



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 03:14 AM UTC

PDB ID : 8ZPY / pdb_00008zpy
Title : Crystal structure of prefusion F of RSV
Authors : Huang, Q.; Lang, Q.; Han, X.; Yan, J.
Deposited on : 2024-05-31
Resolution : 2.92 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

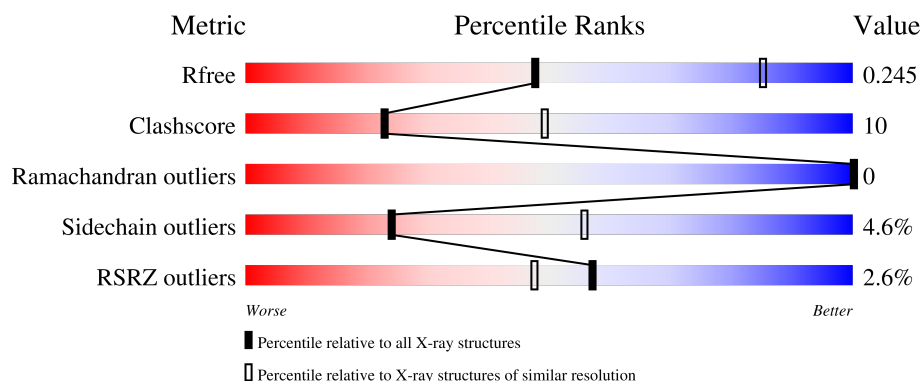
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.92 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	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (2.94-2.90)

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	522	3% 64% 21% • 12%
1	B	522	2% 62% 23% • 14%
1	C	522	0% 62% 23% • 14%
1	D	522	2% 63% 23% • 14%
1	E	522	3% 63% 22% • 14%

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Mol	Chain	Length	Quality of chain
1	F	522	2% 64% 21% • 14%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 20848 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,Fibritin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	457	Total	C	N	O	S	0	0	0
			3510	2215	580	694	21			
1	B	449	Total	C	N	O	S	0	0	0
			3472	2193	572	686	21			
1	C	448	Total	C	N	O	S	0	0	0
			3466	2190	571	684	21			
1	D	450	Total	C	N	O	S	0	0	0
			3472	2192	573	686	21			
1	E	449	Total	C	N	O	S	0	0	0
			3465	2187	572	685	21			
1	F	449	Total	C	N	O	S	0	0	0
			3463	2187	571	684	21			

There are 318 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	MET	-	initiating methionine	UNP P12568
A	11	LYS	-	expression tag	UNP P12568
A	12	CYS	-	expression tag	UNP P12568
A	13	LEU	-	expression tag	UNP P12568
A	14	LEU	-	expression tag	UNP P12568
A	15	TYR	-	expression tag	UNP P12568
A	16	LEU	-	expression tag	UNP P12568
A	17	ALA	-	expression tag	UNP P12568
A	18	PHE	-	expression tag	UNP P12568
A	19	LEU	-	expression tag	UNP P12568
A	20	PHE	-	expression tag	UNP P12568
A	21	ILE	-	expression tag	UNP P12568
A	22	GLY	-	expression tag	UNP P12568
A	23	VAL	-	expression tag	UNP P12568
A	24	ASN	-	expression tag	UNP P12568
A	25	CYS	-	expression tag	UNP P12568
A	67	PRO	ASN	conflict	UNP P12568

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Chain	Residue	Modelled	Actual	Comment	Reference
A	80	LYS	ASN	conflict	UNP P12568
A	100	GLY	-	linker	UNP P12568
A	101	GLY	-	linker	UNP P12568
A	102	GLY	-	linker	UNP P12568
A	103	GLY	-	linker	UNP P12568
A	104	SER	-	linker	UNP P12568
A	105	GLY	-	linker	UNP P12568
A	106	GLY	-	linker	UNP P12568
A	128	GLY	-	linker	UNP P12568
A	129	GLY	-	linker	UNP P12568
A	130	SER	-	linker	UNP P12568
A	131	GLY	-	linker	UNP P12568
A	132	GLY	-	linker	UNP P12568
A	133	GLY	-	linker	UNP P12568
A	134	GLY	-	linker	UNP P12568
A	135	SER	-	linker	UNP P12568
A	138	PRO	LEU	conflict	UNP P12568
A	139	PRO	GLY	conflict	UNP P12568
A	141	PRO	LEU	conflict	UNP P12568
A	152	VAL	ILE	conflict	UNP P12568
A	213	SER	ARG	conflict	UNP P12568
A	215	PRO	SER	conflict	UNP P12568
A	279	PRO	GLN	conflict	UNP P12568
A	377	PRO	SER	conflict	UNP P12568
A	514	SER	-	linker	UNP P12568
A	515	ALA	-	linker	UNP P12568
A	516	ILE	-	linker	UNP P12568
A	517	GLY	-	linker	UNP P12568
A	545	HIS	-	expression tag	UNP A0A346FJN8
A	546	HIS	-	expression tag	UNP A0A346FJN8
A	547	HIS	-	expression tag	UNP A0A346FJN8
A	548	HIS	-	expression tag	UNP A0A346FJN8
A	549	HIS	-	expression tag	UNP A0A346FJN8
A	550	HIS	-	expression tag	UNP A0A346FJN8
A	551	HIS	-	expression tag	UNP A0A346FJN8
A	552	HIS	-	expression tag	UNP A0A346FJN8
B	10	MET	-	initiating methionine	UNP P12568
B	11	LYS	-	expression tag	UNP P12568
B	12	CYS	-	expression tag	UNP P12568
B	13	LEU	-	expression tag	UNP P12568
B	14	LEU	-	expression tag	UNP P12568
B	15	TYR	-	expression tag	UNP P12568

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Chain	Residue	Modelled	Actual	Comment	Reference
B	16	LEU	-	expression tag	UNP P12568
B	17	ALA	-	expression tag	UNP P12568
B	18	PHE	-	expression tag	UNP P12568
B	19	LEU	-	expression tag	UNP P12568
B	20	PHE	-	expression tag	UNP P12568
B	21	ILE	-	expression tag	UNP P12568
B	22	GLY	-	expression tag	UNP P12568
B	23	VAL	-	expression tag	UNP P12568
B	24	ASN	-	expression tag	UNP P12568
B	25	CYS	-	expression tag	UNP P12568
B	67	PRO	ASN	conflict	UNP P12568
B	80	LYS	ASN	conflict	UNP P12568
B	121	GLY	-	linker	UNP P12568
B	122	GLY	-	linker	UNP P12568
B	123	GLY	-	linker	UNP P12568
B	124	GLY	-	linker	UNP P12568
B	125	SER	-	linker	UNP P12568
B	126	GLY	-	linker	UNP P12568
B	127	GLY	-	linker	UNP P12568
B	128	GLY	-	linker	UNP P12568
B	129	GLY	-	linker	UNP P12568
B	130	SER	-	linker	UNP P12568
B	131	GLY	-	linker	UNP P12568
B	132	GLY	-	linker	UNP P12568
B	133	GLY	-	linker	UNP P12568
B	134	GLY	-	linker	UNP P12568
B	135	SER	-	linker	UNP P12568
B	138	PRO	LEU	conflict	UNP P12568
B	139	PRO	GLY	conflict	UNP P12568
B	141	PRO	LEU	conflict	UNP P12568
B	152	VAL	ILE	conflict	UNP P12568
B	213	SER	ARG	conflict	UNP P12568
B	215	PRO	SER	conflict	UNP P12568
B	279	PRO	GLN	conflict	UNP P12568
B	377	PRO	SER	conflict	UNP P12568
B	514	SER	-	linker	UNP P12568
B	515	ALA	-	linker	UNP P12568
B	516	ILE	-	linker	UNP P12568
B	517	GLY	-	linker	UNP P12568
B	545	HIS	-	expression tag	UNP A0A346FJN8
B	546	HIS	-	expression tag	UNP A0A346FJN8
B	547	HIS	-	expression tag	UNP A0A346FJN8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	548	HIS	-	expression tag	UNP A0A346FJN8
B	549	HIS	-	expression tag	UNP A0A346FJN8
B	550	HIS	-	expression tag	UNP A0A346FJN8
B	551	HIS	-	expression tag	UNP A0A346FJN8
B	552	HIS	-	expression tag	UNP A0A346FJN8
C	10	MET	-	initiating methionine	UNP P12568
C	11	LYS	-	expression tag	UNP P12568
C	12	CYS	-	expression tag	UNP P12568
C	13	LEU	-	expression tag	UNP P12568
C	14	LEU	-	expression tag	UNP P12568
C	15	TYR	-	expression tag	UNP P12568
C	16	LEU	-	expression tag	UNP P12568
C	17	ALA	-	expression tag	UNP P12568
C	18	PHE	-	expression tag	UNP P12568
C	19	LEU	-	expression tag	UNP P12568
C	20	PHE	-	expression tag	UNP P12568
C	21	ILE	-	expression tag	UNP P12568
C	22	GLY	-	expression tag	UNP P12568
C	23	VAL	-	expression tag	UNP P12568
C	24	ASN	-	expression tag	UNP P12568
C	25	CYS	-	expression tag	UNP P12568
C	67	PRO	ASN	conflict	UNP P12568
C	80	LYS	ASN	conflict	UNP P12568
C	121	GLY	-	linker	UNP P12568
C	122	GLY	-	linker	UNP P12568
C	123	GLY	-	linker	UNP P12568
C	124	GLY	-	linker	UNP P12568
C	125	SER	-	linker	UNP P12568
C	126	GLY	-	linker	UNP P12568
C	127	GLY	-	linker	UNP P12568
C	128	GLY	-	linker	UNP P12568
C	129	GLY	-	linker	UNP P12568
C	130	SER	-	linker	UNP P12568
C	131	GLY	-	linker	UNP P12568
C	132	GLY	-	linker	UNP P12568
C	133	GLY	-	linker	UNP P12568
C	134	GLY	-	linker	UNP P12568
C	135	SER	-	linker	UNP P12568
C	138	PRO	LEU	conflict	UNP P12568
C	139	PRO	GLY	conflict	UNP P12568
C	141	PRO	LEU	conflict	UNP P12568
C	152	VAL	ILE	conflict	UNP P12568

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Chain	Residue	Modelled	Actual	Comment	Reference
C	213	SER	ARG	conflict	UNP P12568
C	215	PRO	SER	conflict	UNP P12568
C	279	PRO	GLN	conflict	UNP P12568
C	377	PRO	SER	conflict	UNP P12568
C	514	SER	-	linker	UNP P12568
C	515	ALA	-	linker	UNP P12568
C	516	ILE	-	linker	UNP P12568
C	517	GLY	-	linker	UNP P12568
C	545	HIS	-	expression tag	UNP A0A346FJN8
C	546	HIS	-	expression tag	UNP A0A346FJN8
C	547	HIS	-	expression tag	UNP A0A346FJN8
C	548	HIS	-	expression tag	UNP A0A346FJN8
C	549	HIS	-	expression tag	UNP A0A346FJN8
C	550	HIS	-	expression tag	UNP A0A346FJN8
C	551	HIS	-	expression tag	UNP A0A346FJN8
C	552	HIS	-	expression tag	UNP A0A346FJN8
D	10	MET	-	initiating methionine	UNP P12568
D	11	LYS	-	expression tag	UNP P12568
D	12	CYS	-	expression tag	UNP P12568
D	13	LEU	-	expression tag	UNP P12568
D	14	LEU	-	expression tag	UNP P12568
D	15	TYR	-	expression tag	UNP P12568
D	16	LEU	-	expression tag	UNP P12568
D	17	ALA	-	expression tag	UNP P12568
D	18	PHE	-	expression tag	UNP P12568
D	19	LEU	-	expression tag	UNP P12568
D	20	PHE	-	expression tag	UNP P12568
D	21	ILE	-	expression tag	UNP P12568
D	22	GLY	-	expression tag	UNP P12568
D	23	VAL	-	expression tag	UNP P12568
D	24	ASN	-	expression tag	UNP P12568
D	25	CYS	-	expression tag	UNP P12568
D	67	PRO	ASN	conflict	UNP P12568
D	80	LYS	ASN	conflict	UNP P12568
D	121	GLY	-	linker	UNP P12568
D	122	GLY	-	linker	UNP P12568
D	123	GLY	-	linker	UNP P12568
D	124	GLY	-	linker	UNP P12568
D	125	SER	-	linker	UNP P12568
D	126	GLY	-	linker	UNP P12568
D	127	GLY	-	linker	UNP P12568
D	128	GLY	-	linker	UNP P12568

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Chain	Residue	Modelled	Actual	Comment	Reference
D	129	GLY	-	linker	UNP P12568
D	130	SER	-	linker	UNP P12568
D	131	GLY	-	linker	UNP P12568
D	132	GLY	-	linker	UNP P12568
D	133	GLY	-	linker	UNP P12568
D	134	GLY	-	linker	UNP P12568
D	135	SER	-	linker	UNP P12568
D	138	PRO	LEU	conflict	UNP P12568
D	139	PRO	GLY	conflict	UNP P12568
D	141	PRO	LEU	conflict	UNP P12568
D	152	VAL	ILE	conflict	UNP P12568
D	213	SER	ARG	conflict	UNP P12568
D	215	PRO	SER	conflict	UNP P12568
D	279	PRO	GLN	conflict	UNP P12568
D	377	PRO	SER	conflict	UNP P12568
D	514	SER	-	linker	UNP P12568
D	515	ALA	-	linker	UNP P12568
D	516	ILE	-	linker	UNP P12568
D	517	GLY	-	linker	UNP P12568
D	545	HIS	-	expression tag	UNP A0A346FJN8
D	546	HIS	-	expression tag	UNP A0A346FJN8
D	547	HIS	-	expression tag	UNP A0A346FJN8
D	548	HIS	-	expression tag	UNP A0A346FJN8
D	549	HIS	-	expression tag	UNP A0A346FJN8
D	550	HIS	-	expression tag	UNP A0A346FJN8
D	551	HIS	-	expression tag	UNP A0A346FJN8
D	552	HIS	-	expression tag	UNP A0A346FJN8
E	10	MET	-	initiating methionine	UNP P12568
E	11	LYS	-	expression tag	UNP P12568
E	12	CYS	-	expression tag	UNP P12568
E	13	LEU	-	expression tag	UNP P12568
E	14	LEU	-	expression tag	UNP P12568
E	15	TYR	-	expression tag	UNP P12568
E	16	LEU	-	expression tag	UNP P12568
E	17	ALA	-	expression tag	UNP P12568
E	18	PHE	-	expression tag	UNP P12568
E	19	LEU	-	expression tag	UNP P12568
E	20	PHE	-	expression tag	UNP P12568
E	21	ILE	-	expression tag	UNP P12568
E	22	GLY	-	expression tag	UNP P12568
E	23	VAL	-	expression tag	UNP P12568
E	24	ASN	-	expression tag	UNP P12568

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Chain	Residue	Modelled	Actual	Comment	Reference
E	25	CYS	-	expression tag	UNP P12568
E	67	PRO	ASN	conflict	UNP P12568
E	80	LYS	ASN	conflict	UNP P12568
E	121	GLY	-	linker	UNP P12568
E	122	GLY	-	linker	UNP P12568
E	123	GLY	-	linker	UNP P12568
E	124	GLY	-	linker	UNP P12568
E	125	SER	-	linker	UNP P12568
E	126	GLY	-	linker	UNP P12568
E	127	GLY	-	linker	UNP P12568
E	128	GLY	-	linker	UNP P12568
E	129	GLY	-	linker	UNP P12568
E	130	SER	-	linker	UNP P12568
E	131	GLY	-	linker	UNP P12568
E	132	GLY	-	linker	UNP P12568
E	133	GLY	-	linker	UNP P12568
E	134	GLY	-	linker	UNP P12568
E	135	SER	-	linker	UNP P12568
E	138	PRO	LEU	conflict	UNP P12568
E	139	PRO	GLY	conflict	UNP P12568
E	141	PRO	LEU	conflict	UNP P12568
E	152	VAL	ILE	conflict	UNP P12568
E	213	SER	ARG	conflict	UNP P12568
E	215	PRO	SER	conflict	UNP P12568
E	279	PRO	GLN	conflict	UNP P12568
E	377	PRO	SER	conflict	UNP P12568
E	514	SER	-	linker	UNP P12568
E	515	ALA	-	linker	UNP P12568
E	516	ILE	-	linker	UNP P12568
E	517	GLY	-	linker	UNP P12568
E	545	HIS	-	expression tag	UNP A0A346FJN8
E	546	HIS	-	expression tag	UNP A0A346FJN8
E	547	HIS	-	expression tag	UNP A0A346FJN8
E	548	HIS	-	expression tag	UNP A0A346FJN8
E	549	HIS	-	expression tag	UNP A0A346FJN8
E	550	HIS	-	expression tag	UNP A0A346FJN8
E	551	HIS	-	expression tag	UNP A0A346FJN8
E	552	HIS	-	expression tag	UNP A0A346FJN8
F	10	MET	-	initiating methionine	UNP P12568
F	11	LYS	-	expression tag	UNP P12568
F	12	CYS	-	expression tag	UNP P12568
F	13	LEU	-	expression tag	UNP P12568

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Chain	Residue	Modelled	Actual	Comment	Reference
F	14	LEU	-	expression tag	UNP P12568
F	15	TYR	-	expression tag	UNP P12568
F	16	LEU	-	expression tag	UNP P12568
F	17	ALA	-	expression tag	UNP P12568
F	18	PHE	-	expression tag	UNP P12568
F	19	LEU	-	expression tag	UNP P12568
F	20	PHE	-	expression tag	UNP P12568
F	21	ILE	-	expression tag	UNP P12568
F	22	GLY	-	expression tag	UNP P12568
F	23	VAL	-	expression tag	UNP P12568
F	24	ASN	-	expression tag	UNP P12568
F	25	CYS	-	expression tag	UNP P12568
F	67	PRO	ASN	conflict	UNP P12568
F	80	LYS	ASN	conflict	UNP P12568
F	121	GLY	-	linker	UNP P12568
F	122	GLY	-	linker	UNP P12568
F	123	GLY	-	linker	UNP P12568
F	124	GLY	-	linker	UNP P12568
F	125	SER	-	linker	UNP P12568
F	126	GLY	-	linker	UNP P12568
F	127	GLY	-	linker	UNP P12568
F	128	GLY	-	linker	UNP P12568
F	129	GLY	-	linker	UNP P12568
F	130	SER	-	linker	UNP P12568
F	131	GLY	-	linker	UNP P12568
F	132	GLY	-	linker	UNP P12568
F	133	GLY	-	linker	UNP P12568
F	134	GLY	-	linker	UNP P12568
F	135	SER	-	linker	UNP P12568
F	138	PRO	LEU	conflict	UNP P12568
F	139	PRO	GLY	conflict	UNP P12568
F	141	PRO	LEU	conflict	UNP P12568
F	152	VAL	ILE	conflict	UNP P12568
F	213	SER	ARG	conflict	UNP P12568
F	215	PRO	SER	conflict	UNP P12568
F	279	PRO	GLN	conflict	UNP P12568
F	377	PRO	SER	conflict	UNP P12568
F	514	SER	-	linker	UNP P12568
F	515	ALA	-	linker	UNP P12568
F	516	ILE	-	linker	UNP P12568
F	517	GLY	-	linker	UNP P12568
F	545	HIS	-	expression tag	UNP A0A346FJN8

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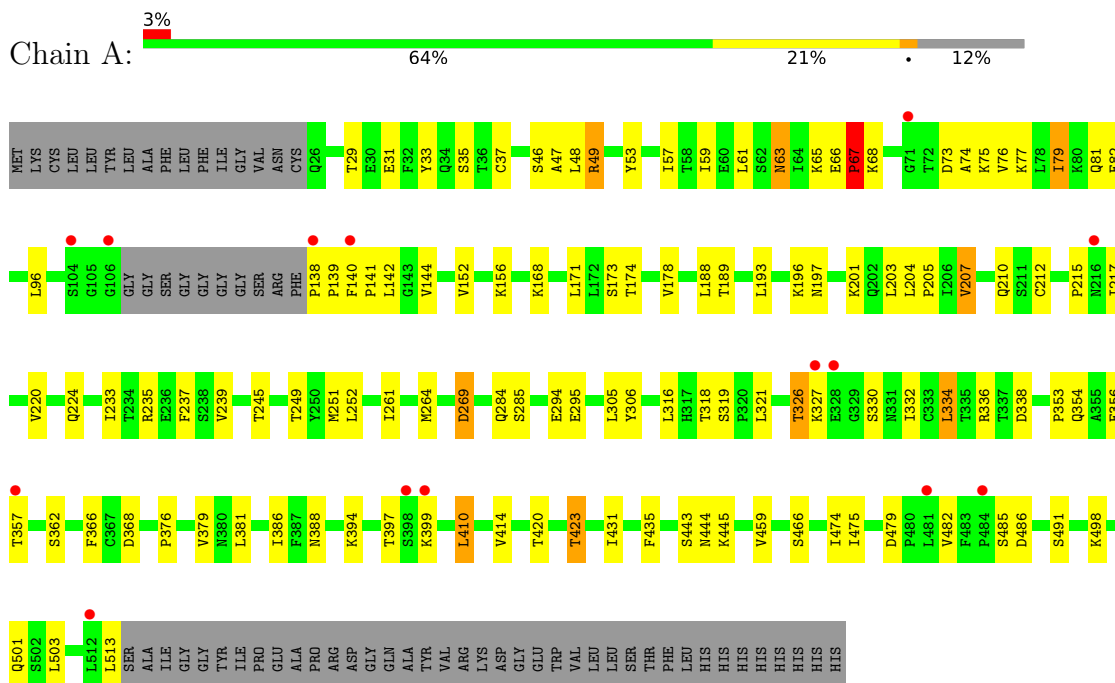
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Chain	Residue	Modelled	Actual	Comment	Reference
F	546	HIS	-	expression tag	UNP A0A346FJN8
F	547	HIS	-	expression tag	UNP A0A346FJN8
F	548	HIS	-	expression tag	UNP A0A346FJN8
F	549	HIS	-	expression tag	UNP A0A346FJN8
F	550	HIS	-	expression tag	UNP A0A346FJN8
F	551	HIS	-	expression tag	UNP A0A346FJN8
F	552	HIS	-	expression tag	UNP A0A346FJN8

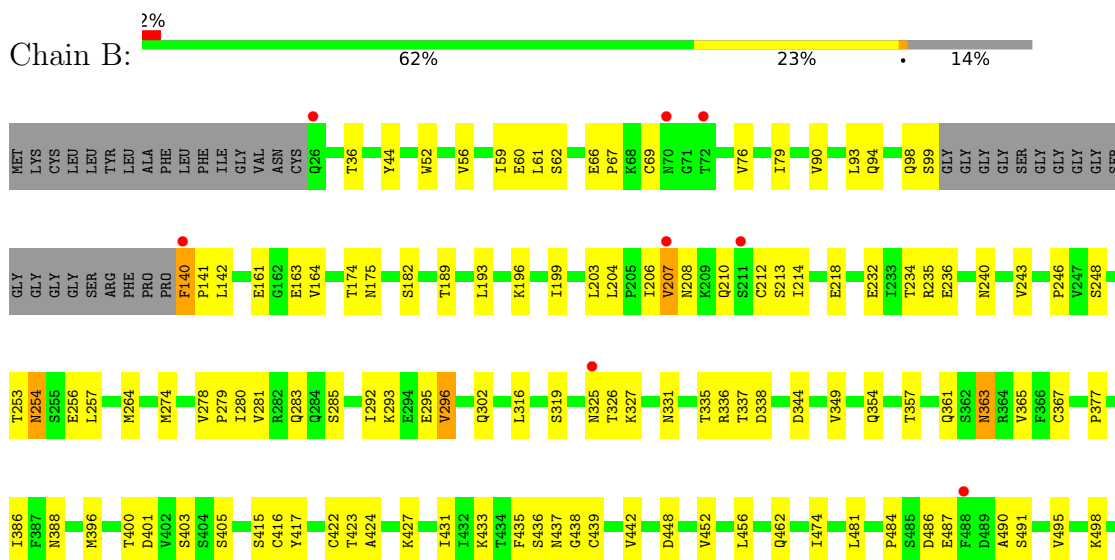
3 Residue-property plots [i](#)

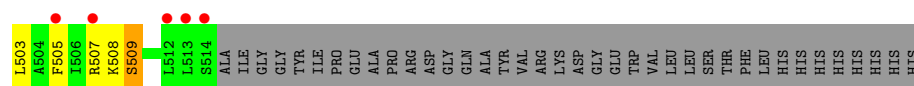
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: Fusion glycoprotein F0,Fibritin

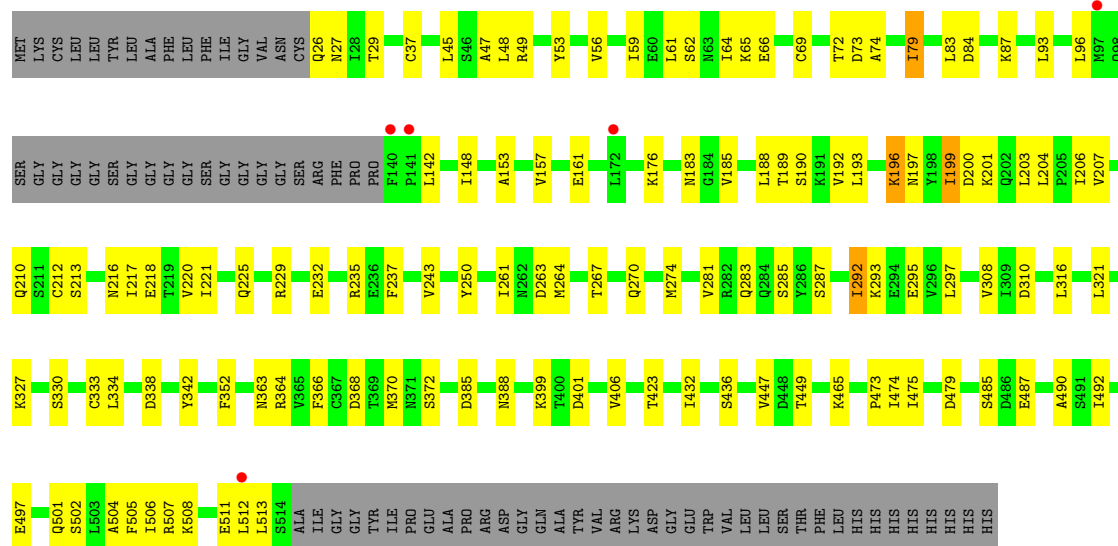


• Molecule 1: Fusion glycoprotein F0,Fibritin

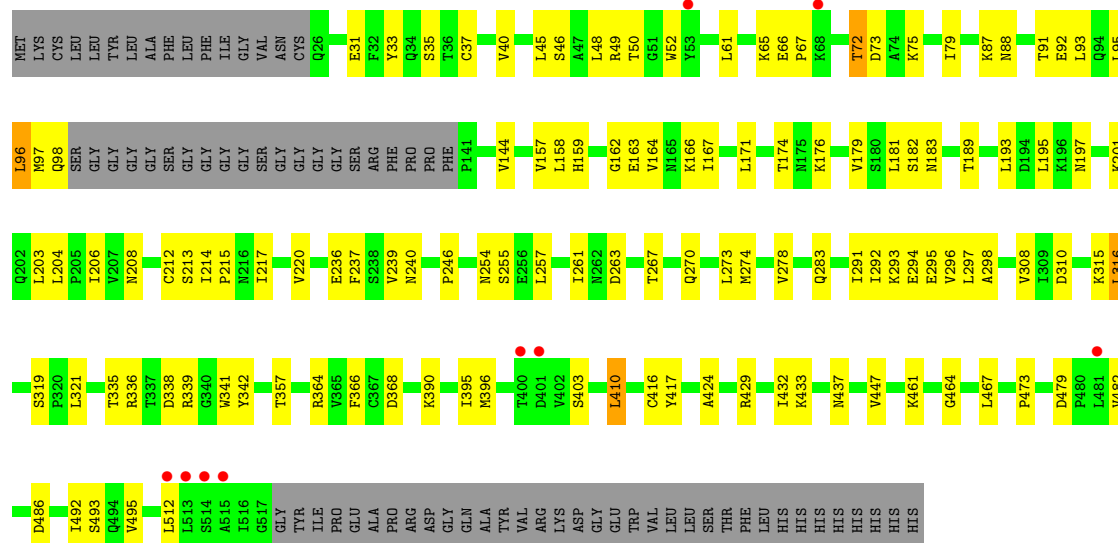




• Molecule 1: Fusion glycoprotein F0,Fibrin

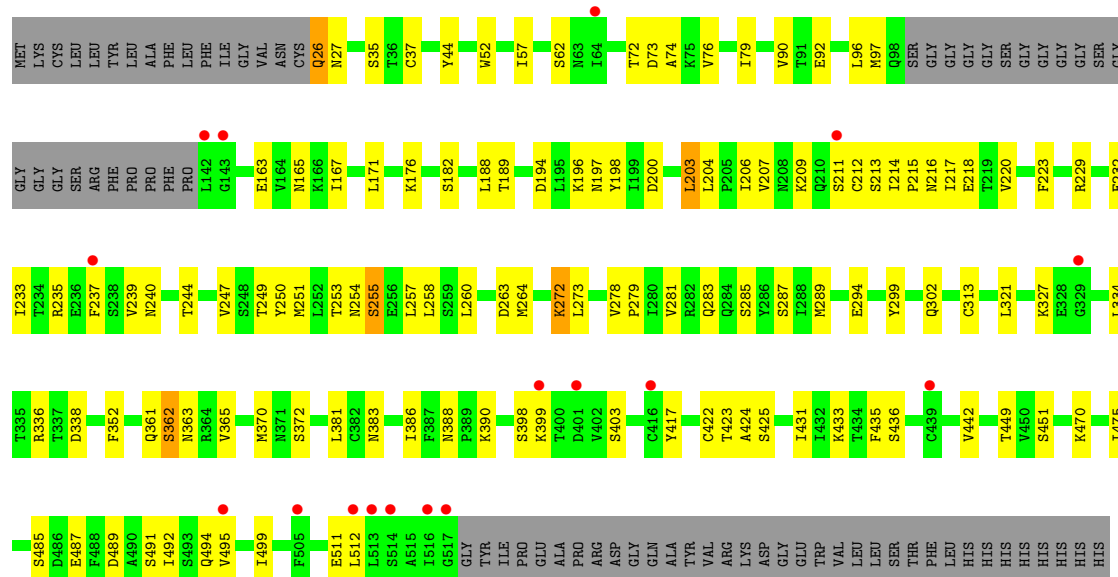


• Molecule 1: Fusion glycoprotein F0,Fibrin

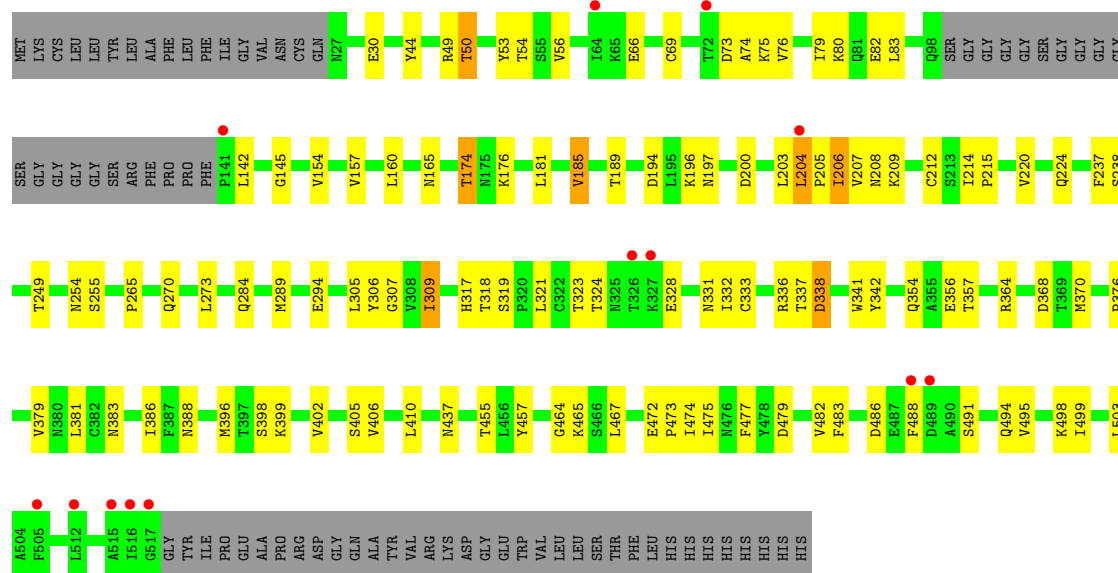


• Molecule 1: Fusion glycoprotein F0,Fibrin





• Molecule 1: Fusion glycoprotein F0,Fibrin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	159.33Å 168.67Å 189.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	126.01 – 2.92 126.01 – 2.92	Depositor EDS
% Data completeness (in resolution range)	67.2 (126.01-2.92) 67.3 (126.01-2.92)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.197 , 0.255 (Not available) , 0.245	Depositor DCC
R_{free} test set	2005 reflections (1.81%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 61.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	20848	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.20	0/3565	0.42	1/4834 (0.0%)
1	B	0.18	0/3525	0.44	2/4781 (0.0%)
1	C	0.19	0/3519	0.44	0/4773
1	D	0.16	0/3524	0.39	0/4779
1	E	0.17	0/3516	0.40	0/4768
1	F	0.17	0/3515	0.42	1/4767 (0.0%)
All	All	0.18	0/21164	0.42	4/28702 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	214	ILE	CG1-CB-CG2	-6.66	90.72	110.70
1	A	67	PRO	N-CA-CB	-5.73	97.23	103.25
1	B	214	ILE	CB-CA-C	5.18	116.08	111.00
1	F	265	PRO	CA-N-CD	-5.03	104.95	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	140	PHE	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3510	0	3550	76	0
1	B	3472	0	3517	73	0
1	C	3466	0	3512	81	0
1	D	3472	0	3523	74	0
1	E	3465	0	3517	80	0
1	F	3463	0	3515	70	0
All	All	20848	0	21134	437	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (437) 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:F:324:THR:HG21	1:F:437:ASN:HB3	1.53	0.90
1:C:216:ASN:OD1	1:C:218:GLU:N	2.08	0.85
1:F:66:GLU:OE2	1:F:66:GLU:N	2.10	0.84
1:A:381:LEU:HB3	1:A:388:ASN:HD22	1.44	0.83
1:D:176:LYS:NZ	1:D:263:ASP:OD2	2.10	0.81
1:D:310:ASP:OD1	1:D:364:ARG:NH2	2.13	0.81
1:F:337:THR:HG22	1:F:396:MET:HG2	1.63	0.79
1:A:332:ILE:HG22	1:A:399:LYS:HE2	1.66	0.77
1:C:26:GLN:OE1	1:C:27:ASN:N	2.18	0.76
1:E:253:THR:HG22	1:E:255:SER:H	1.52	0.75
1:E:403:SER:HB3	1:E:417:TYR:H	1.51	0.75
1:A:139:PRO:HG2	1:A:142:LEU:HD13	1.68	0.73
1:D:167:ILE:HG22	1:D:179:VAL:HG21	1.70	0.72
1:A:141:PRO:HD2	1:A:142:LEU:HD12	1.69	0.72
1:D:273:LEU:HD13	1:D:364:ARG:HH11	1.53	0.72
1:A:49:ARG:HD3	1:A:368:ASP:OD2	1.90	0.71
1:E:26:GLN:O	1:E:27:ASN:ND2	2.24	0.71
1:C:206:ILE:HG13	1:C:207:VAL:HG13	1.73	0.70
1:C:370:MET:HA	1:F:455:THR:HG23	1.74	0.70
1:D:40:VAL:HG12	1:D:316:LEU:HD12	1.73	0.70
1:F:30:GLU:HB2	1:F:410:LEU:HD21	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:45:LEU:HD12	1:C:363:ASN:HD21	1.57	0.69
1:C:196:LYS:HE3	1:C:295:GLU:OE2	1.91	0.69
1:E:73:ASP:OD2	1:E:74:ALA:N	2.26	0.69
1:E:336:ARG:HD3	1:E:386:ILE:HD12	1.73	0.69
1:F:270:GLN:HG2	1:F:309:ILE:HD12	1.75	0.68
1:D:316:LEU:HD23	1:D:339:ARG:HA	1.74	0.68
1:D:395:ILE:HD13	1:D:492:ILE:HD13	1.75	0.67
1:B:204:LEU:HD12	1:B:208:ASN:HB2	1.75	0.67
1:D:479:ASP:HB3	1:D:482:VAL:HG22	1.77	0.67
1:A:171:LEU:HD11	1:A:189:THR:HG22	1.76	0.66
1:D:410:LEU:HD22	1:D:464:GLY:HA3	1.77	0.66
1:B:232:GLU:OE2	1:B:235:ARG:NH1	2.28	0.66
1:D:163:GLU:OE2	1:D:182:SER:HB3	1.96	0.66
1:F:354:GLN:O	1:F:357:THR:HG22	1.95	0.66
1:F:79:ILE:HD12	1:F:203:LEU:HD11	1.78	0.65
1:C:59:ILE:HG23	1:C:193:LEU:HB3	1.78	0.65
1:C:66:GLU:N	1:C:66:GLU:OE1	2.28	0.65
1:B:66:GLU:HG3	1:B:67:PRO:HD2	1.77	0.65
1:A:37:CYS:HB2	1:A:321:LEU:HD13	1.77	0.65
1:C:26:GLN:HG3	1:C:363:ASN:ND2	2.12	0.65
1:E:260:LEU:O	1:E:264:MET:HG3	1.97	0.63
1:E:237:PHE:HD1	1:E:289:MET:HE2	1.62	0.63
1:B:59:ILE:HG12	1:B:193:LEU:HB3	1.80	0.63
1:B:487:GLU:OE2	1:B:498:LYS:HE2	1.99	0.63
1:B:164:VAL:HG11	1:B:293:LYS:HE2	1.81	0.63
1:F:76:VAL:HG12	1:F:80:LYS:HE3	1.80	0.63
1:B:281:VAL:O	1:B:285:SER:OG	2.15	0.62
1:D:48:LEU:HB2	1:D:308:VAL:HB	1.81	0.62
1:F:386:ILE:HG21	1:F:474:ILE:HD13	1.82	0.62
1:D:486:ASP:OD2	1:F:498:LYS:NZ	2.32	0.62
1:A:381:LEU:HB3	1:A:388:ASN:ND2	2.13	0.62
1:B:210:GLN:CD	1:B:210:GLN:H	2.06	0.61
1:E:229:ARG:O	1:E:233:ILE:HG12	2.00	0.61
1:D:79:ILE:HG12	1:D:220:VAL:HG22	1.82	0.61
1:B:93:LEU:HG	1:B:234:THR:HG23	1.83	0.61
1:D:432:ILE:HD11	1:D:447:VAL:HG22	1.83	0.60
1:E:423:THR:HB	1:E:451:SER:HB3	1.83	0.60
1:A:168:LYS:NZ	1:A:294:GLU:O	2.25	0.60
1:E:97:MET:HE1	1:E:289:MET:HG3	1.84	0.59
1:F:206:ILE:HG13	1:F:207:VAL:HG23	1.84	0.59
1:D:174:THR:HG22	1:D:176:LYS:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:336:ARG:NH2	1:E:383:ASN:OD1	2.36	0.59
1:A:178:VAL:HG22	1:A:188:LEU:HD23	1.84	0.59
1:A:82:GLU:HG3	1:A:224:GLN:HG2	1.83	0.59
1:A:46:SER:HB2	1:A:48:LEU:HD13	1.84	0.59
1:B:206:ILE:HG22	1:B:207:VAL:HG23	1.84	0.59
1:E:491:SER:H	1:E:494:GLN:HB2	1.68	0.58
1:A:445:LYS:O	1:A:445:LYS:HG2	2.03	0.58
1:C:321:LEU:HD11	1:C:473:PRO:HB3	1.85	0.58
1:C:153:ALA:O	1:C:157:VAL:HG23	2.02	0.58
1:A:261:ILE:HA	1:A:264:MET:HE2	1.84	0.58
1:E:76:VAL:HG23	1:E:214:ILE:HG22	1.86	0.58
1:E:240:ASN:ND2	1:E:244:THR:HG22	2.18	0.58
1:E:92:GLU:O	1:E:96:LEU:HG	2.03	0.58
1:F:323:THR:O	1:F:331:ASN:ND2	2.34	0.58
1:B:325:ASN:O	1:B:327:LYS:NZ	2.30	0.57
1:C:96:LEU:HD21	1:C:237:PHE:HB3	1.85	0.57
1:D:61:LEU:O	1:D:295:GLU:HB3	2.04	0.57
1:E:338:ASP:OD2	1:E:338:ASP:N	2.36	0.57
1:D:193:LEU:HD21	1:D:195:LEU:HG	1.85	0.57
1:D:65:LYS:H	1:D:65:LYS:HD3	1.68	0.57
1:E:44:TYR:HB2	1:E:313:CYS:HB2	1.86	0.57
1:F:321:LEU:HD11	1:F:473:PRO:HB3	1.86	0.57
1:C:73:ASP:OD1	1:C:74:ALA:N	2.36	0.57
1:E:424:ALA:HB3	1:E:433:LYS:HB3	1.86	0.57
1:F:196:LYS:HG3	1:F:200:ASP:OD2	2.03	0.57
1:A:386:ILE:HG21	1:A:474:ILE:HD13	1.85	0.57
1:B:422:CYS:HB2	1:B:435:PHE:HB2	1.86	0.57
1:C:65:LYS:H	1:C:65:LYS:HD3	1.69	0.57
1:B:99:SER:C	1:E:361:GLN:HB3	2.29	0.57
1:A:318:THR:HG21	1:A:336:ARG:HB2	1.87	0.56
1:E:422:CYS:HB2	1:E:435:PHE:HB2	1.87	0.56
1:B:503:LEU:O	1:B:507:ARG:N	2.39	0.56
1:D:87:LYS:NZ	1:D:87:LYS:HB3	2.20	0.56
1:A:284:GLN:OE1	1:A:306:TYR:OH	2.11	0.56
1:F:76:VAL:HG22	1:F:215:PRO:HD3	1.88	0.56
1:D:171:LEU:HD11	1:D:189:THR:HG22	1.88	0.56
1:F:56:VAL:HB	1:F:189:THR:HG22	1.86	0.56
1:F:472:GLU:HG2	1:F:477:PHE:HE1	1.71	0.56
1:B:163:GLU:OE2	1:B:182:SER:HB3	2.06	0.56
1:A:66:GLU:HG2	1:A:67:PRO:CD	2.36	0.55
1:B:487:GLU:HB3	1:B:490:ALA:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:204:LEU:HG	1:F:208:ASN:HB2	1.88	0.55
1:F:479:ASP:HB3	1:F:482:VAL:HG22	1.88	0.55
1:A:326:THR:HB	1:A:330:SER:HB3	1.87	0.55
1:C:210:GLN:N	1:C:210:GLN:OE1	2.39	0.55
1:E:237:PHE:HE2	1:E:244:THR:HG23	1.71	0.55
1:A:142:LEU:HD11	1:A:353:PRO:HG3	1.87	0.55
1:E:206:ILE:HD13	1:E:215:PRO:HB3	1.89	0.55
1:B:337:THR:HG22	1:B:396:MET:HG2	1.87	0.55
1:E:237:PHE:CD1	1:E:289:MET:HE2	2.41	0.55
1:F:410:LEU:HD13	1:F:464:GLY:HA3	1.88	0.55
1:C:65:LYS:H	1:C:65:LYS:CD	2.19	0.55
1:D:321:LEU:HD11	1:D:473:PRO:HB3	1.88	0.55
1:C:406:VAL:HG22	1:D:144:VAL:HB	1.89	0.54
1:D:97:MET:HG3	1:D:98:GLN:HB3	1.89	0.54
1:F:338:ASP:OD1	1:F:338:ASP:N	2.28	0.54
1:A:220:VAL:O	1:A:224:GLN:HG3	2.08	0.54
1:C:199:ILE:O	1:C:204:LEU:N	2.33	0.54
1:F:376:PRO:O	1:F:379:VAL:HG12	2.07	0.54
1:D:88:ASN:O	1:D:92:GLU:HG3	2.08	0.54
1:D:294:GLU:HA	1:D:294:GLU:OE2	2.08	0.54
1:A:498:LYS:NZ	1:B:486:ASP:OD1	2.37	0.53
1:B:257:LEU:HD23	1:B:278:VAL:HG13	1.91	0.53
1:E:176:LYS:HD3	1:E:263:ASP:OD2	2.09	0.53
1:A:210:GLN:H	1:A:210:GLN:CD	2.16	0.53
1:D:79:ILE:HD12	1:D:203:LEU:HD11	1.91	0.53
1:D:261:ILE:HD13	1:D:274:MET:HB3	1.91	0.53
1:E:206:ILE:HG22	1:E:207:VAL:HG13	1.89	0.53
1:E:272:LYS:HG3	1:E:273:LEU:N	2.23	0.53
1:C:333:CYS:SG	1:C:401:ASP:HB3	2.48	0.53
1:A:66:GLU:HG2	1:A:67:PRO:HD2	1.90	0.53
1:E:362:SER:OG	1:E:363:ASN:N	2.41	0.53
1:E:511:GLU:O	1:E:511:GLU:HG3	2.08	0.53
1:F:354:GLN:O	1:F:356:GLU:N	2.42	0.53
1:A:96:LEU:HD11	1:B:279:PRO:HG2	1.91	0.53
1:F:50:THR:HB	1:F:307:GLY:H	1.74	0.53
1:F:338:ASP:HB2	1:F:342:TYR:OH	2.10	0.52
1:C:48:LEU:HB2	1:C:308:VAL:HB	1.90	0.52
1:E:381:LEU:HD23	1:E:388:ASN:HD22	1.74	0.52
1:C:338:ASP:HB2	1:C:342:TYR:OH	2.09	0.52
1:F:49:ARG:HE	1:F:368:ASP:CG	2.17	0.52
1:C:49:ARG:HE	1:C:368:ASP:CG	2.16	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:247:VAL:HG13	1:E:287:SER:HB2	1.91	0.52
1:A:67:PRO:HA	1:A:207:VAL:HG13	1.90	0.52
1:E:62:SER:HB2	1:E:196:LYS:HA	1.90	0.52
1:E:253:THR:HG22	1:E:255:SER:N	2.22	0.52
1:B:484:PRO:HB3	1:B:498:LYS:HE3	1.92	0.52
1:A:479:ASP:HB3	1:A:482:VAL:HG22	1.91	0.52
1:F:53:TYR:HB2	1:F:305:LEU:HD13	1.90	0.52
1:F:328:GLU:OE2	1:F:328:GLU:HA	2.10	0.52
1:B:62:SER:HB2	1:B:196:LYS:HA	1.92	0.51
1:B:424:ALA:HB3	1:B:433:LYS:HB3	1.91	0.51
1:A:334:LEU:HB3	1:A:475:ILE:HD13	1.91	0.51
1:A:356:GLU:N	1:A:356:GLU:OE1	2.43	0.51
1:E:232:GLU:HB2	1:E:250:TYR:CD1	2.44	0.51
1:C:334:LEU:HD21	1:C:474:ILE:HD11	1.92	0.51
1:E:194:ASP:OD2	1:E:197:ASN:HB2	2.11	0.51
1:F:203:LEU:O	1:F:206:ILE:HG12	2.09	0.51
1:F:79:ILE:HG12	1:F:220:VAL:HG22	1.93	0.51
1:D:338:ASP:O	1:D:342:TYR:OH	2.29	0.51
1:E:26:GLN:CD	1:E:27:ASN:H	2.17	0.51
1:F:237:PHE:CE2	1:F:289:MET:HB2	2.45	0.51
1:B:206:ILE:HG23	1:B:213:SER:O	2.11	0.51
1:D:66:GLU:HG2	1:D:67:PRO:HD2	1.93	0.50
1:F:273:LEU:HD11	1:F:364:ARG:HD3	1.92	0.50
1:D:403:SER:HB3	1:D:417:TYR:H	1.75	0.50
1:F:194:ASP:OD2	1:F:197:ASN:HB2	2.11	0.50
1:C:49:ARG:NH2	1:C:368:ASP:OD1	2.41	0.50
1:C:270:GLN:O	1:C:274:MET:HG3	2.11	0.50
1:B:164:VAL:HG21	1:B:293:LYS:HG3	1.93	0.50
1:D:159:HIS:CD2	1:D:291:ILE:HG22	2.47	0.50
1:A:79:ILE:HD12	1:A:215:PRO:CG	2.41	0.50
1:D:91:THR:O	1:D:95:LEU:HD23	2.12	0.50
1:F:82:GLU:HG3	1:F:224:GLN:HG2	1.92	0.50
1:B:316:LEU:HD23	1:B:338:ASP:O	2.12	0.50
1:A:57:ILE:HD13	1:A:252:LEU:HD13	1.93	0.50
1:C:281:VAL:O	1:C:285:SER:OG	2.20	0.50
1:E:239:VAL:HG23	1:E:240:ASN:OD1	2.12	0.50
1:F:76:VAL:HG21	1:F:214:ILE:HG22	1.94	0.50
1:E:247:VAL:HG12	1:E:251:MET:HB3	1.94	0.49
1:E:492:ILE:O	1:E:495:VAL:HG12	2.12	0.49
1:F:157:VAL:HG11	1:F:181:LEU:HB3	1.94	0.49
1:C:79:ILE:HG12	1:C:220:VAL:HG22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:73:ASP:HB2	1:D:214:ILE:HD12	1.93	0.49
1:D:49:ARG:NH1	1:D:368:ASP:OD2	2.45	0.49
1:B:90:VAL:O	1:B:94:GLN:HG3	2.13	0.49
1:D:31:GLU:OE1	1:D:33:TYR:OH	2.27	0.49
1:A:423:THR:HG23	1:A:431:ILE:HG23	1.94	0.48
1:A:513:LEU:HD11	1:E:512:LEU:HD21	1.95	0.48
1:B:44:TYR:CD2	1:B:363:ASN:HA	2.48	0.48
1:B:174:THR:OG1	1:B:175:ASN:N	2.46	0.48
1:A:245:THR:HG23	1:A:285:SER:O	2.12	0.48
1:D:291:ILE:HG12	1:D:298:ALA:HB3	1.96	0.48
1:C:487:GLU:HB3	1:C:490:ALA:HB2	1.96	0.48
1:A:397:THR:OG1	1:A:485:SER:HA	2.14	0.48
1:D:93:LEU:HD13	1:D:297:LEU:CD1	2.44	0.48
1:A:63:ASN:HD22	1:A:295:GLU:HG2	1.77	0.48
1:A:73:ASP:OD1	1:A:74:ALA:N	2.46	0.48
1:A:338:ASP:OD1	1:A:338:ASP:N	2.44	0.48
1:A:410:LEU:CD1	1:A:466:SER:HB2	2.44	0.48
1:B:491:SER:O	1:B:495:VAL:HG23	2.14	0.48
1:B:505:PHE:O	1:B:509:SER:HB3	2.14	0.48
1:A:388:ASN:OD1	1:A:388:ASN:C	2.55	0.48
1:D:96:LEU:HD13	1:D:237:PHE:HB3	1.94	0.48
1:F:54:THR:OG1	1:F:154:VAL:HG21	2.13	0.48
1:C:310:ASP:OD1	1:C:364:ARG:NH1	2.46	0.48
1:C:200:ASP:HA	1:C:204:LEU:HB3	1.94	0.48
1:A:444:ASN:HB3	1:A:459:VAL:HG11	1.95	0.48
1:B:206:ILE:HD12	1:B:213:SER:O	2.14	0.48
1:C:56:VAL:HB	1:C:189:THR:HG22	1.95	0.48
1:F:488:PHE:CD1	1:F:488:PHE:C	2.92	0.48
1:F:488:PHE:C	1:F:488:PHE:HD1	2.22	0.48
1:C:61:LEU:O	1:C:295:GLU:HB3	2.13	0.47
1:C:502:SER:O	1:C:506:ILE:HG13	2.14	0.47
1:F:270:GLN:CG	1:F:309:ILE:HD12	2.43	0.47
1:B:98:GLN:O	1:B:98:GLN:HG2	2.14	0.47
1:C:293:LYS:HB3	1:C:293:LYS:HE2	1.68	0.47
1:E:240:ASN:HD22	1:E:244:THR:HG22	1.78	0.47
1:A:47:ALA:O	1:A:366:PHE:HA	2.15	0.47
1:A:482:VAL:HG21	1:A:503:LEU:HD21	1.95	0.47
1:B:427:LYS:HB3	1:B:448:ASP:OD1	2.14	0.47
1:A:75:LYS:NZ	1:B:218:GLU:OE2	2.44	0.47
1:B:503:LEU:O	1:B:507:ARG:HB2	2.14	0.47
1:C:26:GLN:HG3	1:C:363:ASN:CG	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:47:ALA:HB2	1:C:364:ARG:HD2	1.96	0.47
1:F:332:ILE:HD12	1:F:483:PHE:CD2	2.50	0.47
1:F:333:CYS:HB2	1:F:398:SER:O	2.15	0.47
1:A:152:VAL:O	1:A:156:LYS:HG3	2.15	0.47
1:E:97:MET:HE1	1:E:289:MET:CG	2.45	0.47
1:E:281:VAL:O	1:E:285:SER:OG	2.25	0.47
1:A:63:ASN:HB2	1:A:295:GLU:OE1	2.15	0.47
1:A:354:GLN:HB2	1:A:357:THR:HG23	1.97	0.47
1:B:56:VAL:HB	1:B:189:THR:HG22	1.97	0.47
1:E:171:LEU:HD11	1:E:189:THR:HG22	1.97	0.47
1:D:246:PRO:HB3	1:D:283:GLN:HA	1.96	0.46
1:E:232:GLU:OE2	1:E:235:ARG:HD2	2.14	0.46
1:B:280:ILE:HG13	1:B:361:GLN:HG3	1.96	0.46
1:E:495:VAL:O	1:E:499:ILE:HG13	2.15	0.46
1:B:335:THR:HG22	1:B:336:ARG:O	2.15	0.46
1:C:216:ASN:ND2	1:C:218:GLU:OE1	2.43	0.46
1:B:349:VAL:HG23	1:B:377:PRO:HA	1.97	0.46
1:A:204:LEU:HB3	1:A:205:PRO:HD3	1.98	0.46
1:A:334:LEU:CB	1:A:475:ILE:HD13	2.44	0.46
1:B:354:GLN:O	1:B:357:THR:HG22	2.16	0.46
1:C:352:PHE:CE1	1:C:372:SER:HB3	2.50	0.46
1:D:273:LEU:HD11	1:D:366:PHE:CZ	2.50	0.46
1:B:36:THR:HG22	1:B:386:ILE:HD12	1.96	0.46
1:B:52:TRP:CE3	1:B:302:GLN:HG2	2.51	0.46
1:F:336:ARG:NH2	1:F:383:ASN:OD1	2.49	0.46
1:C:261:ILE:HA	1:C:264:MET:HG3	1.97	0.46
1:A:249:THR:OG1	1:E:235:ARG:NH1	2.44	0.46
1:A:326:THR:HA	1:A:327:LYS:HZ2	1.81	0.46
1:D:204:LEU:HD11	1:D:208:ASN:ND2	2.31	0.46
1:F:75:LYS:HB2	1:F:215:PRO:HD2	1.98	0.46
1:C:513:LEU:HD12	1:D:512:LEU:HD11	1.98	0.45
1:F:495:VAL:O	1:F:499:ILE:HG12	2.16	0.45
1:A:79:ILE:HD13	1:A:203:LEU:HD11	1.98	0.45
1:D:197:ASN:HB3	1:D:201:LYS:HE3	1.97	0.45
1:E:487:GLU:HA	1:E:487:GLU:OE1	2.16	0.45
1:A:376:PRO:O	1:A:379:VAL:HG12	2.16	0.45
1:D:75:LYS:HD2	1:D:215:PRO:O	2.15	0.45
1:D:338:ASP:OD1	1:D:338:ASP:N	2.37	0.45
1:A:269:ASP:OD1	1:A:269:ASP:N	2.47	0.45
1:F:317:HIS:HB3	1:F:406:VAL:HG11	1.98	0.45
1:F:396:MET:HB3	1:F:488:PHE:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:258:LEU:HD23	1:E:258:LEU:HA	1.78	0.45
1:B:236:GLU:OE1	1:B:248:SER:OG	2.27	0.45
1:D:164:VAL:HG21	1:D:293:LYS:HE2	1.99	0.45
1:C:62:SER:HB2	1:C:196:LYS:HA	1.97	0.45
1:A:77:LYS:HE2	1:A:81:GLN:HE21	1.82	0.45
1:A:197:ASN:O	1:A:201:LYS:HG3	2.17	0.45
1:B:140:PHE:HB3	1:B:142:LEU:HD13	1.99	0.45
1:E:399:LYS:HG3	1:E:485:SER:HB2	1.98	0.45
1:F:204:LEU:N	1:F:205:PRO:HD2	2.32	0.45
1:A:65:LYS:HB2	1:A:68:LYS:HE2	1.97	0.45
1:B:254:ASN:OD1	1:B:278:VAL:HG11	2.17	0.45
1:C:364:ARG:HG2	1:C:366:PHE:CZ	2.51	0.45
1:B:99:SER:HB2	1:E:361:GLN:OE1	2.17	0.44
1:A:443:SER:OG	1:A:445:LYS:HD2	2.17	0.44
1:C:221:ILE:HD12	1:D:217:ILE:HD11	1.99	0.44
1:C:364:ARG:HE	1:C:364:ARG:HB2	1.63	0.44
1:C:479:ASP:C	1:C:479:ASP:OD2	2.60	0.44
1:D:316:LEU:HD11	1:D:336:ARG:NH2	2.32	0.44
1:B:235:ARG:NE	1:E:250:TYR:HE2	2.15	0.44
1:B:235:ARG:CZ	1:E:250:TYR:HE2	2.30	0.44
1:B:240:ASN:HB3	1:B:243:VAL:O	2.18	0.44
1:C:188:LEU:HD21	1:C:263:ASP:HB3	2.00	0.44
1:A:59:ILE:HG23	1:A:193:LEU:HB3	1.98	0.44
1:C:505:PHE:CD1	1:C:505:PHE:C	2.95	0.44
1:B:253:THR:OG1	1:B:256:GLU:HG3	2.17	0.44
1:D:72:THR:O	1:D:72:THR:OG1	2.30	0.44
1:E:52:TRP:CE3	1:E:302:GLN:HG2	2.52	0.44
1:F:154:VAL:HG22	1:F:185:VAL:HG11	1.99	0.44
1:F:318:THR:HG21	1:F:336:ARG:HB2	2.00	0.44
1:A:394:LYS:NZ	1:B:400:THR:OG1	2.51	0.44
1:E:336:ARG:NH1	1:E:338:ASP:OD1	2.50	0.44
1:E:72:THR:O	1:E:72:THR:OG1	2.33	0.43
1:E:423:THR:HG23	1:E:431:ILE:HG13	2.00	0.43
1:B:79:ILE:HD13	1:B:79:ILE:HA	1.93	0.43
1:C:327:LYS:O	1:C:330:SER:OG	2.25	0.43
1:D:66:GLU:CG	1:D:67:PRO:HD2	2.49	0.43
1:C:507:ARG:NH1	1:C:508:LYS:HA	2.33	0.43
1:F:44:TYR:CD2	1:F:341:TRP:HH2	2.36	0.43
1:F:465:LYS:HE2	1:F:465:LYS:HB2	1.58	0.43
1:A:138:PRO:HG2	1:A:144:VAL:HG22	2.01	0.43
1:A:394:LYS:HB3	1:A:394:LYS:HE3	1.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:93:LEU:HB3	1:C:292:ILE:HD11	2.00	0.43
1:C:512:LEU:HD12	1:C:512:LEU:HA	1.65	0.43
1:E:279:PRO:O	1:E:283:GLN:HG3	2.17	0.43
1:B:141:PRO:HD2	1:B:142:LEU:HD12	2.00	0.43
1:B:416:CYS:O	1:B:437:ASN:HA	2.18	0.43
1:C:497:GLU:O	1:C:501:GLN:HG3	2.19	0.43
1:A:31:GLU:OE1	1:A:33:TYR:OH	2.25	0.43
1:C:61:LEU:O	1:C:196:LYS:HB2	2.17	0.43
1:C:83:LEU:HD23	1:C:83:LEU:HA	1.90	0.43
1:C:176:LYS:NZ	1:C:190:SER:HB2	2.33	0.43
1:C:399:LYS:HG3	1:C:485:SER:HB2	2.00	0.43
1:E:352:PHE:CE1	1:E:372:SER:HB3	2.53	0.43
1:A:444:ASN:HB3	1:A:459:VAL:CG1	2.48	0.43
1:D:158:LEU:HD23	1:D:158:LEU:HA	1.88	0.43
1:D:335:THR:HB	1:D:396:MET:HG2	2.01	0.43
1:D:429:ARG:HG3	1:D:429:ARG:HH11	1.84	0.43
1:E:79:ILE:HG12	1:E:220:VAL:HG22	2.01	0.43
1:F:410:LEU:HD23	1:F:410:LEU:N	2.33	0.43
1:A:203:LEU:HD12	1:A:203:LEU:HA	1.72	0.43
1:B:388:ASN:OD1	1:B:388:ASN:C	2.62	0.43
1:C:183:ASN:OD1	1:C:185:VAL:HG12	2.18	0.43
1:F:145:GLY:HA3	1:F:370:MET:SD	2.59	0.43
1:B:235:ARG:CZ	1:E:250:TYR:CE2	3.01	0.43
1:F:73:ASP:OD2	1:F:74:ALA:N	2.52	0.43
1:F:157:VAL:O	1:F:160:LEU:HB2	2.19	0.43
1:F:381:LEU:HB2	1:F:388:ASN:ND2	2.34	0.43
1:B:61:LEU:O	1:B:295:GLU:HB3	2.19	0.43
1:B:326:THR:OG1	1:B:331:ASN:OD1	2.34	0.43
1:B:401:ASP:O	1:B:401:ASP:OD2	2.37	0.43
1:D:46:SER:HB2	1:D:48:LEU:HD13	2.01	0.43
1:F:284:GLN:OE1	1:F:306:TYR:OH	2.18	0.43
1:B:293:LYS:O	1:B:296:VAL:HG12	2.19	0.42
1:D:315:LYS:HB2	1:D:341:TRP:CZ3	2.54	0.42
1:F:332:ILE:HG13	1:F:475:ILE:HD11	2.01	0.42
1:D:403:SER:HB2	1:D:416:CYS:HA	2.02	0.42
1:E:163:GLU:OE2	1:E:182:SER:HB3	2.19	0.42
1:E:390:LYS:HB3	1:E:390:LYS:HE3	1.74	0.42
1:A:217:ILE:HD12	1:A:217:ILE:HA	1.85	0.42
1:B:246:PRO:HB3	1:B:283:GLN:HA	1.99	0.42
1:C:53:TYR:OH	1:C:188:LEU:HD12	2.19	0.42
1:C:492:ILE:HD13	1:C:492:ILE:HA	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:504:ALA:O	1:C:508:LYS:N	2.46	0.42
1:D:45:LEU:HD23	1:D:45:LEU:HA	1.85	0.42
1:B:199:ILE:HA	1:B:203:LEU:HB2	2.01	0.42
1:C:197:ASN:O	1:C:201:LYS:HG3	2.19	0.42
1:C:507:ARG:O	1:C:511:GLU:HG2	2.19	0.42
1:D:157:VAL:O	1:D:163:GLU:HG3	2.19	0.42
1:E:203:LEU:HD21	1:E:223:PHE:CD2	2.55	0.42
1:F:209:LYS:HE2	1:F:209:LYS:HB2	1.81	0.42
1:A:233:ILE:HG23	1:A:251:MET:HE1	2.01	0.42
1:A:394:LYS:HA	1:A:491:SER:HA	2.02	0.42
1:D:236:GLU:O	1:D:240:ASN:HB2	2.19	0.42
1:D:424:ALA:HB3	1:D:433:LYS:HB3	2.01	0.42
1:E:194:ASP:CG	1:E:197:ASN:HB2	2.44	0.42
1:F:503:LEU:HD23	1:F:503:LEU:HA	1.87	0.42
1:C:203:LEU:O	1:C:207:VAL:HG22	2.20	0.42
1:C:217:ILE:HD12	1:C:217:ILE:HA	1.72	0.42
1:D:50:THR:HG21	1:D:308:VAL:HG23	2.01	0.42
1:C:62:SER:OG	1:C:64:ILE:HG12	2.19	0.42
1:A:79:ILE:HG13	1:A:220:VAL:HG22	2.01	0.42
1:B:405:SER:HB2	1:B:452:VAL:HG21	2.02	0.42
1:C:316:LEU:HD23	1:C:338:ASP:O	2.20	0.42
1:D:273:LEU:HD13	1:D:364:ARG:NH1	2.26	0.42
1:E:217:ILE:HD12	1:E:217:ILE:HA	1.92	0.42
1:A:65:LYS:H	1:A:65:LYS:HG2	1.58	0.42
1:C:49:ARG:HH21	1:C:368:ASP:CG	2.28	0.42
1:C:216:ASN:OD1	1:C:217:ILE:N	2.52	0.42
1:C:232:GLU:HG3	1:C:250:TYR:CZ	2.54	0.42
1:D:206:ILE:HG22	1:D:213:SER:HB2	2.02	0.42
1:F:165:ASN:HD21	1:F:294:GLU:CD	2.27	0.42
1:B:481:LEU:HD13	1:B:481:LEU:HA	1.88	0.41
1:C:61:LEU:HD11	1:C:297:LEU:HB2	2.02	0.41
1:C:432:ILE:HD11	1:C:447:VAL:HG22	2.02	0.41
1:E:233:ILE:HG23	1:E:251:MET:HE1	2.01	0.41
1:F:273:LEU:HD11	1:F:364:ARG:CD	2.50	0.41
1:B:365:VAL:HG12	1:B:367:CYS:SG	2.60	0.41
1:D:197:ASN:HD22	1:D:201:LYS:HE3	1.84	0.41
1:E:370:MET:HE2	1:E:370:MET:HB3	1.82	0.41
1:C:475:ILE:HD12	1:C:475:ILE:HA	1.86	0.41
1:E:37:CYS:HB2	1:E:321:LEU:HD13	2.03	0.41
1:B:264:MET:HE1	1:B:274:MET:HE1	2.01	0.41
1:A:235:ARG:O	1:A:239:VAL:HG23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:TYR:HD2	1:B:363:ASN:HA	1.85	0.41
1:B:60:GLU:O	1:B:196:LYS:N	2.53	0.41
1:D:416:CYS:O	1:D:437:ASN:HA	2.21	0.41
1:E:209:LYS:HD2	1:E:211:SER:OG	2.20	0.41
1:F:160:LEU:HD23	1:F:160:LEU:HA	1.95	0.41
1:A:96:LEU:CD2	1:A:237:PHE:HB3	2.51	0.41
1:B:403:SER:HA	1:B:415:SER:O	2.21	0.41
1:E:254:ASN:OD1	1:E:278:VAL:HG11	2.20	0.41
1:A:53:TYR:HB2	1:A:305:LEU:HD13	2.02	0.41
1:D:193:LEU:CD2	1:D:195:LEU:HG	2.50	0.41
1:D:157:VAL:HG11	1:D:181:LEU:HB3	2.03	0.41
1:D:267:THR:HG23	1:D:270:GLN:H	1.85	0.41
1:F:174:THR:HB	1:F:176:LYS:H	1.86	0.41
1:A:233:ILE:HG12	1:A:251:MET:HE2	2.03	0.41
1:C:221:ILE:O	1:C:225:GLN:HG3	2.21	0.41
1:C:235:ARG:HD3	1:F:249:THR:OG1	2.21	0.41
1:D:157:VAL:HG21	1:D:183:ASN:ND2	2.36	0.41
1:D:162:GLY:O	1:D:166:LYS:HB2	2.21	0.41
1:D:257:LEU:HD13	1:D:278:VAL:HG13	2.03	0.41
1:E:165:ASN:ND2	1:E:294:GLU:OE1	2.53	0.41
1:A:61:LEU:C	1:A:196:LYS:HB2	2.46	0.41
1:A:414:VAL:HG21	1:A:435:PHE:CE2	2.56	0.41
1:B:396:MET:HE3	1:B:396:MET:HB2	1.94	0.41
1:C:37:CYS:HB2	1:C:321:LEU:HB2	2.03	0.41
1:C:148:ILE:HG21	1:C:243:VAL:HG11	2.02	0.41
1:E:167:ILE:HG23	1:E:189:THR:HG21	2.03	0.41
1:E:198:TYR:CD1	1:E:198:TYR:C	2.99	0.41
1:F:405:SER:HB3	1:F:457:TYR:CE2	2.56	0.41
1:F:491:SER:H	1:F:494:GLN:HB2	1.86	0.41
1:B:431:ILE:H	1:B:431:ILE:HD12	1.87	0.40
1:C:87:LYS:NZ	1:C:87:LYS:HB3	2.36	0.40
1:D:37:CYS:SG	1:D:319:SER:HB3	2.61	0.40
1:E:57:ILE:HB	1:E:299:TYR:CE1	2.57	0.40
1:C:385:ASP:O	1:C:388:ASN:HB3	2.21	0.40
1:E:334:LEU:HB3	1:E:475:ILE:HD13	2.03	0.40
1:E:489:ASP:OD2	1:E:489:ASP:C	2.64	0.40
1:C:29:THR:HA	1:C:465:LYS:O	2.20	0.40
1:D:49:ARG:HH21	1:D:52:TRP:NE1	2.20	0.40
1:E:200:ASP:HA	1:E:204:LEU:HB2	2.04	0.40
1:E:203:LEU:HA	1:E:203:LEU:HD12	1.81	0.40
1:E:470:LYS:HE3	1:E:470:LYS:HB2	1.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:331:ASN:O	1:F:399:LYS:HD3	2.22	0.40
1:B:417:TYR:HE2	1:B:438:GLY:HA2	1.86	0.40
1:C:192:VAL:HB	1:C:229:ARG:HH12	1.86	0.40
1:C:192:VAL:HB	1:C:229:ARG:NH1	2.37	0.40
1:D:461:LYS:HA	1:D:461:LYS:HD2	1.75	0.40
1:E:216:ASN:ND2	1:E:218:GLU:HB2	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	453/522 (87%)	420 (93%)	33 (7%)	0	100	100
1	B	445/522 (85%)	427 (96%)	18 (4%)	0	100	100
1	C	444/522 (85%)	426 (96%)	18 (4%)	0	100	100
1	D	446/522 (85%)	436 (98%)	10 (2%)	0	100	100
1	E	445/522 (85%)	423 (95%)	22 (5%)	0	100	100
1	F	445/522 (85%)	418 (94%)	27 (6%)	0	100	100
All	All	2678/3132 (86%)	2550 (95%)	128 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	413/463 (89%)	390 (94%)	23 (6%)	19	48
1	B	411/463 (89%)	391 (95%)	20 (5%)	22	52
1	C	410/463 (89%)	393 (96%)	17 (4%)	27	60
1	D	410/463 (89%)	394 (96%)	16 (4%)	28	61
1	E	409/463 (88%)	390 (95%)	19 (5%)	24	56
1	F	409/463 (88%)	391 (96%)	18 (4%)	25	57
All	All	2462/2778 (89%)	2349 (95%)	113 (5%)	24	56

All (113) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	THR
1	A	35	SER
1	A	49	ARG
1	A	63	ASN
1	A	67	PRO
1	A	76	VAL
1	A	79	ILE
1	A	140	PHE
1	A	173	SER
1	A	174	THR
1	A	207	VAL
1	A	212	CYS
1	A	269	ASP
1	A	316	LEU
1	A	319	SER
1	A	326	THR
1	A	334	LEU
1	A	362	SER
1	A	410	LEU
1	A	420	THR
1	A	423	THR
1	A	486	ASP
1	A	501	GLN
1	B	69	CYS
1	B	76	VAL
1	B	161	GLU
1	B	207	VAL
1	B	212	CYS
1	B	254	ASN
1	B	292	ILE

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Mol	Chain	Res	Type
1	B	296	VAL
1	B	319	SER
1	B	344	ASP
1	B	363	ASN
1	B	423	THR
1	B	436	SER
1	B	439	CYS
1	B	442	VAL
1	B	456	LEU
1	B	462	GLN
1	B	474	ILE
1	B	508	LYS
1	B	509	SER
1	C	69	CYS
1	C	72	THR
1	C	79	ILE
1	C	84	ASP
1	C	142	LEU
1	C	161	GLU
1	C	196	LYS
1	C	199	ILE
1	C	212	CYS
1	C	213	SER
1	C	267	THR
1	C	283	GLN
1	C	287	SER
1	C	292	ILE
1	C	423	THR
1	C	436	SER
1	C	449	THR
1	D	35	SER
1	D	72	THR
1	D	96	LEU
1	D	212	CYS
1	D	239	VAL
1	D	254	ASN
1	D	255	SER
1	D	292	ILE
1	D	296	VAL
1	D	316	LEU
1	D	357	THR
1	D	390	LYS

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Mol	Chain	Res	Type
1	D	410	LEU
1	D	467	LEU
1	D	493	SER
1	D	495	VAL
1	E	26	GLN
1	E	35	SER
1	E	90	VAL
1	E	188	LEU
1	E	203	LEU
1	E	212	CYS
1	E	213	SER
1	E	249	THR
1	E	255	SER
1	E	257	LEU
1	E	272	LYS
1	E	327	LYS
1	E	362	SER
1	E	365	VAL
1	E	398	SER
1	E	425	SER
1	E	436	SER
1	E	442	VAL
1	E	449	THR
1	F	50	THR
1	F	69	CYS
1	F	83	LEU
1	F	142	LEU
1	F	174	THR
1	F	185	VAL
1	F	204	LEU
1	F	206	ILE
1	F	212	CYS
1	F	238	SER
1	F	254	ASN
1	F	255	SER
1	F	309	ILE
1	F	319	SER
1	F	338	ASP
1	F	402	VAL
1	F	467	LEU
1	F	486	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	ASN
1	A	81	GLN
1	A	380	ASN
1	B	94	GLN
1	B	270	GLN
1	B	361	GLN
1	B	380	ASN
1	B	460	ASN
1	B	494	GLN
1	C	268	ASN
1	C	270	GLN
1	C	283	GLN
1	C	363	ASN
1	C	437	ASN
1	C	462	GLN
1	C	496	ASN
1	D	208	ASN
1	D	262	ASN
1	D	277	ASN
1	D	283	GLN
1	E	159	HIS
1	E	165	ASN
1	E	268	ASN
1	E	388	ASN
1	E	501	GLN
1	F	317	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	457/522 (87%)	0.18	14 (3%)	51 41	16, 39, 79, 113	0
1	B	449/522 (86%)	0.03	13 (2%)	53 44	16, 35, 80, 118	0
1	C	448/522 (85%)	0.07	5 (1%)	78 71	15, 41, 76, 103	0
1	D	450/522 (86%)	0.02	9 (2%)	65 56	17, 37, 77, 122	0
1	E	449/522 (86%)	0.26	17 (3%)	44 36	18, 41, 83, 122	0
1	F	449/522 (86%)	0.20	13 (2%)	53 44	19, 40, 84, 120	0
All	All	2702/3132 (86%)	0.13	71 (2%)	57 47	15, 39, 80, 122	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	140	PHE	5.6
1	E	142	LEU	4.6
1	E	516	ILE	4.5
1	A	104	SER	4.2
1	C	141	PRO	4.1
1	A	140	PHE	3.9
1	D	512	LEU	3.8
1	E	401	ASP	3.8
1	F	326	THR	3.4
1	B	325	ASN	3.3
1	C	172	LEU	3.3
1	E	505	PHE	3.3
1	E	64	ILE	3.2
1	F	516	ILE	3.2
1	B	512	LEU	3.2
1	E	513	LEU	3.1
1	B	140	PHE	3.1
1	E	329	GLY	3.0
1	F	517	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	399	LYS	3.0
1	F	515	ALA	2.8
1	F	204	LEU	2.8
1	A	71	GLY	2.8
1	E	514	SER	2.8
1	B	72	THR	2.7
1	E	143	GLY	2.7
1	B	26	GLN	2.7
1	B	488	PHE	2.6
1	F	488	PHE	2.6
1	D	515	ALA	2.6
1	A	106	GLY	2.6
1	C	512	LEU	2.6
1	B	514	SER	2.6
1	D	481	LEU	2.6
1	D	53	TYR	2.5
1	B	505	PHE	2.5
1	E	399	LYS	2.4
1	B	513	LEU	2.4
1	D	400	THR	2.4
1	B	207	VAL	2.4
1	F	64	ILE	2.4
1	F	141	PRO	2.3
1	B	70	ASN	2.3
1	E	237	PHE	2.3
1	A	481	LEU	2.2
1	E	512	LEU	2.2
1	D	401	ASP	2.2
1	B	211	SER	2.2
1	E	517	GLY	2.2
1	A	138	PRO	2.2
1	A	328	GLU	2.2
1	F	489	ASP	2.2
1	A	398	SER	2.2
1	D	68	LYS	2.2
1	A	512	LEU	2.2
1	D	514	SER	2.2
1	B	507	ARG	2.1
1	F	327	LYS	2.1
1	D	513	LEU	2.1
1	A	357	THR	2.1
1	F	505	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	416	CYS	2.1
1	A	327	LYS	2.1
1	C	97	MET	2.1
1	E	495	VAL	2.1
1	A	484	PRO	2.1
1	A	216	ASN	2.1
1	E	211	SER	2.0
1	F	512	LEU	2.0
1	E	439	CYS	2.0
1	F	72	THR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.