PRO:CG	2.42	0.46
3:U:197:THR:HG22	3:U:204:PRO:HB3	1.97	0.46
1:A:167:ILE:HD12	1:A:179:VAL:HG21	1.97	0.46
1:C:341:TRP:CZ3	1:C:341:TRP:CZ2	2.89	0.46
1:E:145:GLY:HA2	1:F:407:ILE:HD12	1.97	0.46
2:J:53:VAL:HG11	2:J:100:VAL:HG21	1.96	0.46
1:B:252:LEU:HD12	1:B:252:LEU:HA	1.82	0.46
1:B:480:PRO:C	1:B:482:VAL:H	2.24	0.46
1:C:351:PHE:C	1:C:351:PHE:CD2	2.94	0.46
1:D:394:LYS:HE2	1:E:400:THR:HG23	1.96	0.46
1:G:137:PHE:HE1	1:I:140:PHE:HB2	1.80	0.46
1:H:69:CYS:O	1:H:80:LYS:NZ	2.28	0.46
1:H:280:ILE:HG21	1:H:366:PHE:CG	2.51	0.46
1:C:188:LEU:HD21	1:C:263:ASP:HB3	1.98	0.46
1:E:178:VAL:HG12	1:E:188:LEU:HD12	1.98	0.46
1:G:142:LEU:HA	1:G:373:LEU:HD21	1.98	0.46
1:H:224:GLN:OE1	1:I:225:GLN:NE2	2.49	0.46
2:J:18:VAL:HB	2:J:82(C):LEU:HD11	1.98	0.46
2:K:170:LEU:HD13	2:K:176:TYR:CE1	2.50	0.46
3:P:11:LEU:HD11	3:P:104:VAL:HG13	1.98	0.46
1:A:261:ILE:HD12	1:A:274:MET:HB3	1.98	0.45
1:D:370:MET:HG3	1:E:457:TYR:CE1	2.51	0.45
1:G:345:ASN:O	1:H:454:ASN:ND2	2.49	0.45
1:H:235:ARG:O	1:H:239:VAL:HG23	2.16	0.45
1:I:97:THR:HG21	1:I:291:ILE:HA	1.97	0.45
1:I:167:ILE:HD12	1:I:189:THR:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:108:ARG:HD2	3:Q:171:SER:HB2	1.97	0.45
1:A:73:ASP:OD1	1:A:74:THR:N	2.49	0.45
1:C:370:MET:HE2	1:C:370:MET:HB3	1.79	0.45
1:E:387:PHE:HZ	1:E:474:ILE:HG23	1.81	0.45
1:G:241:ALA:HA	1:H:279:GLN:CG	2.43	0.45
1:H:261:ILE:HD12	1:H:274:MET:HB3	1.97	0.45
2:J:184:VAL:HG21	2:J:194:TYR:OH	2.16	0.45
2:N:166:PHE:CE1	3:T:176:SER:HB3	2.52	0.45
3:T:33:LEU:HD22	3:T:71:PHE:CG	2.51	0.45
1:F:334:LEU:HD11	1:F:395:ILE:HB	1.97	0.45
1:H:243:VAL:HA	1:H:287:SER:O	2.15	0.45
1:I:142:LEU:HD23	1:I:373:LEU:HG	1.98	0.45
1:I:214:ILE:HD11	1:I:219:THR:CB	2.46	0.45
3:S:4:MET:HB2	3:S:99:GLY:HA2	1.99	0.45
1:A:77:LYS:HD2	1:A:77:LYS:HA	1.59	0.45
1:B:192:VAL:HG11	1:B:229:ARG:NH2	2.31	0.45
1:D:52:TRP:CE3	1:D:302:GLN:HG2	2.51	0.45
1:E:235:ARG:HG3	1:F:249:THR:OG1	2.17	0.45
1:F:140:PHE:HD1	1:F:140:PHE:H	1.64	0.45
1:F:320:PRO:O	1:F:417:TYR:OH	2.32	0.45
1:F:405:SER:HB3	1:F:457:TYR:CD2	2.51	0.45
1:I:220:VAL:O	1:I:224:GLN:HB2	2.17	0.45
1:I:452:VAL:O	1:I:455:THR:OG1	2.33	0.45
2:L:211:VAL:O	2:L:212:GLU:HG3	2.15	0.45
2:M:36:TRP:CZ3	2:M:92:CYS:HB2	2.52	0.45
2:M:143:LYS:HG2	2:M:144:ASP:CG	2.42	0.45
1:A:87:LYS:O	1:A:91:THR:OG1	2.28	0.45
1:D:405:SER:HB3	1:D:457:TYR:CD2	2.52	0.45
1:D:414:VAL:HG21	1:D:435:PHE:HE2	1.80	0.45
1:F:426:ASN:OD1	1:F:427:LYS:N	2.50	0.45
1:G:181:LEU:HD12	1:G:185:VAL:HG23	1.99	0.45
1:G:223:PHE:O	1:G:227:ASN:N	2.44	0.45
1:H:204:LEU:N	1:H:205:PRO:HD2	2.32	0.45
1:H:231:LEU:HA	1:H:234:THR:HG22	1.98	0.45
2:N:18:VAL:HB	2:N:82(C):LEU:HD11	1.99	0.45
2:O:63:PHE:HB3	2:O:67:VAL:HG21	1.97	0.45
3:T:28:ASP:OD1	3:T:68:GLY:HA2	2.16	0.45
3:T:83:VAL:HG11	3:T:166:GLN:HB3	1.97	0.45
1:A:49:ARG:HE	1:A:368:ASP:CG	2.25	0.45
1:A:176:LYS:HZ3	1:A:190:PHE:HE2	1.55	0.45
1:A:442:VAL:HG11	1:A:447:VAL:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:193:LEU:HD23	1:B:193:LEU:HA	1.79	0.45
1:C:315:LYS:HE2	1:C:341:TRP:CE3	2.49	0.45
1:E:62:SER:HB3	1:E:196:LYS:HA	1.99	0.45
1:F:87:LYS:O	1:F:91:THR:OG1	2.28	0.45
1:G:199:ILE:HG23	1:G:204:LEU:HD23	1.99	0.45
2:J:29:LEU:HG	2:J:76:ASP:HA	1.98	0.45
2:L:163:VAL:HG12	2:L:182:VAL:HB	1.98	0.45
3:S:18:ARG:NH2	3:S:74:THR:HG21	2.32	0.45
1:A:192:VAL:HG23	1:A:193:LEU:H	1.82	0.45
1:C:317:HIS:CD2	1:C:408:THR:HA	2.52	0.45
1:D:328:GLU:OE1	1:D:328:GLU:N	2.29	0.45
1:E:56:VAL:HB	1:E:189:THR:HG22	1.99	0.45
1:E:480:PRO:C	1:E:482:VAL:H	2.24	0.45
1:H:39:ALA:HB2	1:H:413:ILE:HD11	1.99	0.45
1:I:338:ASP:HB2	1:I:342:TYR:OH	2.16	0.45
2:M:186:SER:HA	2:M:189:LEU:HD13	1.97	0.45
1:D:176:LYS:HG2	1:D:190:PHE:CZ	2.52	0.45
1:G:338:ASP:HB2	1:G:342:TYR:OH	2.16	0.45
1:H:241:ALA:H	1:I:279:GLN:NE2	2.15	0.45
1:I:386:ILE:HG12	1:I:492:ILE:HG13	1.99	0.45
1:I:461:LYS:HD2	1:I:461:LYS:HA	1.68	0.45
2:J:72:ASP:OD1	2:J:74:SER:OG	2.25	0.45
1:A:257:LEU:O	1:A:261:ILE:HG12	2.16	0.45
1:B:266:ILE:HG13	1:B:271:LYS:HG3	1.98	0.45
1:F:336:ARG:HB3	1:F:338:ASP:OD1	2.16	0.45
3:S:35:TRP:HB2	3:S:48:ILE:HB	1.99	0.45
3:U:166:GLN:NE2	3:U:171:SER:HB3	2.32	0.45
1:B:498:LYS:HZ3	1:C:486:ASP:HB3	1.80	0.45
1:C:202:GLN:O	1:C:206:ILE:HG13	2.16	0.45
1:D:260:LEU:HD22	1:D:303:LEU:HD12	1.99	0.45
1:E:73:ASP:OD1	1:E:74:THR:N	2.50	0.45
1:E:338:ASP:OD1	1:E:338:ASP:N	2.50	0.45
1:H:93:LEU:HD23	1:H:96:LEU:HD12	1.99	0.45
1:I:76:VAL:HG22	1:I:212:CYS:O	2.16	0.45
1:I:318:THR:O	1:I:406:VAL:HG21	2.16	0.45
2:M:181:VAL:HG11	3:S:135:LEU:HD22	1.99	0.45
1:C:209:GLN:HE22	2:K:101:ASP:HB2	1.82	0.44
1:F:90:VAL:HG13	1:F:292:ILE:HD11	1.99	0.44
1:F:171:LEU:HD21	1:F:189:THR:HB	1.99	0.44
1:F:235:ARG:O	1:F:239:VAL:HG23	2.17	0.44
1:G:289:MET:HE1	1:G:297:LEU:HG	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:480:PRO:C	1:G:482:VAL:H	2.25	0.44
1:H:198:TYR:CE2	1:H:223:PHE:HD1	2.35	0.44
1:H:432:ILE:HD11	1:H:447:VAL:HG22	1.99	0.44
1:B:52:TRP:CE3	1:B:302:GLN:HG2	2.52	0.44
1:B:146:SER:HB2	1:B:149:ALA:HB2	1.98	0.44
1:B:226:LYS:HD3	1:B:226:LYS:HA	1.65	0.44
1:D:99:ASN:O	1:D:100:THR:HG22	2.17	0.44
1:D:270:GLN:NE2	1:D:307:GLY:HA2	2.31	0.44
1:D:509:SER:HA	1:E:512:LEU:HD21	1.99	0.44
1:G:396:MET:HE3	1:G:488:PHE:HA	1.98	0.44
1:G:507:ARG:HH12	1:G:508:ARG:HH21	1.65	0.44
1:H:394:LYS:HZ1	1:I:402:ILE:HD12	1.82	0.44
1:C:209:GLN:HG2	3:Q:49:TYR:CZ	2.53	0.44
1:D:56:VAL:O	1:D:189:THR:HA	2.17	0.44
1:E:31:GLU:O	1:E:39:ALA:HA	2.18	0.44
1:F:193:LEU:HD23	1:F:193:LEU:HA	1.88	0.44
1:G:56:VAL:O	1:G:189:THR:HA	2.17	0.44
1:I:190:PHE:HE2	1:I:260:LEU:HB2	1.83	0.44
2:O:166:PHE:CD2	3:U:164:THR:HG23	2.52	0.44
1:A:315:LYS:HD2	1:A:341:TRP:CZ2	2.51	0.44
1:A:415:SER:HB3	1:A:417:TYR:CE2	2.52	0.44
1:B:267:THR:HG22	1:B:269:ASP:H	1.83	0.44
1:E:309:ILE:HG22	1:E:310:ASP:CG	2.42	0.44
1:E:370:MET:HE2	1:E:370:MET:HB3	1.72	0.44
1:E:484:PRO:HG2	1:E:495:VAL:HG13	1.99	0.44
1:E:508:ARG:HD3	1:F:509:SER:OG	2.18	0.44
1:F:33:TYR:CE2	1:F:383:ASN:HB3	2.52	0.44
1:F:195:LEU:HD23	1:F:195:LEU:HA	1.81	0.44
1:G:235:ARG:O	1:G:239:VAL:HG23	2.17	0.44
1:G:507:ARG:HH22	1:G:508:ARG:NH2	2.16	0.44
1:H:318:THR:O	1:H:339:ARG:NH2	2.50	0.44
2:J:1:GLN:OE1	2:J:1:GLN:N	2.44	0.44
3:U:143:GLU:OE1	3:U:143:GLU:N	2.49	0.44
1:B:202:GLN:HB2	1:F:429:ARG:HD2	1.98	0.44
1:B:235:ARG:O	1:B:239:VAL:HG23	2.18	0.44
1:B:308:VAL:HG21	1:B:345:ASN:HD21	1.83	0.44
1:C:318:THR:OG1	1:C:339:ARG:NH2	2.50	0.44
1:D:171:LEU:HD21	1:D:189:THR:OG1	2.17	0.44
1:D:243:VAL:HG22	1:D:288:ILE:HG22	1.99	0.44
1:E:64:ILE:HG21	1:E:83:LEU:HD11	1.99	0.44
1:E:217:ILE:O	1:E:220:VAL:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:50:THR:HG22	1:G:307:GLY:H	1.82	0.44
1:I:33:TYR:CE2	1:I:383:ASN:HB3	2.50	0.44
2:J:166:PHE:CD2	3:P:164:THR:HG23	2.52	0.44
2:L:170:LEU:HD13	2:L:176:TYR:CE1	2.53	0.44
3:P:108:ARG:HD3	3:P:109:THR:O	2.17	0.44
1:A:235:ARG:O	1:A:239:VAL:HG23	2.17	0.44
1:A:241:ALA:HA	1:B:279:GLN:HG2	1.99	0.44
1:B:235:ARG:HD3	1:C:250:TYR:CE2	2.53	0.44
1:C:75:LYS:O	1:C:79:ILE:HG12	2.18	0.44
1:D:414:VAL:HG11	1:D:435:PHE:HD2	1.83	0.44
1:E:270:GLN:NE2	1:E:306:TYR:O	2.51	0.44
1:E:387:PHE:CE2	2:J:158:ALA:HB2	2.52	0.44
1:F:405:SER:HB2	1:F:452:VAL:HG21	2.00	0.44
1:F:480:PRO:C	1:F:482:VAL:H	2.25	0.44
1:G:406:VAL:HG13	1:I:144:VAL:HG22	2.00	0.44
1:H:49:ARG:HE	1:H:368:ASP:CG	2.26	0.44
2:N:123:PRO:HB3	2:N:211:VAL:HG12	2.00	0.44
2:O:123:PRO:CB	2:O:211:VAL:HG12	2.46	0.44
3:P:186:TYR:O	3:P:192:TYR:OH	2.35	0.44
1:A:291:ILE:CD1	1:A:291:ILE:C	2.91	0.44
1:B:49:ARG:HE	1:B:368:ASP:CG	2.26	0.44
1:E:209:GLN:HE22	1:I:442:VAL:HG13	1.82	0.44
1:E:335:THR:HB	1:E:396:MET:HG2	1.98	0.44
1:F:31:GLU:OE1	1:F:33:TYR:OH	2.26	0.44
1:F:97:THR:HG21	1:F:292:ILE:HG22	1.99	0.44
1:G:487:GLU:HA	1:H:486:ASP:OD2	2.18	0.44
1:H:159:HIS:CE1	1:H:291:ILE:HD13	2.52	0.44
1:E:50:THR:HG22	1:E:369:THR:HG21	1.99	0.44
1:E:291:ILE:HG22	1:E:298:ALA:O	2.18	0.44
1:F:386:ILE:HG21	1:F:474:ILE:HG13	2.00	0.44
1:I:480:PRO:C	1:I:482:VAL:H	2.26	0.44
2:J:66:ARG:NH1	2:J:82:LEU:HD11	2.33	0.44
2:O:33:ILE:HD11	2:O:100(D):TYR:CD2	2.52	0.44
3:Q:143:GLU:OE1	3:Q:143:GLU:N	2.49	0.44
1:G:317:HIS:CD2	1:G:408:THR:HA	2.52	0.44
1:I:309:ILE:HG22	1:I:310:ASP:CG	2.43	0.44
1:I:432:ILE:HD11	1:I:447:VAL:HG22	1.99	0.44
1:I:491:SER:H	1:I:494:GLN:HB2	1.83	0.44
2:L:195:ILE:HD12	2:L:195:ILE:N	2.33	0.44
1:G:402:ILE:HD13	1:I:373:LEU:HD13	1.99	0.43
1:G:512:LEU:HD13	1:H:515:ALA:C	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:95:LEU:HD13	1:I:278:VAL:HG21	2.00	0.43
1:I:316:LEU:HD21	1:I:336:ARG:HH21	1.83	0.43
2:O:100(G):HIS:O	3:U:34:ASN:ND2	2.51	0.43
3:S:66:GLY:HA3	3:S:71:PHE:HA	1.99	0.43
3:S:124:GLN:O	3:S:127:SER:OG	2.31	0.43
3:U:33:LEU:HD22	3:U:71:PHE:CG	2.52	0.43
1:A:246:PRO:HG2	1:C:239:VAL:CG1	2.48	0.43
1:E:210:GLN:OE1	1:E:213:ARG:HB3	2.19	0.43
1:G:156:LYS:HE2	1:G:156:LYS:HB2	1.60	0.43
1:H:352:PHE:CE2	1:H:367:CYS:HB3	2.53	0.43
1:I:65:LYS:HA	1:I:65:LYS:HD3	1.81	0.43
1:I:209:GLN:NE2	2:O:101:ASP:OD2	2.39	0.43
2:K:29:LEU:HG	2:K:76:ASP:HA	2.00	0.43
2:K:114:ALA:HB3	2:K:146:PHE:CE2	2.53	0.43
2:M:169:VAL:HG21	3:S:160:GLN:HB3	2.00	0.43
1:A:414:VAL:HG21	1:A:435:PHE:CE2	2.53	0.43
1:C:164:VAL:HG21	1:C:293:LYS:HD3	1.99	0.43
1:F:315:LYS:HD2	1:F:341:TRP:CE2	2.53	0.43
1:G:30:GLU:OE1	1:G:441:TYR:OH	2.16	0.43
1:G:379:VAL:HG22	1:G:391:TYR:CZ	2.54	0.43
1:I:337:THR:HG22	1:I:394:LYS:C	2.43	0.43
2:K:100(B):GLU:O	2:K:100(C):THR:OG1	2.36	0.43
2:M:19:MET:HE2	2:M:81:GLU:HB2	2.01	0.43
1:C:266:ILE:HG13	1:C:271:LYS:HG3	2.00	0.43
1:D:490:ALA:HB2	1:E:486:ASP:OD2	2.18	0.43
1:I:59:ILE:HG12	1:I:192:VAL:HG23	2.01	0.43
1:I:426:ASN:ND2	1:I:446:GLY:O	2.50	0.43
2:K:166:PHE:HA	3:Q:164:THR:HG22	1.99	0.43
2:L:100(D):TYR:HD1	2:L:100(E):LEU:H	1.66	0.43
2:O:33:ILE:HG12	2:O:52:ILE:HG23	2.01	0.43
3:P:119:PRO:HB3	3:P:209:PHE:CE1	2.53	0.43
1:C:44:TYR:CD2	1:C:341:TRP:HZ3	2.36	0.43
1:C:315:LYS:CD	1:C:341:TRP:CD2	3.01	0.43
1:C:446:GLY:HA3	1:H:205:PRO:CB	2.45	0.43
1:D:293:LYS:HG2	1:D:294:GLU:N	2.33	0.43
1:F:361:GLN:C	1:F:362:SER:HG	2.22	0.43
1:G:76:VAL:HG22	1:G:212:CYS:O	2.18	0.43
1:G:97:THR:HG21	1:G:289:MET:HE3	2.00	0.43
1:H:480:PRO:C	1:H:482:VAL:H	2.27	0.43
2:J:193:THR:HG22	2:J:195:ILE:HD11	1.99	0.43
2:L:123:PRO:O	3:R:121:SER:OG	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:33:LEU:HD11	3:P:88:CYS:HB2	2.01	0.43
3:S:137:ASN:OD1	3:S:138:ASN:ND2	2.44	0.43
1:G:79:ILE:HG22	1:G:220:VAL:HG23	2.00	0.43
1:G:442:VAL:CG1	1:G:447:VAL:HG21	2.48	0.43
2:N:150:VAL:HG22	2:N:200:HIS:HB2	2.01	0.43
3:P:4:MET:HE1	3:P:25:ALA:HB2	2.00	0.43
3:P:40:PRO:CB	3:P:165:GLU:HG3	2.48	0.43
3:P:151:ASP:OD1	3:P:189:HIS:ND1	2.52	0.43
3:R:190:LYS:NZ	3:R:210:ASN:HB3	2.34	0.43
1:B:335:THR:HB	1:B:396:MET:HG2	2.00	0.43
1:C:207:LEU:HA	1:C:207:LEU:HD12	1.75	0.43
1:D:458:TYR:CE2	1:F:150:SER:HB3	2.54	0.43
1:A:193:LEU:HD23	1:A:193:LEU:HA	1.84	0.43
1:A:403:SER:OG	1:A:416:CYS:HA	2.18	0.43
1:D:144:VAL:CG2	1:E:406:VAL:HG13	2.48	0.43
1:F:94:GLN:HG3	1:F:292:ILE:HD13	1.99	0.43
1:G:314:TRP:NE1	1:G:342:TYR:HB2	2.33	0.43
1:H:488:PHE:HB2	1:I:488:PHE:CZ	2.54	0.43
1:B:379:VAL:HG22	1:B:391:TYR:CZ	2.53	0.43
1:C:73:ASP:OD2	1:C:213:ARG:NH2	2.52	0.43
1:C:210:GLN:O	1:C:213:ARG:HG3	2.19	0.43
1:D:319:SER:OG	1:D:320:PRO:HD2	2.19	0.43
1:E:426:ASN:OD1	1:E:427:LYS:N	2.51	0.43
1:F:243:VAL:HA	1:F:287:SER:O	2.18	0.43
1:H:153:ALA:O	1:H:157:VAL:HG23	2.19	0.43
1:H:395:ILE:HD13	1:H:492:ILE:HD13	2.01	0.43
2:K:195:ILE:HD12	2:K:210:ARG:HG2	2.01	0.43
2:L:170:LEU:HD13	2:L:176:TYR:CZ	2.53	0.43
2:M:11:VAL:HA	2:M:110:THR:O	2.19	0.43
3:S:119:PRO:HB3	3:S:209:PHE:CE1	2.54	0.43
1:A:369:THR:HG23	1:B:455:THR:HG23	2.00	0.43
1:D:369:THR:O	1:E:455:THR:HG22	2.19	0.43
1:E:137:PHE:HD2	1:E:337:THR:HA	1.84	0.43
3:P:113:PRO:HB3	3:P:139:PHE:HB3	2.00	0.43
1:A:217:ILE:HD12	1:A:217:ILE:HA	1.87	0.42
1:A:235:ARG:HD2	1:B:250:TYR:CE2	2.54	0.42
1:C:315:LYS:HE2	1:C:315:LYS:HB2	1.14	0.42
1:F:49:ARG:HG3	1:F:304:PRO:CB	2.49	0.42
1:F:59:ILE:HG12	1:F:192:VAL:HG23	2.00	0.42
1:F:395:ILE:HG12	1:F:491:SER:HA	2.00	0.42
1:G:427:LYS:HG2	1:G:448:ASP:OD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:193:LEU:HD23	1:H:193:LEU:HA	1.89	0.42
1:I:78:LEU:HD12	1:I:78:LEU:HA	1.86	0.42
1:I:441:TYR:OH	1:I:466:ASN:ND2	2.45	0.42
2:J:33:ILE:HG13	2:J:97:ALA:HB2	2.01	0.42
2:M:209:LYS:HD2	2:M:209:LYS:HA	1.66	0.42
3:R:50:VAL:HG22	3:R:91:TYR:OH	2.18	0.42
1:C:324:THR:HG21	1:C:437:ASN:C	2.43	0.42
1:E:45:PHE:HB3	1:E:310:ASP:HA	2.00	0.42
1:E:138:LEU:HD12	1:E:140:PHE:HE1	1.84	0.42
1:F:207:LEU:HD12	1:F:207:LEU:HA	1.66	0.42
1:G:77:LYS:O	1:G:81:GLN:HG2	2.19	0.42
2:K:19:MET:HE2	2:K:81:GLU:HB2	2.00	0.42
2:L:63:PHE:HB3	2:L:67:VAL:HG21	2.01	0.42
3:S:179:LEU:HG	3:S:181:LEU:HD11	2.01	0.42
1:A:76:VAL:O	1:A:80:LYS:HB3	2.20	0.42
1:B:49:ARG:NH1	1:B:51:GLY:O	2.51	0.42
1:B:157:VAL:HG11	1:B:181:LEU:HB3	2.01	0.42
1:C:313:CYS:HA	1:C:342:TYR:O	2.20	0.42
1:C:491:SER:H	1:C:494:GLN:HB2	1.83	0.42
1:D:67:THR:HG22	2:L:99:VAL:HG13	2.01	0.42
1:D:285:SER:OG	1:D:304:PRO:HD3	2.18	0.42
1:E:236:GLU:OE2	1:E:248:SER:OG	2.35	0.42
1:G:61:LEU:O	1:G:295:GLU:HB2	2.19	0.42
1:G:252:LEU:HD12	1:G:252:LEU:HA	1.84	0.42
1:G:354:GLN:O	1:G:357:THR:OG1	2.37	0.42
2:L:193:THR:CG2	2:L:210:ARG:HD3	2.49	0.42
2:M:121:VAL:HA	2:M:141:LEU:O	2.19	0.42
1:B:498:LYS:HZ1	1:C:486:ASP:HB3	1.82	0.42
1:C:71:GLY:O	1:C:76:VAL:HG11	2.19	0.42
1:D:92:GLU:HG2	1:E:254:ASN:CG	2.45	0.42
1:D:193:LEU:HD23	1:D:193:LEU:HA	1.69	0.42
1:D:508:ARG:HG2	1:D:508:ARG:HH11	1.84	0.42
1:E:445:LYS:HZ1	1:E:464:GLY:N	2.12	0.42
1:F:261:ILE:HD12	1:F:274:MET:HB3	2.01	0.42
1:I:171:LEU:HD21	1:I:189:THR:HB	2.02	0.42
2:L:36:TRP:CH2	2:L:92:CYS:HB2	2.54	0.42
1:B:157:VAL:HG21	1:B:183:ASN:ND2	2.34	0.42
1:D:338:ASP:HB2	1:D:342:TYR:OH	2.18	0.42
1:E:240:ASN:HB3	1:E:243:VAL:O	2.19	0.42
1:G:294:GLU:O	1:G:295:GLU:HG2	2.19	0.42
1:G:426:ASN:OD1	1:G:427:LYS:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:240:ASN:HB3	1:H:243:VAL:O	2.20	0.42
2:N:63:PHE:HB3	2:N:67:VAL:HG21	2.02	0.42
1:A:65:LYS:HG3	2:J:100(B):GLU:OE1	2.20	0.42
1:E:192:VAL:CG1	1:E:229:ARG:NH1	2.82	0.42
1:G:246:PRO:HG2	1:I:239:VAL:HG12	2.01	0.42
1:I:34:GLN:HB2	1:I:468:TYR:HE1	1.84	0.42
2:J:126:PRO:HD3	2:J:138:LEU:HB3	1.99	0.42
2:K:29:LEU:HD11	2:K:77:THR:C	2.45	0.42
3:Q:113:PRO:HB3	3:Q:139:PHE:HB3	2.01	0.42
1:A:252:LEU:HD22	1:A:301:VAL:HG11	2.02	0.42
1:B:487:GLU:OE2	1:B:498:LYS:HD3	2.20	0.42
1:C:423:THR:CG2	1:C:431:ILE:HG13	2.46	0.42
1:D:59:ILE:HB	1:D:297:LEU:CD2	2.49	0.42
1:D:279:GLN:CG	1:F:241:ALA:HA	2.49	0.42
1:D:426:ASN:OD1	1:D:427:LYS:N	2.52	0.42
1:E:332:ILE:HD13	1:E:332:ILE:HA	1.93	0.42
1:F:318:THR:O	1:F:339:ARG:NH2	2.53	0.42
1:F:327:LYS:HB3	1:F:327:LYS:HE2	1.78	0.42
1:F:396:MET:HE3	1:F:396:MET:HB2	1.81	0.42
1:H:192:VAL:HG23	1:H:193:LEU:H	1.84	0.42
1:H:267:THR:HG22	1:H:269:ASP:H	1.85	0.42
2:K:166:PHE:CD2	3:Q:164:THR:HG23	2.55	0.42
2:M:205:THR:HG22	2:M:207:VAL:HG23	2.02	0.42
2:N:33:ILE:O	2:N:94:THR:HA	2.19	0.42
2:O:83:ARG:O	2:O:111:VAL:HG11	2.19	0.42
1:A:68:LYS:HD2	1:A:68:LYS:HA	1.82	0.42
1:E:150:SER:HB3	1:F:458:TYR:CD2	2.54	0.42
1:E:239:VAL:HG12	1:F:246:PRO:HG2	2.00	0.42
1:H:387:PHE:HZ	1:H:474:ILE:HG23	1.85	0.42
1:I:82:GLU:OE2	1:I:224:GLN:HG3	2.19	0.42
1:I:193:LEU:HD23	1:I:193:LEU:HA	1.91	0.42
2:J:186:SER:HA	2:J:189:LEU:HD13	2.00	0.42
1:A:280:ILE:HG21	1:A:366:PHE:CG	2.55	0.42
1:A:406:VAL:HG13	1:C:144:VAL:CG2	2.50	0.42
1:B:30:GLU:OE2	1:B:408:THR:HB	2.20	0.42
1:C:480:PRO:C	1:C:482:VAL:H	2.28	0.42
1:D:225:GLN:HE21	1:F:224:GLN:NE2	2.17	0.42
1:E:60:GLU:OE1	1:E:196:LYS:HD3	2.20	0.42
1:E:79:ILE:CG2	1:E:220:VAL:HG23	2.48	0.42
1:F:44:TYR:HA	1:F:363:ASN:OD1	2.19	0.42
1:H:338:ASP:O	1:H:342:TYR:OH	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:198:HIS:H	3:R:201:LEU:HD11	1.84	0.42
1:C:196:LYS:NZ	2:K:100(C):THR:OG1	2.53	0.42
1:D:176:LYS:HE2	1:D:190:PHE:CE2	2.55	0.42
1:E:176:LYS:HZ3	1:E:190:PHE:HE1	1.64	0.42
1:I:405:SER:HB2	1:I:452:VAL:HG21	2.02	0.42
1:D:352:PHE:CD1	1:D:352:PHE:N	2.88	0.41
1:D:505:PHE:CG	1:E:505:PHE:HE1	2.38	0.41
1:G:204:LEU:HD13	1:G:204:LEU:HA	1.90	0.41
2:M:100(H):TYR:HB3	3:S:34:ASN:ND2	2.35	0.41
1:D:318:THR:O	1:D:339:ARG:NH2	2.53	0.41
1:E:192:VAL:HG11	1:E:229:ARG:CZ	2.50	0.41
1:I:37:CYS:SG	1:I:319:SER:HB3	2.60	0.41
2:K:48:MET:HG2	2:K:63:PHE:CE2	2.56	0.41
2:L:146:PHE:CD1	2:L:147:PRO:HA	2.55	0.41
2:M:45:PRO:HG2	3:S:98:PHE:CD2	2.54	0.41
2:O:36:TRP:CE2	2:O:80:MET:HB2	2.55	0.41
3:S:108:ARG:HH12	3:S:111:ALA:HB2	1.85	0.41
1:A:75:LYS:H	1:A:75:LYS:HG2	1.71	0.41
1:B:151:GLY:HA3	1:B:288:ILE:HD12	2.02	0.41
1:C:375:LEU:HB3	1:C:379:VAL:HG21	2.02	0.41
1:G:423:THR:HG23	1:G:431:ILE:HG23	2.01	0.41
2:J:11:VAL:HA	2:J:110:THR:O	2.20	0.41
2:M:98:LEU:HD23	2:M:98:LEU:HA	1.84	0.41
3:R:197:THR:HG22	3:R:204:PRO:HB3	2.02	0.41
1:D:188:LEU:HD23	1:D:188:LEU:HA	1.88	0.41
1:F:397:THR:HB	1:F:483:PHE:CE2	2.55	0.41
1:G:319:SER:OG	1:G:320:PRO:HD2	2.20	0.41
2:J:94:THR:OG1	2:J:102:ASN:HB3	2.20	0.41
2:J:139:GLY:HA2	2:J:154:TRP:HH2	1.85	0.41
2:K:19:MET:HA	2:K:80:MET:O	2.21	0.41
2:O:33:ILE:HG23	2:O:52:ILE:HG12	2.02	0.41
1:A:237:PHE:CE2	1:A:289:MET:HB2	2.56	0.41
1:C:167:ILE:HD13	1:C:179:VAL:HG11	2.02	0.41
1:C:171:LEU:HD21	1:C:189:THR:HB	2.03	0.41
1:C:217:ILE:O	1:C:220:VAL:HG12	2.21	0.41
1:C:258:LEU:HD11	1:C:278:VAL:HG11	2.02	0.41
1:D:50:THR:HG22	1:D:307:GLY:H	1.85	0.41
1:G:192:VAL:HG23	1:G:193:LEU:H	1.86	0.41
1:G:314:TRP:CE2	1:G:342:TYR:HB2	2.56	0.41
2:O:121:VAL:HG22	2:O:142:VAL:HG22	2.01	0.41
3:P:149:LYS:HG2	3:P:154:LEU:HG	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S:140:TYR:CG	3:S:141:PRO:HA	2.54	0.41
3:U:107:LYS:HA	3:U:140:TYR:OH	2.20	0.41
1:C:151:GLY:HA3	1:C:288:ILE:CD1	2.50	0.41
1:C:171:LEU:HD21	1:C:189:THR:CB	2.50	0.41
1:C:321:LEU:HD11	1:C:473:PRO:HB3	2.02	0.41
1:C:503:LEU:HA	1:C:506:ILE:HB	2.01	0.41
1:D:279:GLN:HE22	1:F:238:SER:C	2.27	0.41
1:D:407:ILE:HD13	1:D:458:TYR:O	2.20	0.41
1:E:146:SER:H	1:F:407:ILE:HD12	1.85	0.41
1:F:204:LEU:HD23	1:F:204:LEU:HA	1.77	0.41
1:I:204:LEU:O	1:I:208:ASN:HB2	2.20	0.41
1:I:231:LEU:HD23	1:I:231:LEU:HA	1.86	0.41
1:I:252:LEU:HD23	1:I:257:LEU:HD13	2.01	0.41
2:K:116:THR:HG22	2:K:203:SER:HB3	2.01	0.41
2:L:23:GLN:NE2	2:L:24:ALA:O	2.52	0.41
3:Q:140:TYR:CG	3:Q:141:PRO:HA	2.55	0.41
1:A:163:GLU:OE1	1:A:163:GLU:HA	2.20	0.41
1:C:442:VAL:HA	1:H:209:GLN:HG3	2.03	0.41
1:D:142:LEU:HD23	1:D:373:LEU:HG	2.03	0.41
1:D:399:LYS:HB2	1:F:494:GLN:NE2	2.35	0.41
1:D:507:ARG:HH22	1:D:508:ARG:NH2	2.19	0.41
1:E:452:VAL:O	1:E:455:THR:OG1	2.37	0.41
1:G:167:ILE:HD11	1:G:181:LEU:HD21	2.02	0.41
1:G:193:LEU:HD23	1:G:193:LEU:HA	1.91	0.41
1:H:406:VAL:O	1:H:413:ILE:N	2.44	0.41
1:H:442:VAL:HG11	1:H:447:VAL:HG21	2.03	0.41
1:I:199:ILE:O	1:I:204:LEU:HD23	2.20	0.41
2:O:100(D):TYR:CZ	2:O:100(G):HIS:HE1	2.38	0.41
1:B:207:LEU:HD12	1:B:207:LEU:HA	1.89	0.41
1:C:317:HIS:HD2	1:C:408:THR:CG2	2.33	0.41
1:C:324:THR:HB	1:C:437:ASN:HB3	2.03	0.41
1:D:509:SER:CA	1:E:512:LEU:HD21	2.49	0.41
1:E:140:PHE:CD1	1:E:140:PHE:N	2.88	0.41
1:E:165:ASN:ND2	1:E:294:GLU:OE2	2.53	0.41
1:F:387:PHE:CZ	1:F:474:ILE:HG23	2.56	0.41
1:G:507:ARG:O	1:G:511:GLU:HB3	2.21	0.41
1:I:204:LEU:HD13	1:I:204:LEU:HA	1.83	0.41
2:N:184:VAL:HG21	2:N:194:TYR:OH	2.20	0.41
1:A:426:ASN:OD1	1:A:427:LYS:N	2.53	0.41
1:A:491:SER:HB2	1:A:494:GLN:HG3	2.03	0.41
1:B:334:LEU:HD11	1:B:395:ILE:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:461:LYS:HA	1:B:461:LYS:HD2	1.61	0.41
1:C:50:THR:HG23	1:C:307:GLY:H	1.85	0.41
1:C:65:LYS:HB2	2:K:100:VAL:O	2.21	0.41
1:C:217:ILE:HD12	1:C:217:ILE:HA	1.78	0.41
1:C:332:ILE:HD13	1:C:332:ILE:HA	1.96	0.41
1:D:75:LYS:HG3	1:E:218:GLU:OE2	2.21	0.41
1:E:338:ASP:O	1:E:342:TYR:OH	2.38	0.41
1:F:387:PHE:CE2	1:F:474:ILE:HD12	2.56	0.41
1:G:28:ILE:HD12	1:G:44:TYR:CE1	2.56	0.41
1:G:67:THR:HA	2:N:99:VAL:HG22	2.02	0.41
1:G:176:LYS:HG2	1:G:190:PHE:CZ	2.56	0.41
1:G:266:ILE:HG13	1:G:271:LYS:HG3	2.03	0.41
1:H:197:SER:O	1:H:201:ASN:HB2	2.21	0.41
2:J:11:VAL:HB	2:J:147:PRO:HG3	2.03	0.41
2:J:139:GLY:HA2	2:J:154:TRP:CH2	2.56	0.41
2:J:152:VAL:HG23	2:J:198:VAL:HG22	2.02	0.41
2:L:63:PHE:HB3	2:L:67:VAL:CG2	2.51	0.41
2:M:6:GLN:HA	2:M:21:SER:O	2.21	0.41
2:M:150:VAL:HG22	2:M:200:HIS:HB2	2.03	0.41
2:N:163:VAL:HG12	2:N:182:VAL:HB	2.03	0.41
2:O:19:MET:HE3	2:O:19:MET:HB2	1.85	0.41
3:Q:198:HIS:H	3:Q:201:LEU:HD11	1.85	0.41
3:T:198:HIS:H	3:T:201:LEU:HD11	1.85	0.41
1:A:156:LYS:HE3	1:B:462:LEU:HD23	2.03	0.41
1:B:189:THR:O	1:B:190:PHE:HD1	2.04	0.41
1:C:395:ILE:HD13	1:C:492:ILE:HD13	2.03	0.41
1:D:352:PHE:CE2	1:D:372:SER:HB3	2.56	0.41
1:E:52:TRP:CE3	1:E:302:GLN:HG2	2.56	0.41
1:F:352:PHE:CE2	1:F:367:CYS:HB3	2.56	0.41
1:F:370:MET:HE2	1:F:370:MET:HB3	1.80	0.41
1:I:478:TYR:HB3	1:I:483:PHE:HD2	1.86	0.41
2:L:100(D):TYR:HE1	2:L:100(G):HIS:CD2	2.39	0.41
2:N:141:LEU:HD12	2:N:178:LEU:O	2.20	0.41
2:O:17:SER:HA	2:O:82(A):SER:HA	2.03	0.41
2:O:103:TRP:CE3	3:U:44:PRO:HD2	2.56	0.41
3:Q:192:TYR:HB2	3:Q:209:PHE:CZ	2.56	0.41
3:T:11:LEU:HD11	3:T:104:VAL:HG13	2.02	0.41
1:A:323:THR:HG23	1:A:475:ILE:HG13	2.03	0.40
1:B:332:ILE:HG23	1:B:483:PHE:CE2	2.56	0.40
1:E:49:ARG:O	1:E:369:THR:HG23	2.21	0.40
1:G:352:PHE:CD1	1:G:352:PHE:N	2.88	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:394:LYS:HZ1	1:I:402:ILE:CD1	2.34	0.40
1:I:59:ILE:HB	1:I:297:LEU:CD2	2.51	0.40
2:K:30:GLU:HA	2:K:52(A):PRO:HB2	2.04	0.40
3:R:192:TYR:HB2	3:R:209:PHE:CE2	2.57	0.40
1:A:204:LEU:HD23	1:A:204:LEU:HA	1.82	0.40
1:B:201:ASN:HB3	1:F:426:ASN:HD21	1.86	0.40
1:B:503:LEU:HD23	1:B:503:LEU:HA	1.94	0.40
1:C:426:ASN:OD1	1:C:427:LYS:N	2.54	0.40
1:E:162:GLY:O	1:E:166:LYS:HG3	2.21	0.40
1:F:394:LYS:HE2	1:F:394:LYS:HB3	1.91	0.40
1:H:37:CYS:SG	1:H:319:SER:HB3	2.61	0.40
1:H:373:LEU:HD13	1:I:402:ILE:HD13	2.03	0.40
2:O:195:ILE:HD12	2:O:210:ARG:HG2	2.04	0.40
1:A:64:ILE:HA	2:J:100(A):SER:HA	2.03	0.40
1:A:474:ILE:HA	1:A:477:TYR:HD2	1.87	0.40
1:C:209:GLN:NE2	3:Q:55:GLU:OE2	2.54	0.40
1:C:408:THR:OG1	1:C:411:GLY:N	2.54	0.40
1:D:176:LYS:NZ	1:D:259:SER:OG	2.54	0.40
1:F:49:ARG:HE	1:F:368:ASP:CG	2.29	0.40
1:G:461:LYS:HD2	1:G:461:LYS:HA	1.77	0.40
2:L:100(E):LEU:HB2	2:L:100(G):HIS:HE1	1.86	0.40
2:M:100(A):SER:O	2:M:100(D):TYR:HB2	2.21	0.40
1:B:138:LEU:HD21	1:B:337:THR:OG1	2.21	0.40
1:B:157:VAL:HG12	1:B:163:GLU:HG2	2.03	0.40
1:B:323:THR:HG23	1:B:475:ILE:HG13	2.03	0.40
1:D:288:ILE:O	1:D:288:ILE:HG13	2.21	0.40
1:D:293:LYS:HG2	1:D:294:GLU:H	1.86	0.40
1:H:59:ILE:HB	1:H:297:LEU:CD2	2.50	0.40
1:H:405:SER:HB3	1:H:457:TYR:CE2	2.57	0.40
1:I:58:THR:HG22	1:I:298:ALA:HB2	2.03	0.40
1:I:270:GLN:HG2	1:I:309:ILE:CD1	2.51	0.40
3:Q:4:MET:HB2	3:Q:99:GLY:HA2	2.02	0.40
1:A:168:LYS:NZ	1:A:295:GLU:HB2	2.37	0.40
1:B:338:ASP:OD1	1:B:338:ASP:N	2.46	0.40
1:D:102:ALA:HA	1:D:152:ILE:HD13	2.04	0.40
1:F:45:PHE:HB3	1:F:310:ASP:HA	2.03	0.40
1:F:334:LEU:CB	1:F:475:ILE:HD13	2.52	0.40
1:F:442:VAL:HG11	1:F:447:VAL:HG21	2.03	0.40
1:I:352:PHE:CE2	1:I:372:SER:HB3	2.57	0.40
2:N:143:LYS:HG2	2:N:144:ASP:CG	2.47	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:173:SER:O	2:K:206:LYS:NZ[5_555]	1.98	0.22
3:Q:5:THR:OG1	3:U:5:THR:OG1[4_555]	1.98	0.22

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	445/568 (78%)	420 (94%)	25 (6%)	0	100	100
1	B	448/568 (79%)	427 (95%)	20 (4%)	1 (0%)	43	77
1	C	446/568 (78%)	426 (96%)	18 (4%)	2 (0%)	30	66
1	D	451/568 (79%)	430 (95%)	20 (4%)	1 (0%)	43	77
1	E	447/568 (79%)	428 (96%)	18 (4%)	1 (0%)	43	77
1	F	448/568 (79%)	429 (96%)	18 (4%)	1 (0%)	43	77
1	G	449/568 (79%)	427 (95%)	21 (5%)	1 (0%)	43	77
1	H	447/568 (79%)	429 (96%)	17 (4%)	1 (0%)	43	77
1	I	444/568 (78%)	422 (95%)	19 (4%)	3 (1%)	18	55
2	J	220/228 (96%)	214 (97%)	6 (3%)	0	100	100
2	K	216/228 (95%)	209 (97%)	7 (3%)	0	100	100
2	L	217/228 (95%)	208 (96%)	9 (4%)	0	100	100
2	M	217/228 (95%)	211 (97%)	6 (3%)	0	100	100
2	N	217/228 (95%)	210 (97%)	7 (3%)	0	100	100
2	O	210/228 (92%)	204 (97%)	6 (3%)	0	100	100
3	P	210/214 (98%)	201 (96%)	8 (4%)	1 (0%)	24	62
3	Q	209/214 (98%)	199 (95%)	9 (4%)	1 (0%)	24	62
3	R	209/214 (98%)	200 (96%)	8 (4%)	1 (0%)	24	62
3	S	209/214 (98%)	199 (95%)	8 (4%)	2 (1%)	12	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	T	209/214 (98%)	201 (96%)	6 (3%)	2 (1%)	12	47
3	U	204/214 (95%)	195 (96%)	8 (4%)	1 (0%)	24	62
All	All	6572/7764 (85%)	6289 (96%)	264 (4%)	19 (0%)	36	71

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	P	30	VAL
3	Q	30	VAL
3	R	30	VAL
3	S	30	VAL
3	T	30	VAL
3	U	30	VAL
1	C	295	GLU
1	I	71	GLY
1	I	215	SER
3	S	151	ASP
3	T	151	ASP
1	B	184	GLY
1	C	184	GLY
1	E	184	GLY
1	H	184	GLY
1	I	184	GLY
1	D	100	THR
1	F	184	GLY
1	G	184	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	411/512 (80%)	411 (100%)	0	100	100
1	B	413/512 (81%)	413 (100%)	0	100	100
1	C	412/512 (80%)	411 (100%)	1 (0%)	87	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	415/512 (81%)	415 (100%)	0	100	100
1	E	413/512 (81%)	413 (100%)	0	100	100
1	F	414/512 (81%)	414 (100%)	0	100	100
1	G	414/512 (81%)	414 (100%)	0	100	100
1	H	412/512 (80%)	412 (100%)	0	100	100
1	I	410/512 (80%)	410 (100%)	0	100	100
2	J	189/193 (98%)	189 (100%)	0	100	100
2	K	186/193 (96%)	186 (100%)	0	100	100
2	L	187/193 (97%)	187 (100%)	0	100	100
2	M	187/193 (97%)	187 (100%)	0	100	100
2	N	187/193 (97%)	187 (100%)	0	100	100
2	O	184/193 (95%)	184 (100%)	0	100	100
3	P	186/188 (99%)	186 (100%)	0	100	100
3	Q	186/188 (99%)	186 (100%)	0	100	100
3	R	186/188 (99%)	186 (100%)	0	100	100
3	S	186/188 (99%)	186 (100%)	0	100	100
3	T	186/188 (99%)	186 (100%)	0	100	100
3	U	183/188 (97%)	183 (100%)	0	100	100
All	All	5947/6894 (86%)	5946 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	251	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	201	ASN
1	A	216	ASN
1	A	240	ASN
1	A	371	ASN
1	A	437	ASN
1	A	454	ASN
1	B	345	ASN

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Mol	Chain	Res	Type
1	B	363	ASN
1	C	317	HIS
1	C	345	ASN
1	C	454	ASN
1	D	227	ASN
1	D	240	ASN
1	D	454	ASN
1	D	476	ASN
1	E	201	ASN
1	E	240	ASN
1	E	262	ASN
1	E	277	ASN
1	E	325	ASN
1	E	428	ASN
1	F	99	ASN
1	F	224	GLN
1	F	302	GLN
1	F	325	ASN
1	F	466	ASN
1	G	27	ASN
1	G	240	ASN
1	H	81	GLN
1	H	159	HIS
1	H	165	ASN
1	H	476	ASN
1	I	201	ASN
1	I	224	GLN
1	I	227	ASN
1	I	325	ASN
2	J	192	GLN
2	L	100(G)	HIS
2	L	192	GLN
2	O	58	HIS
3	P	53	ASN
3	Q	27	GLN
3	Q	158	ASN
3	R	53	ASN
3	R	79	GLN
3	T	53	ASN
3	T	138	ASN
3	U	79	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

15 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	B	601	-	4,4,4	0.21	0	6,6,6	0.11	0
4	SO4	H	602	-	4,4,4	0.26	0	6,6,6	0.11	0
4	SO4	D	601	-	4,4,4	0.25	0	6,6,6	0.10	0
4	SO4	C	601	-	4,4,4	0.24	0	6,6,6	0.04	0
4	SO4	J	301	-	4,4,4	0.24	0	6,6,6	0.09	0
4	SO4	B	603	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	I	601	-	4,4,4	0.23	0	6,6,6	0.11	0
4	SO4	A	601	-	4,4,4	0.24	0	6,6,6	0.05	0
4	SO4	L	301	-	4,4,4	0.23	0	6,6,6	0.09	0
4	SO4	B	604	-	4,4,4	0.25	0	6,6,6	0.06	0
4	SO4	H	601	-	4,4,4	0.23	0	6,6,6	0.14	0
4	SO4	B	602	-	4,4,4	0.24	0	6,6,6	0.06	0
4	SO4	E	601	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	G	601	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	C	602	-	4,4,4	0.26	0	6,6,6	0.08	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	449/568 (79%)	0.22	1 (0%) 91 83	62, 85, 113, 126	0
1	B	452/568 (79%)	0.19	4 (0%) 81 66	61, 83, 112, 128	0
1	C	450/568 (79%)	0.17	4 (0%) 81 66	58, 91, 118, 139	0
1	D	455/568 (80%)	0.24	2 (0%) 88 77	59, 84, 117, 135	0
1	E	451/568 (79%)	0.17	4 (0%) 81 66	62, 82, 115, 132	0
1	F	452/568 (79%)	0.16	3 (0%) 84 71	66, 88, 116, 140	0
1	G	453/568 (79%)	0.18	2 (0%) 88 77	63, 82, 112, 123	0
1	H	451/568 (79%)	0.18	4 (0%) 81 66	66, 84, 112, 128	0
1	I	448/568 (78%)	0.17	5 (1%) 78 62	60, 88, 111, 128	0
2	J	224/228 (98%)	0.22	1 (0%) 88 77	83, 103, 126, 145	0
2	K	220/228 (96%)	0.60	9 (4%) 41 35	97, 167, 209, 241	0
2	L	221/228 (96%)	0.24	1 (0%) 87 75	90, 111, 137, 156	0
2	M	221/228 (96%)	0.10	1 (0%) 87 75	75, 97, 137, 160	0
2	N	221/228 (96%)	0.12	0 100 100	75, 93, 116, 142	0
2	O	216/228 (94%)	0.65	9 (4%) 40 34	90, 168, 201, 232	0
3	P	212/214 (99%)	0.27	2 (0%) 81 66	84, 114, 156, 175	0
3	Q	211/214 (98%)	0.46	4 (1%) 66 51	92, 137, 210, 225	0
3	R	211/214 (98%)	0.24	1 (0%) 87 75	87, 122, 169, 186	0
3	S	211/214 (98%)	0.21	1 (0%) 87 75	79, 108, 142, 150	0
3	T	211/214 (98%)	0.17	1 (0%) 87 75	77, 106, 141, 164	0
3	U	208/214 (97%)	0.64	8 (3%) 44 36	87, 167, 211, 226	0
All	All	6648/7764 (85%)	0.24	67 (1%) 79 64	58, 94, 173, 241	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	K	125	ALA	3.6
1	B	256	GLU	3.5
2	O	170	LEU	3.4
2	O	173	SER	3.3
2	O	144	ASP	3.3
3	U	111	ALA	3.3
1	I	222	GLU	3.2
3	T	130	ALA	3.2
2	K	190	GLY	3.1
2	O	203	SER	3.0
1	I	432	ILE	3.0
2	K	128	SER	3.0
3	Q	184	ALA	2.8
2	K	87	THR	2.7
1	A	303	LEU	2.6
2	K	195	ILE	2.6
1	E	451	SER	2.6
1	C	222	GLU	2.6
1	I	454	ASN	2.5
1	E	209	GLN	2.5
2	M	212	GLU	2.5
3	U	100	GLY	2.5
2	O	186	SER	2.5
2	K	170	LEU	2.5
1	B	400	THR	2.4
1	C	218	GLU	2.4
3	P	130	ALA	2.4
1	H	488	PHE	2.3
3	Q	134	CYS	2.3
1	F	402	ILE	2.3
2	O	212	GLU	2.3
1	D	100	THR	2.3
1	G	72	THR	2.3
3	U	104	VAL	2.3
1	D	404	SER	2.3
3	Q	207	LYS	2.3
1	H	238	SER	2.2
2	O	113	SER	2.2
2	O	213	PRO	2.2
2	K	112	SER	2.2
1	H	209	GLN	2.2
2	L	194	TYR	2.2
3	P	212	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
3	Q	127	SER	2.2
3	U	200	GLY	2.2
2	K	204	ASN	2.2
3	U	178	THR	2.1
1	F	497	GLU	2.1
2	J	125	ALA	2.1
1	H	491	SER	2.1
3	U	149	LYS	2.1
1	B	215	SER	2.1
3	U	191	VAL	2.1
1	E	423	THR	2.1
3	R	100	GLY	2.1
1	E	472	GLU	2.1
1	I	447	VAL	2.1
1	F	375	LEU	2.0
1	C	71	GLY	2.0
1	I	72	THR	2.0
2	K	212	GLU	2.0
2	O	188	SER	2.0
3	S	200	GLY	2.0
1	C	72	THR	2.0
1	G	400	THR	2.0
3	U	126	LYS	2.0
1	B	137	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SO4	B	602	5/5	0.75	0.15	172,172,172,172	0
4	SO4	H	601	5/5	0.76	0.10	119,119,119,119	0
4	SO4	C	602	5/5	0.78	0.12	121,121,122,122	0
4	SO4	B	603	5/5	0.78	0.12	145,145,145,145	0
4	SO4	G	601	5/5	0.82	0.11	119,120,120,120	0
4	SO4	C	601	5/5	0.82	0.14	138,138,138,138	0
4	SO4	J	301	5/5	0.83	0.10	128,129,129,129	0
4	SO4	D	601	5/5	0.84	0.12	147,147,147,147	0
4	SO4	A	601	5/5	0.87	0.10	145,146,146,146	0
4	SO4	I	601	5/5	0.87	0.17	136,136,136,136	0
4	SO4	B	601	5/5	0.87	0.08	132,132,132,132	0
4	SO4	H	602	5/5	0.88	0.09	103,103,103,104	0
4	SO4	E	601	5/5	0.90	0.08	96,96,97,97	0
4	SO4	L	301	5/5	0.91	0.08	115,115,115,116	0
4	SO4	B	604	5/5	0.94	0.14	105,106,106,107	0

6.5 Other polymers [i](#)

There are no such residues in this entry.