Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 08:46 PM GMT

PDB ID	:	4U39
Title	:	Crystal Structure of FtsZ:MciZ Complex from Bacillus subtilis
Authors	:	Bisson-Filho, A.W.; Discola, K.F.; Castellen, P.; Blasios, V.; Martins, A.; Sforca, M.L.; Garcia, W.; Zeri, A.C.; Erickson, H.P.; Dessen, A.; Gueiros-Filho, F.J.
Deposited on	:	2014-07-19
Resolution	:	3.19 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

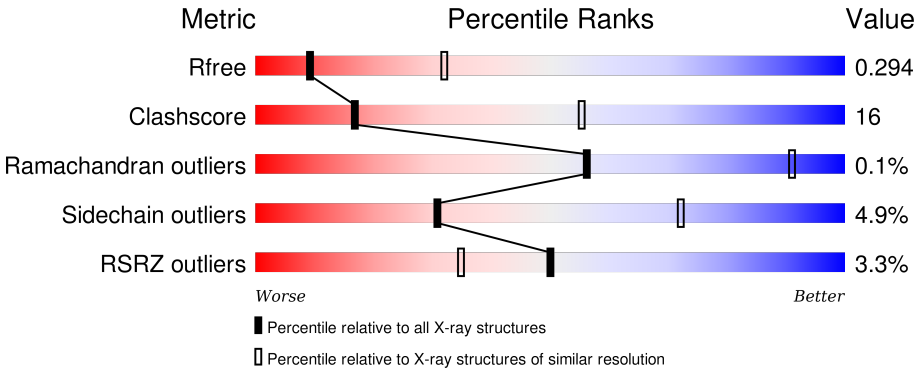
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 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}	91344	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	305	56% 39%
1	B	305	4% 67% 28% 5%
1	C	305	% 60% 32% 6%
1	D	305	3% 64% 26% 8%
1	E	305	3% 60% 31% 6%

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Mol	Chain	Length	Quality of chain
1	F	305	2% 62% 30% 7%
1	G	305	5% 61% 30% 9%
1	H	305	4% 59% 29% 12%
1	I	305	6% 62% 25% 11%
2	J	60	33% 23% 40%
2	K	60	17% 8% 75%
2	L	60	2% 35% 13% 50%
2	M	60	32% 8% 58%
2	N	60	32% 10% 55%
2	O	60	28% 17% 53%
2	P	60	27% 8% 65%
2	Q	60	2% 38% 5% 55%
2	R	60	5% 25% 5% 70%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PO4	C	401	-	-	-	X
3	PO4	H	402	-	-	X	-
3	PO4	I	401	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19225 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 Cell division protein FtsZ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	0	0
			2074	1288	360	417	9			
1	B	289	Total	C	N	O	S	0	0	0
			1951	1205	349	389	8			
1	C	288	Total	C	N	O	S	0	0	0
			2030	1259	356	406	9			
1	D	280	Total	C	N	O	S	0	0	0
			1951	1211	342	389	9			
1	E	286	Total	C	N	O	S	0	0	0
			1970	1223	346	392	9			
1	F	284	Total	C	N	O	S	0	0	0
			1991	1235	350	396	10			
1	G	279	Total	C	N	O	S	0	0	0
			1935	1197	338	390	10			
1	H	269	Total	C	N	O	S	0	0	0
			1854	1151	331	363	9			
1	I	270	Total	C	N	O	S	0	0	0
			1849	1151	326	362	10			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MET	-	initiating methionine	UNP P17865
B	11	MET	-	initiating methionine	UNP P17865
C	11	MET	-	initiating methionine	UNP P17865
D	11	MET	-	initiating methionine	UNP P17865
E	11	MET	-	initiating methionine	UNP P17865
F	11	MET	-	initiating methionine	UNP P17865
G	11	MET	-	initiating methionine	UNP P17865
H	11	MET	-	initiating methionine	UNP P17865
I	11	MET	-	initiating methionine	UNP P17865

- Molecule 2 is a protein called Cell division factor.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	J	36	Total C N O S 268 178 44 45 1	0	0	0
2	K	15	Total C N O 86 55 16 15	0	0	0
2	L	30	Total C N O 221 149 33 39	0	0	0
2	M	25	Total C N O 147 90 29 28	0	0	0
2	N	27	Total C N O 189 127 32 30	0	0	0
2	O	28	Total C N O 205 137 34 34	0	0	0
2	P	21	Total C N O 149 99 25 25	0	0	0
2	Q	27	Total C N O 161 106 28 27	0	0	0
2	R	18	Total C N O 114 73 22 19	0	0	0

There are 180 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	-19	MET	-	expression tag	UNP L8EBJ9
J	-18	GLY	-	expression tag	UNP L8EBJ9
J	-17	SER	-	expression tag	UNP L8EBJ9
J	-16	SER	-	expression tag	UNP L8EBJ9
J	-15	HIS	-	expression tag	UNP L8EBJ9
J	-14	HIS	-	expression tag	UNP L8EBJ9
J	-13	HIS	-	expression tag	UNP L8EBJ9
J	-12	HIS	-	expression tag	UNP L8EBJ9
J	-11	HIS	-	expression tag	UNP L8EBJ9
J	-10	HIS	-	expression tag	UNP L8EBJ9
J	-9	SER	-	expression tag	UNP L8EBJ9
J	-8	SER	-	expression tag	UNP L8EBJ9
J	-7	GLY	-	expression tag	UNP L8EBJ9
J	-6	LEU	-	expression tag	UNP L8EBJ9
J	-5	VAL	-	expression tag	UNP L8EBJ9
J	-4	PRO	-	expression tag	UNP L8EBJ9
J	-3	ARG	-	expression tag	UNP L8EBJ9
J	-2	GLY	-	expression tag	UNP L8EBJ9
J	-1	SER	-	expression tag	UNP L8EBJ9
J	0	HIS	-	expression tag	UNP L8EBJ9
K	-19	MET	-	expression tag	UNP L8EBJ9
K	-18	GLY	-	expression tag	UNP L8EBJ9

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-17	SER	-	expression tag	UNP L8EBJ9
K	-16	SER	-	expression tag	UNP L8EBJ9
K	-15	HIS	-	expression tag	UNP L8EBJ9
K	-14	HIS	-	expression tag	UNP L8EBJ9
K	-13	HIS	-	expression tag	UNP L8EBJ9
K	-12	HIS	-	expression tag	UNP L8EBJ9
K	-11	HIS	-	expression tag	UNP L8EBJ9
K	-10	HIS	-	expression tag	UNP L8EBJ9
K	-9	SER	-	expression tag	UNP L8EBJ9
K	-8	SER	-	expression tag	UNP L8EBJ9
K	-7	GLY	-	expression tag	UNP L8EBJ9
K	-6	LEU	-	expression tag	UNP L8EBJ9
K	-5	VAL	-	expression tag	UNP L8EBJ9
K	-4	PRO	-	expression tag	UNP L8EBJ9
K	-3	ARG	-	expression tag	UNP L8EBJ9
K	-2	GLY	-	expression tag	UNP L8EBJ9
K	-1	SER	-	expression tag	UNP L8EBJ9
K	0	HIS	-	expression tag	UNP L8EBJ9
L	-19	MET	-	expression tag	UNP L8EBJ9
L	-18	GLY	-	expression tag	UNP L8EBJ9
L	-17	SER	-	expression tag	UNP L8EBJ9
L	-16	SER	-	expression tag	UNP L8EBJ9
L	-15	HIS	-	expression tag	UNP L8EBJ9
L	-14	HIS	-	expression tag	UNP L8EBJ9
L	-13	HIS	-	expression tag	UNP L8EBJ9
L	-12	HIS	-	expression tag	UNP L8EBJ9
L	-11	HIS	-	expression tag	UNP L8EBJ9
L	-10	HIS	-	expression tag	UNP L8EBJ9
L	-9	SER	-	expression tag	UNP L8EBJ9
L	-8	SER	-	expression tag	UNP L8EBJ9
L	-7	GLY	-	expression tag	UNP L8EBJ9
L	-6	LEU	-	expression tag	UNP L8EBJ9
L	-5	VAL	-	expression tag	UNP L8EBJ9
L	-4	PRO	-	expression tag	UNP L8EBJ9
L	-3	ARG	-	expression tag	UNP L8EBJ9
L	-2	GLY	-	expression tag	UNP L8EBJ9
L	-1	SER	-	expression tag	UNP L8EBJ9
L	0	HIS	-	expression tag	UNP L8EBJ9
M	-19	MET	-	expression tag	UNP L8EBJ9
M	-18	GLY	-	expression tag	UNP L8EBJ9
M	-17	SER	-	expression tag	UNP L8EBJ9
M	-16	SER	-	expression tag	UNP L8EBJ9

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Chain	Residue	Modelled	Actual	Comment	Reference
M	-15	HIS	-	expression tag	UNP L8EBJ9
M	-14	HIS	-	expression tag	UNP L8EBJ9
M	-13	HIS	-	expression tag	UNP L8EBJ9
M	-12	HIS	-	expression tag	UNP L8EBJ9
M	-11	HIS	-	expression tag	UNP L8EBJ9
M	-10	HIS	-	expression tag	UNP L8EBJ9
M	-9	SER	-	expression tag	UNP L8EBJ9
M	-8	SER	-	expression tag	UNP L8EBJ9
M	-7	GLY	-	expression tag	UNP L8EBJ9
M	-6	LEU	-	expression tag	UNP L8EBJ9
M	-5	VAL	-	expression tag	UNP L8EBJ9
M	-4	PRO	-	expression tag	UNP L8EBJ9
M	-3	ARG	-	expression tag	UNP L8EBJ9
M	-2	GLY	-	expression tag	UNP L8EBJ9
M	-1	SER	-	expression tag	UNP L8EBJ9
M	0	HIS	-	expression tag	UNP L8EBJ9
N	-19	MET	-	expression tag	UNP L8EBJ9
N	-18	GLY	-	expression tag	UNP L8EBJ9
N	-17	SER	-	expression tag	UNP L8EBJ9
N	-16	SER	-	expression tag	UNP L8EBJ9
N	-15	HIS	-	expression tag	UNP L8EBJ9
N	-14	HIS	-	expression tag	UNP L8EBJ9
N	-13	HIS	-	expression tag	UNP L8EBJ9
N	-12	HIS	-	expression tag	UNP L8EBJ9
N	-11	HIS	-	expression tag	UNP L8EBJ9
N	-10	HIS	-	expression tag	UNP L8EBJ9
N	-9	SER	-	expression tag	UNP L8EBJ9
N	-8	SER	-	expression tag	UNP L8EBJ9
N	-7	GLY	-	expression tag	UNP L8EBJ9
N	-6	LEU	-	expression tag	UNP L8EBJ9
N	-5	VAL	-	expression tag	UNP L8EBJ9
N	-4	PRO	-	expression tag	UNP L8EBJ9
N	-3	ARG	-	expression tag	UNP L8EBJ9
N	-2	GLY	-	expression tag	UNP L8EBJ9
N	-1	SER	-	expression tag	UNP L8EBJ9
N	0	HIS	-	expression tag	UNP L8EBJ9
O	-19	MET	-	expression tag	UNP L8EBJ9
O	-18	GLY	-	expression tag	UNP L8EBJ9
O	-17	SER	-	expression tag	UNP L8EBJ9
O	-16	SER	-	expression tag	UNP L8EBJ9
O	-15	HIS	-	expression tag	UNP L8EBJ9
O	-14	HIS	-	expression tag	UNP L8EBJ9

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-13	HIS	-	expression tag	UNP L8EBJ9
O	-12	HIS	-	expression tag	UNP L8EBJ9
O	-11	HIS	-	expression tag	UNP L8EBJ9
O	-10	HIS	-	expression tag	UNP L8EBJ9
O	-9	SER	-	expression tag	UNP L8EBJ9
O	-8	SER	-	expression tag	UNP L8EBJ9
O	-7	GLY	-	expression tag	UNP L8EBJ9
O	-6	LEU	-	expression tag	UNP L8EBJ9
O	-5	VAL	-	expression tag	UNP L8EBJ9
O	-4	PRO	-	expression tag	UNP L8EBJ9
O	-3	ARG	-	expression tag	UNP L8EBJ9
O	-2	GLY	-	expression tag	UNP L8EBJ9
O	-1	SER	-	expression tag	UNP L8EBJ9
O	0	HIS	-	expression tag	UNP L8EBJ9
P	-19	MET	-	expression tag	UNP L8EBJ9
P	-18	GLY	-	expression tag	UNP L8EBJ9
P	-17	SER	-	expression tag	UNP L8EBJ9
P	-16	SER	-	expression tag	UNP L8EBJ9
P	-15	HIS	-	expression tag	UNP L8EBJ9
P	-14	HIS	-	expression tag	UNP L8EBJ9
P	-13	HIS	-	expression tag	UNP L8EBJ9
P	-12	HIS	-	expression tag	UNP L8EBJ9
P	-11	HIS	-	expression tag	UNP L8EBJ9
P	-10	HIS	-	expression tag	UNP L8EBJ9
P	-9	SER	-	expression tag	UNP L8EBJ9
P	-8	SER	-	expression tag	UNP L8EBJ9
P	-7	GLY	-	expression tag	UNP L8EBJ9
P	-6	LEU	-	expression tag	UNP L8EBJ9
P	-5	VAL	-	expression tag	UNP L8EBJ9
P	-4	PRO	-	expression tag	UNP L8EBJ9
P	-3	ARG	-	expression tag	UNP L8EBJ9
P	-2	GLY	-	expression tag	UNP L8EBJ9
P	-1	SER	-	expression tag	UNP L8EBJ9
P	0	HIS	-	expression tag	UNP L8EBJ9
Q	-19	MET	-	expression tag	UNP L8EBJ9
Q	-18	GLY	-	expression tag	UNP L8EBJ9
Q	-17	SER	-	expression tag	UNP L8EBJ9
Q	-16	SER	-	expression tag	UNP L8EBJ9
Q	-15	HIS	-	expression tag	UNP L8EBJ9
Q	-14	HIS	-	expression tag	UNP L8EBJ9
Q	-13	HIS	-	expression tag	UNP L8EBJ9
Q	-12	HIS	-	expression tag	UNP L8EBJ9

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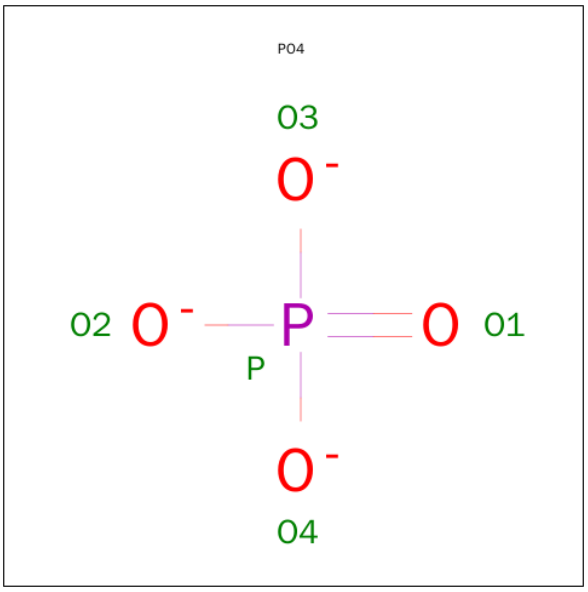
Chain	Residue	Modelled	Actual	Comment	Reference
Q	-11	HIS	-	expression tag	UNP L8EBJ9
Q	-10	HIS	-	expression tag	UNP L8EBJ9
Q	-9	SER	-	expression tag	UNP L8EBJ9
Q	-8	SER	-	expression tag	UNP L8EBJ9
Q	-7	GLY	-	expression tag	UNP L8EBJ9
Q	-6	LEU	-	expression tag	UNP L8EBJ9
Q	-5	VAL	-	expression tag	UNP L8EBJ9
Q	-4	PRO	-	expression tag	UNP L8EBJ9
Q	-3	ARG	-	expression tag	UNP L8EBJ9
Q	-2	GLY	-	expression tag	UNP L8EBJ9
Q	-1	SER	-	expression tag	UNP L8EBJ9
Q	0	HIS	-	expression tag	UNP L8EBJ9
R	-19	MET	-	expression tag	UNP L8EBJ9
R	-18	GLY	-	expression tag	UNP L8EBJ9
R	-17	SER	-	expression tag	UNP L8EBJ9
R	-16	SER	-	expression tag	UNP L8EBJ9
R	-15	HIS	-	expression tag	UNP L8EBJ9
R	-14	HIS	-	expression tag	UNP L8EBJ9
R	-13	HIS	-	expression tag	UNP L8EBJ9
R	-12	HIS	-	expression tag	UNP L8EBJ9
R	-11	HIS	-	expression tag	UNP L8EBJ9
R	-10	HIS	-	expression tag	UNP L8EBJ9
R	-9	SER	-	expression tag	UNP L8EBJ9
R	-8	SER	-	expression tag	UNP L8EBJ9
R	-7	GLY	-	expression tag	UNP L8EBJ9
R	-6	LEU	-	expression tag	UNP L8EBJ9
R	-5	VAL	-	expression tag	UNP L8EBJ9
R	-4	PRO	-	expression tag	UNP L8EBJ9
R	-3	ARG	-	expression tag	UNP L8EBJ9
R	-2	GLY	-	expression tag	UNP L8EBJ9
R	-1	SER	-	expression tag	UNP L8EBJ9
R	0	HIS	-	expression tag	UNP L8EBJ9

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0
3	A	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0
3	C	1	Total O P 5 4 1	0	0
3	C	1	Total O P 5 4 1	0	0
3	D	1	Total O P 5 4 1	0	0
3	D	1	Total O P 5 4 1	0	0
3	E	1	Total O P 5 4 1	0	0
3	F	1	Total O P 5 4 1	0	0
3	G	1	Total O P 5 4 1	0	0
3	G	1	Total O P 5 4 1	0	0
3	H	1	Total O P 5 4 1	0	0
3	H	1	Total O P 5 4 1	0	0

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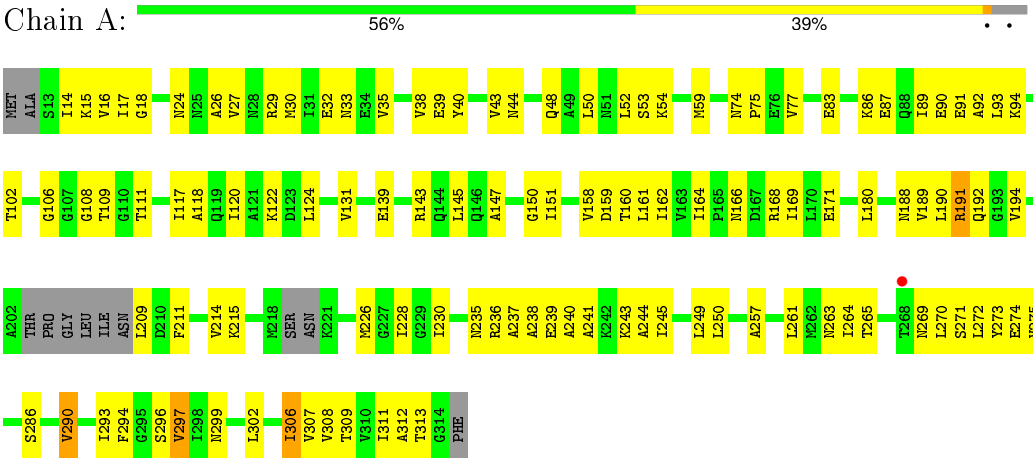
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	I	1	Total O P 5 4 1	0	0
3	I	1	Total O P 5 4 1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

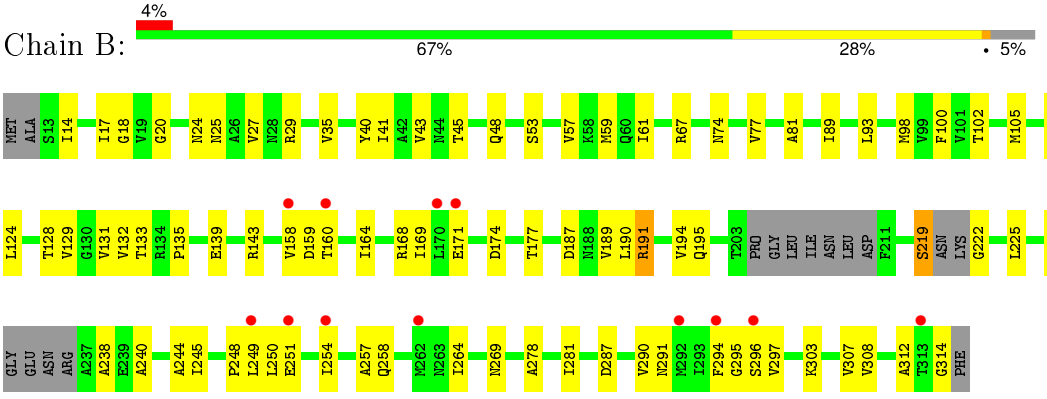
- Molecule 1: Cell division protein FtsZ

Chain A:



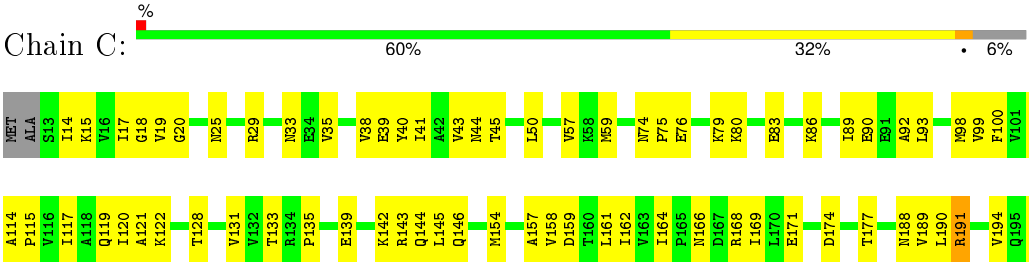
- Molecule 1: Cell division protein FtsZ

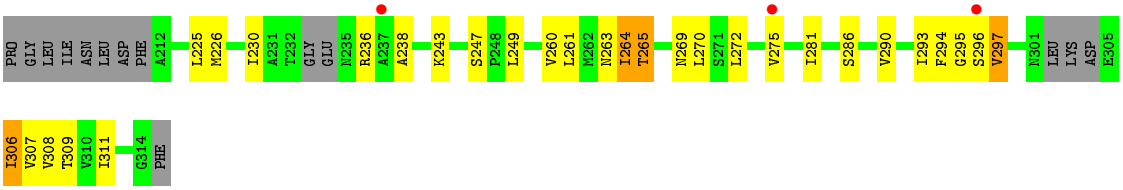
Chain B:



- Molecule 1: Cell division protein FtsZ

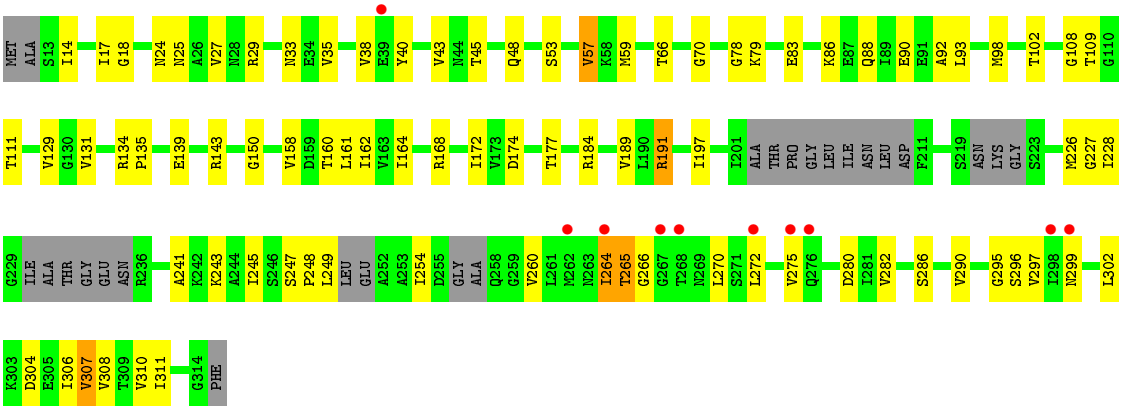
Chain C:





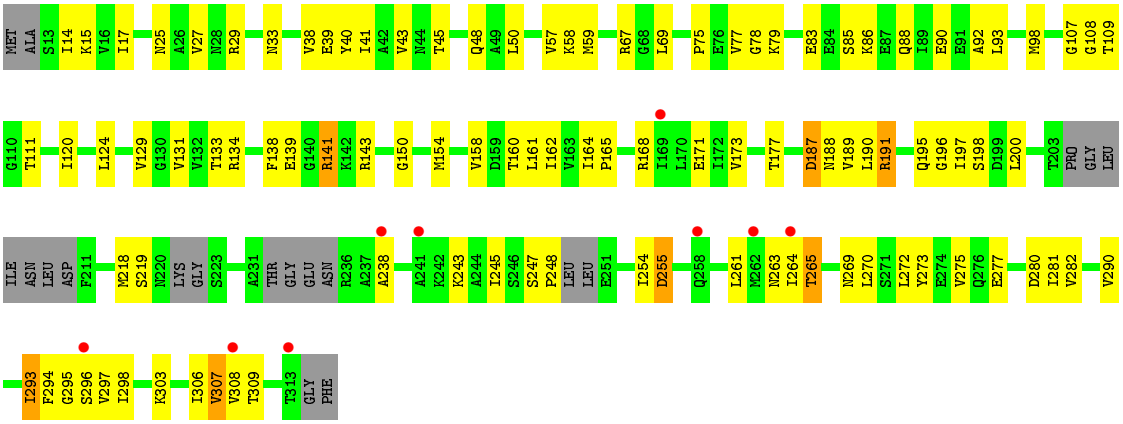
• Molecule 1: Cell division protein FtsZ

Chain D:



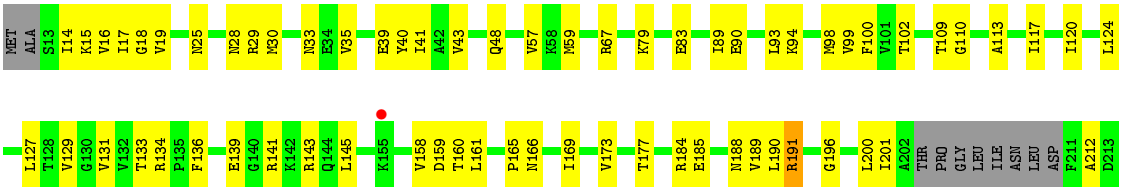
• Molecule 1: Cell division protein FtsZ

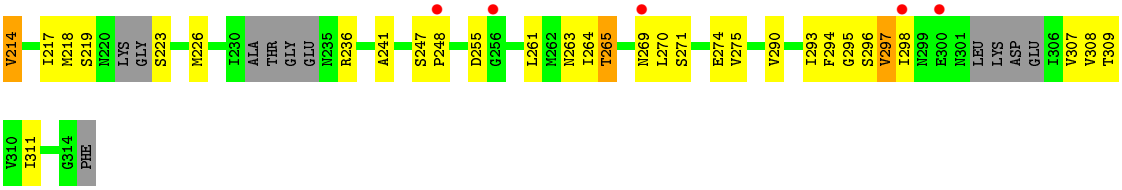
Chain E:



• Molecule 1: Cell division protein FtsZ

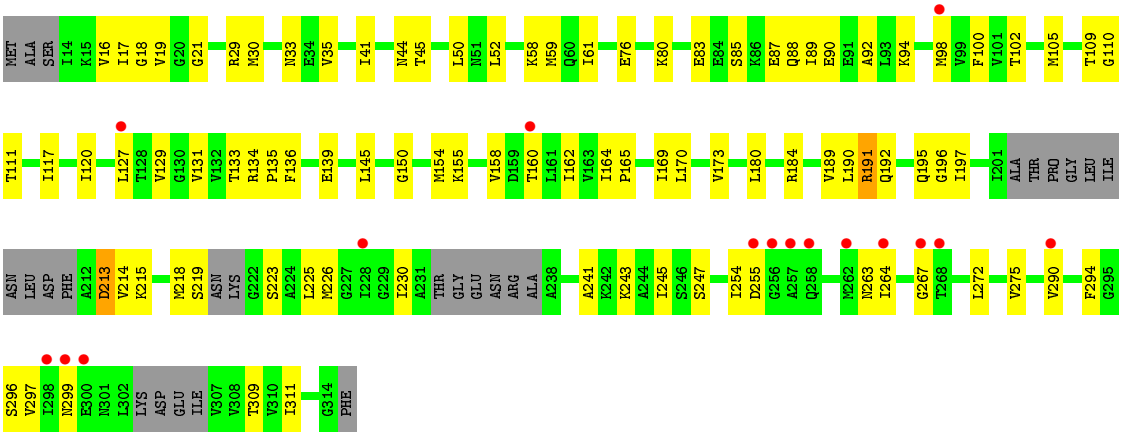
Chain F:





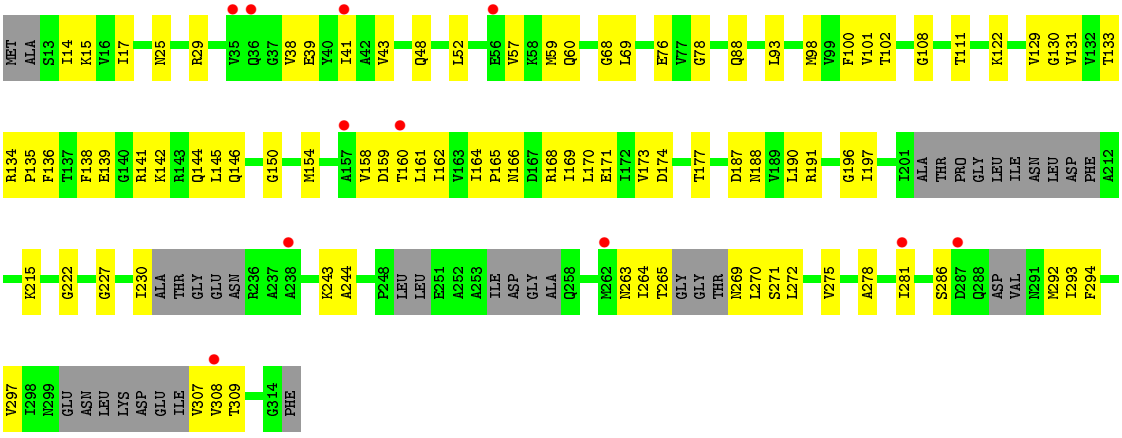
• Molecule 1: Cell division protein FtsZ

Chain G:



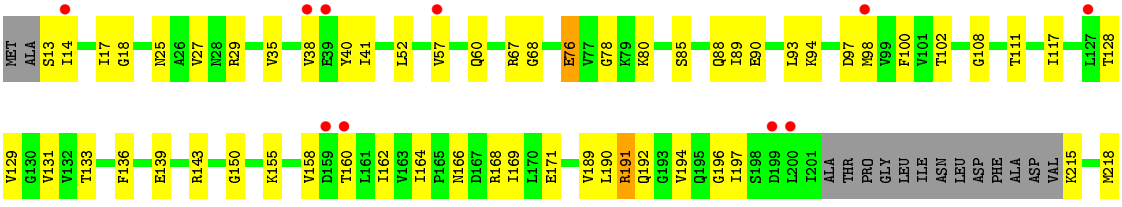
• Molecule 1: Cell division protein FtsZ

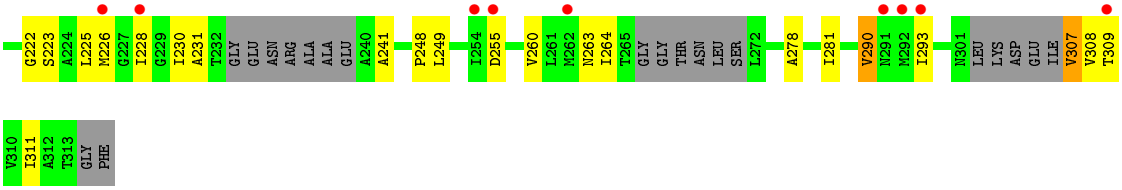
Chain H:



• Molecule 1: Cell division protein FtsZ

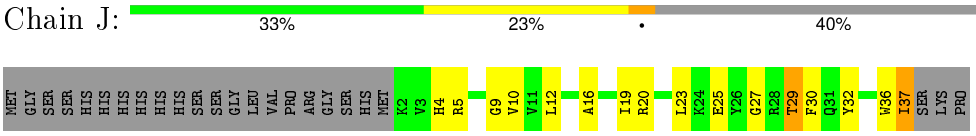
Chain I:





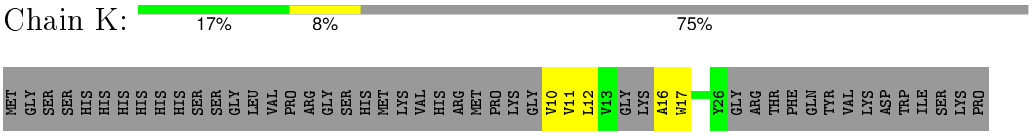
- Molecule 2: Cell division factor

Chain J:



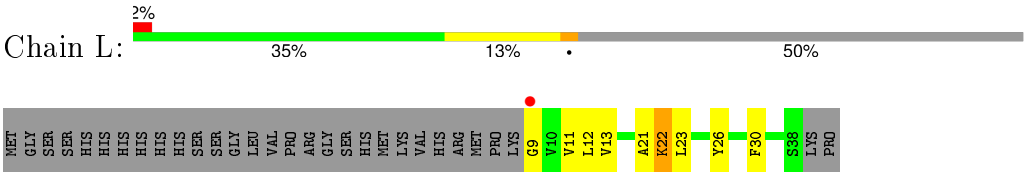
- Molecule 2: Cell division factor

Chain K:



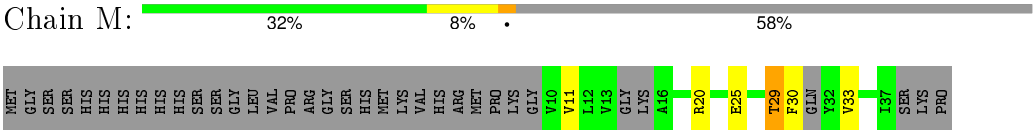
- Molecule 2: Cell division factor

Chain L:



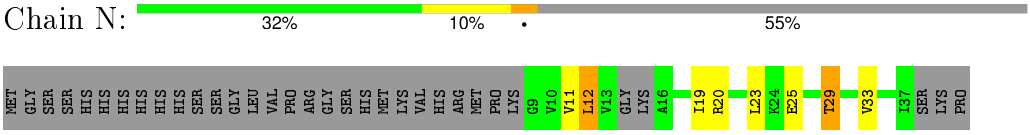
- Molecule 2: Cell division factor

Chain M:



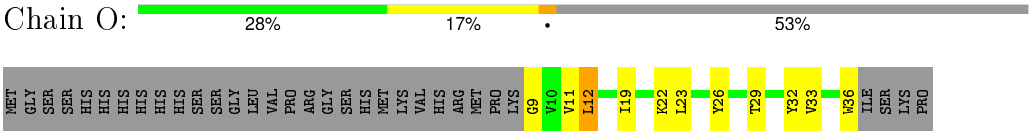
- Molecule 2: Cell division factor

Chain N:



- Molecule 2: Cell division factor

Chain O:

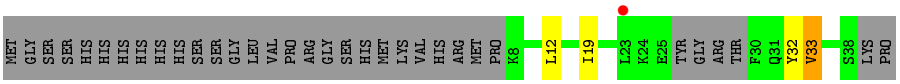


- Molecule 2: Cell division factor

Chain P:

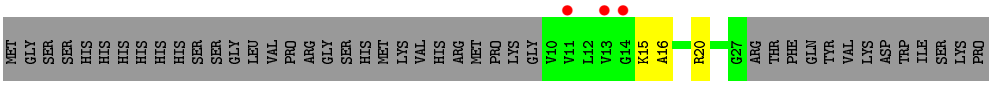
• Molecule 2: Cell division factor

Chain Q:



• Molecule 2: Cell division factor

Chain R:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	167.36Å 167.36Å 528.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.59 – 3.19 46.59 – 3.19	Depositor EDS
% Data completeness (in resolution range)	97.8 (46.59-3.19) 98.0 (46.59-3.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	10.94 (at 3.19Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.232 , 0.292 0.233 , 0.294	Depositor DCC
R_{free} test set	3664 reflections (5.09%)	DCC
Wilson B-factor (Å^2)	80.4	Xtriage
Anisotropy	0.308	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 82.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.26$	Xtriage
Outliers	12 of 72065 reflections (0.017%)	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	19225	wwPDB-VP
Average B, all atoms (Å^2)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.89 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 7.8760e-03.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.59	0/2085	0.76	0/2819
1	B	0.49	0/1959	0.68	0/2653
1	C	0.57	0/2039	0.70	0/2755
1	D	0.53	0/1957	0.71	0/2643
1	E	0.51	0/1977	0.67	0/2677
1	F	0.48	0/1999	0.68	0/2700
1	G	0.49	0/1942	0.69	0/2626
1	H	0.49	0/1858	0.68	0/2505
1	I	0.50	0/1856	0.68	0/2512
2	J	0.51	0/276	0.64	0/378
2	K	0.48	0/86	0.52	0/118
2	L	0.46	0/227	0.59	0/311
2	M	0.39	0/146	0.58	0/198
2	N	0.44	0/194	0.58	0/266
2	O	0.45	0/210	0.61	0/287
2	P	0.42	0/152	0.71	0/208
2	Q	0.45	0/162	0.61	0/222
2	R	0.43	0/116	0.74	0/159
All	All	0.51	0/19241	0.69	0/26037

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2074	0	2080	92	0
1	B	1951	0	1875	60	0
1	C	2030	0	2042	78	0
1	D	1951	0	1946	56	0
1	E	1970	0	1946	74	0
1	F	1991	0	1999	73	0
1	G	1935	0	1917	65	0
1	H	1854	0	1827	53	0
1	I	1849	0	1819	56	0
2	J	268	0	235	16	0
2	K	86	0	49	4	0
2	L	221	0	193	8	0
2	M	147	0	89	5	0
2	N	189	0	145	10	0
2	O	205	0	184	14	0
2	P	149	0	130	2	0
2	Q	161	0	116	3	0
2	R	114	0	83	2	0
3	A	10	0	0	2	0
3	B	10	0	0	0	0
3	C	10	0	0	2	0
3	D	10	0	0	2	0
3	E	5	0	0	1	0
3	F	5	0	0	1	0
3	G	10	0	0	1	0
3	H	10	0	0	2	0
3	I	10	0	0	1	0
All	All	19225	0	18675	620	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 16.

All (620) 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:A:17:ILE:HD11	1:A:93:LEU:HD21	1.36	1.07
1:D:17:ILE:HD11	1:D:93:LEU:HD21	1.45	0.98
1:C:17:ILE:HD11	1:C:93:LEU:HD21	1.45	0.95
1:I:263:ASN:HB3	1:I:309:THR:HB	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:217:ILE:HD12	1:F:293:ILE:HG13	1.55	0.88
1:E:295:GLY:HA3	2:N:11:VAL:HG22	1.54	0.88
1:A:15:LYS:NZ	1:A:39:GLU:OE1	2.06	0.87
1:E:17:ILE:HD11	1:E:93:LEU:HD21	1.55	0.87
1:F:17:ILE:HD11	1:F:93:LEU:HD21	1.57	0.86
1:B:191:ARG:NH1	1:B:195:GLN:OE1	2.08	0.86
1:E:141:ARG:H	1:E:141:ARG:HE	1.24	0.84
1:C:265:THR:HB	1:C:297:VAL:HG23	1.60	0.84
1:B:17:ILE:HD11	1:B:93:LEU:HD21	1.58	0.84
1:C:270:LEU:HD13	1:C:306:ILE:HD11	1.59	0.84
1:E:14:ILE:HG22	1:E:98:MET:HB3	1.60	0.83
1:I:14:ILE:HG22	1:I:98:MET:HB3	1.60	0.81
1:D:33:ASN:OD1	1:D:191:ARG:NH1	2.14	0.81
1:G:230:ILE:O	1:G:243:LYS:NZ	2.14	0.81
1:I:17:ILE:HD11	1:I:93:LEU:HD21	1.62	0.80
1:H:17:ILE:HD11	1:H:93:LEU:HD21	1.63	0.80
1:C:230:ILE:O	1:C:243:LYS:NZ	2.13	0.79
1:B:295:GLY:HA2	2:K:11:VAL:HA	1.66	0.78
1:D:14:ILE:HG22	1:D:98:MET:HB3	1.65	0.77
1:E:173:VAL:HB	1:E:177:THR:HG21	1.64	0.77
1:B:269:ASN:ND2	1:B:303:LYS:O	2.19	0.76
1:C:164:ILE:HD13	1:C:189:VAL:HG12	1.67	0.76
1:A:147:ALA:O	1:A:151:ILE:N	2.13	0.76
1:E:168:ARG:HB3	1:E:248:PRO:HB2	1.68	0.76
1:E:265:THR:HG23	1:E:307:VAL:HG13	1.68	0.75
1:C:236:ARG:NH2	1:C:269:ASN:OD1	2.20	0.74
1:D:78:GLY:HA3	1:D:108:GLY:O	1.87	0.74
1:E:263:ASN:HB3	1:E:309:THR:HB	1.70	0.74
1:B:294:PHE:O	2:K:12:LEU:N	2.21	0.73
2:O:12:LEU:HD12	2:O:19:ILE:HG23	1.70	0.73
1:G:160:THR:HB	1:G:218:MET:O	1.89	0.73
1:G:191:ARG:HH21	1:G:192:GLN:HG2	1.55	0.72
1:E:33:ASN:OD1	1:E:191:ARG:NH1	2.24	0.71
1:H:271:SER:HA	2:Q:32:TYR:HA	1.73	0.71
1:D:168:ARG:HB3	1:D:248:PRO:HB2	1.73	0.71
1:A:230:ILE:HG12	1:A:307:VAL:HG13	1.71	0.70
1:F:159:ASP:HB3	1:F:219:SER:HA	1.74	0.70
1:C:295:GLY:HA2	2:L:11:VAL:HA	1.74	0.69
1:B:89:ILE:HD13	1:B:117:ILE:HG12	1.75	0.68
1:A:236:ARG:NH2	1:A:269:ASN:OD1	2.27	0.68
1:D:158:VAL:HG21	1:D:161:LEU:HB2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:33:ASN:OD1	1:C:191:ARG:NH1	2.28	0.67
1:G:214:VAL:HG12	1:G:218:MET:HG2	1.75	0.67
1:G:33:ASN:OD1	1:G:191:ARG:NH1	2.28	0.67
1:E:158:VAL:HG21	1:E:161:LEU:HB2	1.77	0.67
1:I:290:VAL:HG12	2:R:16:ALA:HB2	1.77	0.67
1:C:263:ASN:HB3	1:C:309:THR:HB	1.75	0.66
1:A:29:ARG:NH2	1:A:188:ASN:HB2	2.10	0.66
1:B:27:VAL:HG13	1:B:40:TYR:CD1	2.31	0.66
1:C:168:ARG:HB2	1:C:249:LEU:HD23	1.77	0.65
1:D:14:ILE:HG13	1:D:38:VAL:HG12	1.79	0.65
1:E:298:ILE:HD11	2:N:33:VAL:HG23	1.78	0.65
1:F:139:GLU:HB3	1:F:143:ARG:HG3	1.79	0.64
1:C:76:GLU:HG3	1:C:80:LYS:HE2	1.79	0.64
1:E:270:LEU:HD23	2:N:33:VAL:HG21	1.78	0.64
1:H:264:ILE:HD13	1:H:308:VAL:HG22	1.79	0.64
1:F:297:VAL:HA	2:O:9:GLY:HA3	1.79	0.64
1:A:241:ALA:O	1:A:245:ILE:HG12	1.96	0.64
2:P:15:LYS:O	2:P:19:ILE:HD12	1.98	0.64
1:D:265:THR:HG23	1:D:307:VAL:HG13	1.80	0.64
1:I:241:ALA:HB3	1:I:281:ILE:HD12	1.79	0.64
1:H:14:ILE:HG13	1:H:38:VAL:HG12	1.79	0.63
1:F:14:ILE:HG22	1:F:98:MET:HB3	1.80	0.63
1:F:109:THR:N	3:F:401:PO4:O2	2.30	0.63
1:A:164:ILE:HD13	1:A:189:VAL:HG12	1.80	0.63
1:H:15:LYS:NZ	1:H:39:GLU:OE1	2.18	0.63
1:B:164:ILE:HD13	1:B:189:VAL:HG12	1.78	0.63
1:B:100:PHE:CD2	1:B:194:VAL:HG13	2.34	0.62
1:B:14:ILE:HG22	1:B:98:MET:HB3	1.80	0.62
1:F:294:PHE:HB3	2:O:19:ILE:HD13	1.80	0.62
1:G:127:LEU:HD21	1:G:218:MET:HG3	1.79	0.62
1:A:264:ILE:HD11	1:A:308:VAL:HG22	1.80	0.62
1:A:200:LEU:HD12	1:A:261:LEU:HD11	1.80	0.62
1:A:214:VAL:HA	1:A:293:ILE:HD11	1.82	0.61
1:E:141:ARG:N	1:E:141:ARG:HE	1.96	0.61
1:A:14:ILE:HG22	1:A:98:MET:HB3	1.83	0.61
1:C:196:GLY:HA2	1:C:263:ASN:HD22	1.65	0.61
1:C:109:THR:N	3:C:401:PO4:O2	2.29	0.61
1:F:214:VAL:HA	1:F:293:ILE:HD11	1.82	0.61
1:H:265:THR:HG23	1:H:307:VAL:HG13	1.82	0.61
1:E:270:LEU:O	2:N:33:VAL:HG22	2.01	0.60
1:E:162:ILE:HD11	1:E:197:ILE:HD11	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:162:ILE:HD11	1:C:197:ILE:HD11	1.82	0.60
1:H:14:ILE:HG22	1:H:98:MET:HB3	1.82	0.60
3:D:402:PO4:O4	1:F:67:ARG:NH2	2.33	0.60
1:F:33:ASN:OD1	1:F:191:ARG:NH1	2.34	0.60
1:E:25:ASN:HB3	1:E:187:ASP:OD2	2.01	0.60
1:F:263:ASN:HB3	1:F:309:THR:HB	1.82	0.60
1:G:80:LYS:HA	1:G:83:GLU:HB2	1.84	0.60
1:A:211:PHE:O	1:A:215:LYS:N	2.32	0.59
1:F:160:THR:HB	1:F:218:MET:O	2.03	0.59
1:I:129:VAL:HG13	1:I:160:THR:HG23	1.85	0.59
1:G:197:ILE:HD11	1:G:311:ILE:HD13	1.84	0.59
1:D:299:ASN:HB3	1:D:302:LEU:HD12	1.85	0.59
1:E:129:VAL:HG22	1:E:160:THR:HG22	1.85	0.59
1:E:164:ILE:HD13	1:E:189:VAL:HG12	1.83	0.58
1:A:264:ILE:CD1	1:A:308:VAL:HG22	2.32	0.58
1:E:14:ILE:HG13	1:E:38:VAL:HG12	1.86	0.58
1:C:168:ARG:NH1	1:C:171:GLU:OE2	2.34	0.58
1:C:14:ILE:HG13	1:C:38:VAL:HG12	1.85	0.58
1:E:111:THR:HG23	1:E:150:GLY:HA3	1.84	0.58
1:B:41:ILE:HG12	1:B:57:VAL:CG1	2.33	0.58
1:C:15:LYS:NZ	1:C:39:GLU:OE1	2.22	0.58
1:G:131:VAL:HG22	1:G:162:ILE:HD12	1.85	0.58
1:C:270:LEU:CD1	1:C:306:ILE:HD11	2.34	0.57
1:I:13:SER:HB3	1:I:97:ASP:H	1.68	0.57
1:A:236:ARG:CZ	1:A:306:ILE:HD12	2.34	0.57
1:C:226:MET:HB3	1:C:311:ILE:HG12	1.85	0.57
1:E:133:THR:HG23	1:E:190:LEU:HD22	1.87	0.57
1:E:141:ARG:NE	1:E:141:ARG:H	1.98	0.57
1:C:79:LYS:HE3	1:C:83:GLU:OE2	2.04	0.57
1:C:139:GLU:HB3	1:C:143:ARG:HG3	1.85	0.57
1:D:162:ILE:HD11	1:D:197:ILE:HD11	1.87	0.57
1:I:108:GLY:N	3:I:401:PO4:O3	2.34	0.57
1:H:170:LEU:HA	1:H:173:VAL:HG22	1.87	0.57
1:D:164:ILE:HD13	1:D:189:VAL:HG12	1.87	0.57
1:H:174:ASP:HB2	1:H:177:THR:HG23	1.85	0.57
1:F:294:PHE:O	2:O:12:LEU:N	2.38	0.56
1:H:111:THR:HG23	1:H:150:GLY:HA3	1.87	0.56
1:F:264:ILE:O	1:F:296:SER:HA	2.05	0.56
1:B:168:ARG:HB2	1:B:249:LEU:HD23	1.87	0.56
1:E:245:ILE:HD11	1:E:282:VAL:HA	1.87	0.56
1:C:59:MET:HE1	1:C:92:ALA:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:219:SER:O	1:B:222:GLY:N	2.38	0.56
1:I:102:THR:HA	1:I:131:VAL:O	2.06	0.56
1:D:45:THR:OG1	1:D:70:GLY:HA2	2.06	0.56
1:F:15:LYS:NZ	1:F:39:GLU:OE1	2.25	0.56
1:G:133:THR:HG23	1:G:190:LEU:HD22	1.88	0.56
1:G:263:ASN:HB3	1:G:309:THR:HB	1.88	0.56
1:E:59:MET:HE1	1:E:92:ALA:CB	2.36	0.56
1:H:215:LYS:HA	1:H:293:ILE:HD11	1.88	0.56
1:D:18:GLY:HA2	1:D:102:THR:HG23	1.88	0.55
1:G:136:PHE:HB2	1:G:139:GLU:HG3	1.88	0.55
1:C:89:ILE:HD13	1:C:117:ILE:HG12	1.87	0.55
1:H:43:VAL:HG22	1:H:59:MET:HB3	1.88	0.55
1:C:294:PHE:O	2:L:12:LEU:N	2.36	0.55
1:A:139:GLU:HB3	1:A:143:ARG:HG3	1.88	0.55
1:I:264:ILE:HD13	1:I:308:VAL:HG22	1.88	0.55
1:D:226:MET:HB3	1:D:311:ILE:HG12	1.87	0.55
1:H:168:ARG:NH1	1:H:171:GLU:OE2	2.31	0.55
1:H:230:ILE:O	1:H:243:LYS:NZ	2.29	0.55
1:H:133:THR:HG23	1:H:190:LEU:HD13	1.89	0.55
1:G:213:ASP:OD1	1:G:214:VAL:N	2.39	0.55
1:F:295:GLY:HA2	2:O:11:VAL:HA	1.87	0.55
1:C:14:ILE:HG22	1:C:98:MET:HB3	1.89	0.55
1:A:131:VAL:O	1:A:190:LEU:HD11	2.07	0.55
1:G:90:GLU:HG2	1:G:120:ILE:HG23	1.88	0.54
1:C:90:GLU:HG2	1:C:120:ILE:HG23	1.88	0.54
1:F:264:ILE:HD13	1:F:308:VAL:HG22	1.88	0.54
1:I:89:ILE:HD13	1:I:117:ILE:HG12	1.89	0.54
1:B:45:THR:HG22	1:B:61:ILE:HG13	1.88	0.54
1:A:33:ASN:OD1	1:A:191:ARG:NH1	2.40	0.54
3:C:402:PO4:O4	1:E:67:ARG:NH2	2.40	0.54
1:A:273:TYR:O	1:A:277:GLU:HB2	2.07	0.54
1:C:158:VAL:HG21	1:C:161:LEU:HB2	1.90	0.54
1:C:264:ILE:O	1:C:296:SER:HA	2.08	0.54
1:F:270:LEU:HD23	2:O:33:VAL:HG21	1.89	0.54
1:C:243:LYS:O	1:C:247:SER:N	2.40	0.54
1:A:131:VAL:HG22	1:A:162:ILE:HD12	1.89	0.54
1:E:79:LYS:HE3	1:E:83:GLU:OE2	2.08	0.54
1:C:275:VAL:HG13	1:C:294:PHE:HZ	1.72	0.53
1:B:229:GLY:O	1:B:308:VAL:N	2.36	0.53
1:F:139:GLU:HG2	1:H:69:LEU:HD21	1.90	0.53
1:C:122:LYS:HE3	1:C:159:ASP:OD1	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:VAL:HG22	1:A:59:MET:HB3	1.89	0.53
1:E:168:ARG:HD2	1:E:248:PRO:HB3	1.91	0.53
1:B:43:VAL:HG22	1:B:59:MET:HB3	1.91	0.53
1:I:162:ILE:HD11	1:I:197:ILE:HD11	1.91	0.53
2:J:25:GLU:O	2:J:29:THR:HG22	2.09	0.53
1:G:19:VAL:HG12	1:G:110:GLY:HA2	1.90	0.53
1:C:35:VAL:HB	1:C:40:TYR:OH	2.09	0.53
1:A:214:VAL:HA	1:A:293:ILE:CD1	2.38	0.53
1:A:265:THR:HA	1:A:297:VAL:O	2.09	0.53
1:E:160:THR:HB	1:E:218:MET:O	2.09	0.53
1:A:270:LEU:HD13	1:A:306:ILE:HD11	1.91	0.53
1:E:264:ILE:O	1:E:296:SER:HA	2.08	0.53
1:F:236:ARG:NE	1:F:274:GLU:OE2	2.42	0.52
1:I:88:GLN:N	1:I:88:GLN:OE1	2.43	0.52
1:I:226:MET:HB3	1:I:311:ILE:HG12	1.91	0.52
1:A:299:ASN:HB3	1:A:302:LEU:HD12	1.90	0.52
1:B:24:ASN:OD1	1:B:53:SER:HB2	2.09	0.52
1:A:77:VAL:HG23	1:G:145:LEU:HD21	1.91	0.52
1:E:196:GLY:HA2	1:E:263:ASN:HD22	1.75	0.52
2:J:16:ALA:O	2:J:20:ARG:HG3	2.10	0.52
1:H:264:ILE:CD1	1:H:308:VAL:HG22	2.39	0.52
1:B:278:ALA:HA	1:B:281:ILE:HD12	1.91	0.52
1:F:133:THR:HG23	1:F:190:LEU:HD13	1.92	0.52
1:C:164:ILE:HG21	1:C:189:VAL:HG11	1.91	0.52
1:E:275:VAL:HG13	1:E:294:PHE:HZ	1.74	0.52
1:A:158:VAL:HG21	1:A:161:LEU:HB2	1.91	0.52
1:A:235:ASN:OD1	1:A:238:ALA:HB3	2.10	0.52
1:E:45:THR:HG23	1:E:109:THR:HG23	1.90	0.52
1:D:243:LYS:O	1:D:247:SER:N	2.42	0.52
1:A:35:VAL:HB	1:A:40:TYR:OH	2.10	0.52
1:I:41:ILE:HG12	1:I:57:VAL:CG1	2.40	0.52
2:L:22:LYS:NZ	2:L:26:TYR:OH	2.43	0.52
1:A:27:VAL:HG13	1:A:40:TYR:CD1	2.45	0.52
1:H:135:PRO:HG2	1:H:144:GLN:NE2	2.25	0.52
1:A:122:LYS:HE3	1:A:159:ASP:OD1	2.10	0.52
1:H:270:LEU:O	2:Q:33:VAL:HG23	2.10	0.52
1:F:16:VAL:HG22	1:F:100:PHE:HB2	1.91	0.52
1:G:111:THR:HG23	1:G:150:GLY:HA3	1.90	0.51
1:A:109:THR:N	3:A:401:PO4:O4	2.42	0.51
1:C:41:ILE:HA	1:C:57:VAL:HG13	1.93	0.51
1:I:85:SER:HB3	1:I:88:GLN:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:139:GLU:HB3	1:B:143:ARG:HG3	1.93	0.51
1:A:272:LEU:HD21	2:J:36:TRP:CE3	2.45	0.51
1:G:50:LEU:HG	1:G:58:LYS:HB3	1.93	0.51
1:H:275:VAL:HG13	1:H:294:PHE:HZ	1.76	0.51
1:F:271:SER:HA	2:O:32:TYR:HA	1.93	0.51
1:E:245:ILE:HG12	1:E:254:ILE:HD11	1.93	0.51
1:F:270:LEU:O	2:O:33:VAL:HG23	2.10	0.51
2:J:23:LEU:O	2:J:27:GLY:N	2.44	0.51
1:F:19:VAL:HG12	1:F:110:GLY:HA2	1.92	0.51
1:I:25:ASN:O	1:I:29:ARG:HG2	2.11	0.51
1:E:139:GLU:HB3	1:E:143:ARG:HG3	1.93	0.51
1:D:88:GLN:OE1	1:D:88:GLN:N	2.44	0.51
1:G:18:GLY:HA2	1:G:102:THR:HG23	1.92	0.51
1:F:275:VAL:HG13	1:F:294:PHE:HZ	1.75	0.51
1:G:243:LYS:O	1:G:247:SER:N	2.44	0.51
1:A:18:GLY:HA2	1:A:102:THR:HG23	1.91	0.51
1:I:191:ARG:HH21	1:I:192:GLN:HG2	1.76	0.51
1:A:14:ILE:HG13	1:A:38:VAL:HG12	1.91	0.50
1:G:245:ILE:HG22	1:G:254:ILE:HD12	1.92	0.50
1:I:129:VAL:HG22	1:I:160:THR:HG22	1.93	0.50
1:G:29:ARG:HH12	1:G:184:ARG:HG2	1.76	0.50
1:C:19:VAL:HG12	1:C:110:GLY:HA2	1.92	0.50
1:G:272:LEU:HD12	1:G:272:LEU:H	1.75	0.50
1:H:136:PHE:HB2	1:H:139:GLU:HG3	1.94	0.50
1:A:240:ALA:HB1	1:A:308:VAL:HG23	1.93	0.50
1:E:15:LYS:NZ	1:E:39:GLU:OE1	2.28	0.50
1:I:76:GLU:HG3	1:I:80:LYS:HE2	1.92	0.50
1:C:174:ASP:HB2	1:C:177:THR:HG23	1.92	0.50
1:E:196:GLY:HA3	1:E:309:THR:HG21	1.93	0.50
1:B:225:LEU:HD13	1:B:251:GLU:H	1.77	0.50
1:I:231:ALA:H	1:I:307:VAL:HG22	1.77	0.50
1:F:275:VAL:HG12	2:O:23:LEU:HD13	1.94	0.50
1:D:241:ALA:O	1:D:245:ILE:HG12	2.12	0.50
1:A:89:ILE:HD13	1:A:117:ILE:HG12	1.94	0.50
1:F:134:ARG:HB3	1:F:165:PRO:HA	1.94	0.50
1:D:264:ILE:HG21	1:D:275:VAL:HG22	1.92	0.50
1:H:129:VAL:HG22	1:H:160:THR:HG22	1.94	0.50
1:D:83:GLU:O	1:D:86:LYS:HB3	2.12	0.50
1:B:45:THR:HG23	1:B:109:THR:HG23	1.94	0.49
1:G:191:ARG:NH2	1:G:192:GLN:HG2	2.25	0.49
1:D:29:ARG:HH12	1:D:184:ARG:HG2	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:122:LYS:HE3	1:H:159:ASP:OD1	2.11	0.49
1:I:90:GLU:O	1:I:94:LYS:N	2.40	0.49
1:E:134:ARG:HB3	1:E:165:PRO:HA	1.92	0.49
1:H:15:LYS:O	1:H:100:PHE:N	2.41	0.49
1:F:298:ILE:HD11	2:O:33:VAL:HB	1.94	0.49
1:B:131:VAL:HG12	1:B:190:LEU:HD12	1.94	0.49
1:I:27:VAL:HG13	1:I:40:TYR:CD1	2.48	0.49
1:D:282:VAL:O	1:D:286:SER:OG	2.24	0.49
1:G:213:ASP:O	1:G:215:LYS:N	2.32	0.49
2:O:33:VAL:HG13	2:O:36:TRP:HE3	1.78	0.49
1:A:59:MET:HE1	1:A:92:ALA:CB	2.42	0.49
2:J:5:ARG:HA	2:J:10:VAL:HG12	1.94	0.49
1:H:294:PHE:HB3	2:Q:19:ILE:HD13	1.94	0.49
1:D:108:GLY:N	3:D:401:PO4:O3	2.42	0.49
1:H:263:ASN:HB3	1:H:309:THR:HB	1.94	0.49
2:R:16:ALA:O	2:R:20:ARG:HG3	2.12	0.49
1:E:264:ILE:HG21	1:E:275:VAL:HG22	1.94	0.49
1:D:228:ILE:HA	1:D:308:VAL:O	2.13	0.49
1:B:35:VAL:HB	1:B:40:TYR:OH	2.13	0.49
1:A:257:ALA:HB2	1:A:312:ALA:HB1	1.94	0.49
1:E:69:LEU:HD21	1:I:139:GLU:HG2	1.94	0.49
1:F:90:GLU:HG2	1:F:120:ILE:HG23	1.94	0.49
1:A:91:GLU:OE1	1:A:91:GLU:HA	2.13	0.49
3:A:402:PO4:O1	1:B:67:ARG:NH2	2.45	0.49
1:B:295:GLY:CA	2:K:11:VAL:HA	2.41	0.48
1:B:43:VAL:HG11	1:B:117:ILE:HD11	1.95	0.48
1:E:238:ALA:HB2	1:E:277:GLU:HG2	1.93	0.48
1:H:29:ARG:NH2	1:H:188:ASN:HB2	2.28	0.48
1:G:21:GLY:H	3:G:401:PO4:P	2.35	0.48
1:A:239:GLU:HG2	1:A:243:LYS:HE2	1.94	0.48
1:F:136:PHE:CE1	1:F:166:ASN:HB3	2.48	0.48
1:H:292:MET:HG2	1:H:293:ILE:N	2.29	0.48
1:G:241:ALA:O	1:G:245:ILE:HG12	2.14	0.48
1:C:142:LYS:HE3	1:C:146:GLN:OE1	2.14	0.48
1:I:111:THR:HG23	1:I:150:GLY:HA3	1.95	0.48
1:D:129:VAL:HG22	1:D:160:THR:HG22	1.93	0.48
1:D:265:THR:HB	1:D:297:VAL:HB	1.96	0.48
1:G:76:GLU:OE2	1:G:80:LYS:HE2	2.14	0.48
1:C:145:LEU:HD21	1:E:77:VAL:HG23	1.96	0.48
1:A:16:VAL:HA	1:A:100:PHE:HB2	1.95	0.48
1:I:215:LYS:HA	1:I:293:ILE:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:133:THR:HG23	1:I:190:LEU:HD22	1.94	0.48
1:I:168:ARG:HB2	1:I:249:LEU:HD23	1.94	0.48
1:A:226:MET:HB3	1:A:311:ILE:HG12	1.94	0.48
2:O:22:LYS:HG3	2:O:26:TYR:CE2	2.48	0.48
1:E:27:VAL:HG13	1:E:40:TYR:CD1	2.48	0.48
2:J:30:PHE:CD1	2:J:36:TRP:HA	2.49	0.48
1:F:29:ARG:NH2	1:F:188:ASN:HB2	2.29	0.48
1:H:166:ASN:O	1:H:169:ILE:HG12	2.13	0.48
1:C:100:PHE:CD2	1:C:194:VAL:HG13	2.49	0.48
1:I:226:MET:CB	1:I:311:ILE:HG12	2.43	0.48
1:I:196:GLY:HA3	1:I:309:THR:HG21	1.96	0.47
1:G:164:ILE:HG21	1:G:189:VAL:HG12	1.95	0.47
1:H:278:ALA:HA	1:H:281:ILE:HD12	1.96	0.47
1:A:313:THR:O	1:A:313:THR:OG1	2.26	0.47
1:H:141:ARG:N	3:H:402:PO4:O3	2.47	0.47
1:B:225:LEU:HB3	1:B:250:LEU:HD12	1.96	0.47
1:F:43:VAL:HG22	1:F:59:MET:HB3	1.95	0.47
1:F:102:THR:HA	1:F:131:VAL:O	2.14	0.47
1:E:255:ASP:N	1:E:255:ASP:OD2	2.34	0.47
1:A:264:ILE:O	1:A:296:SER:HA	2.15	0.47
1:E:131:VAL:HG22	1:E:162:ILE:HD12	1.96	0.47
1:H:265:THR:HA	1:H:297:VAL:O	2.15	0.47
1:D:45:THR:HG23	1:D:109:THR:HG23	1.97	0.47
1:D:45:THR:HB	1:D:66:THR:HG21	1.97	0.47
1:A:237:ALA:HB2	1:A:274:GLU:HB3	1.95	0.47
1:D:139:GLU:HB3	1:D:143:ARG:HG3	1.95	0.47
1:C:86:LYS:O	1:C:90:GLU:HG3	2.15	0.47
1:E:109:THR:N	3:E:401:PO4:O2	2.31	0.47
1:D:227:GLY:HA2	1:D:249:LEU:HB2	1.96	0.47
1:A:32:GLU:HG2	1:A:54:LYS:NZ	2.29	0.47
1:G:44:ASN:HA	1:G:109:THR:HG21	1.97	0.47
1:A:83:GLU:O	1:A:86:LYS:HB3	2.14	0.47
1:D:35:VAL:HB	1:D:40:TYR:OH	2.15	0.47
1:A:272:LEU:HD13	2:J:30:PHE:O	2.14	0.47
1:E:138:PHE:O	1:I:67:ARG:HD2	2.15	0.47
1:C:45:THR:HG23	1:C:109:THR:HG23	1.95	0.47
1:E:43:VAL:HG22	1:E:59:MET:HB3	1.97	0.47
2:J:10:VAL:HG21	2:J:36:TRP:CZ3	2.50	0.47
1:A:111:THR:HG23	1:A:150:GLY:HA3	1.97	0.47
1:F:109:THR:O	1:F:113:ALA:HB3	2.15	0.47
1:C:102:THR:HA	1:C:131:VAL:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:43:VAL:HG22	1:D:59:MET:HB3	1.97	0.47
1:B:230:ILE:HA	1:B:307:VAL:HA	1.97	0.47
1:C:169:ILE:HD13	1:C:249:LEU:HD21	1.97	0.46
1:I:241:ALA:HA	1:I:308:VAL:HG11	1.97	0.46
2:L:21:ALA:HA	2:P:17:TRP:HZ3	1.79	0.46
1:B:257:ALA:HB2	1:B:312:ALA:HB1	1.97	0.46
1:C:25:ASN:O	1:C:29:ARG:HG2	2.15	0.46
1:C:133:THR:HG23	1:C:190:LEU:HD22	1.96	0.46
1:I:230:ILE:HA	1:I:307:VAL:N	2.31	0.46
1:C:43:VAL:HG11	1:C:117:ILE:HD11	1.98	0.46
1:E:280:ASP:OD1	2:N:20:ARG:NH2	2.45	0.46
1:F:169:ILE:HD12	1:F:189:VAL:HG21	1.97	0.46
1:A:294:PHE:O	2:J:12:LEU:N	2.46	0.46
1:E:168:ARG:NH1	1:E:171:GLU:OE2	2.36	0.46
1:A:271:SER:HA	2:J:32:TYR:HA	1.98	0.46
1:C:272:LEU:HD13	2:L:30:PHE:O	2.15	0.46
1:D:14:ILE:CG2	1:D:98:MET:HB3	2.42	0.46
1:G:162:ILE:HD11	1:G:197:ILE:HD11	1.98	0.46
1:H:150:GLY:O	1:H:154:MET:N	2.48	0.46
1:A:244:ALA:HB2	1:A:308:VAL:HB	1.97	0.46
1:I:78:GLY:HA3	1:I:108:GLY:O	2.16	0.46
1:G:90:GLU:O	1:G:94:LYS:N	2.44	0.46
1:D:86:LYS:O	1:D:90:GLU:HG3	2.16	0.46
2:J:37:ILE:H	2:J:37:ILE:HG13	1.54	0.46
2:O:33:VAL:HG13	2:O:36:TRP:CE3	2.51	0.46
2:L:22:LYS:HD2	2:L:22:LYS:HA	1.76	0.46
1:G:52:LEU:HD23	1:G:52:LEU:HA	1.74	0.46
1:C:297:VAL:HA	2:L:9:GLY:HA3	1.98	0.46
1:I:218:MET:SD	1:I:293:ILE:HG13	2.56	0.46
1:F:30:MET:HE2	1:F:40:TYR:HE1	1.81	0.46
1:I:128:THR:HG22	1:I:158:VAL:HG12	1.98	0.46
1:C:15:LYS:O	1:C:99:VAL:HA	2.16	0.46
1:B:240:ALA:O	1:B:244:ALA:N	2.42	0.46
1:I:155:LYS:HD3	1:I:223:SER:HB3	1.98	0.46
1:F:158:VAL:HG21	1:F:161:LEU:HB2	1.97	0.46
1:C:93:LEU:HD13	1:C:121:ALA:HB2	1.98	0.45
1:G:16:VAL:HG22	1:G:100:PHE:HB2	1.98	0.45
2:M:25:GLU:O	2:M:29:THR:HG22	2.15	0.45
1:B:290:VAL:HG13	1:B:291:ASN:O	2.16	0.45
1:F:136:PHE:CD1	1:F:166:ASN:HB3	2.52	0.45
1:C:29:ARG:HD2	1:C:29:ARG:HA	1.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:185:GLU:O	1:F:189:VAL:HG23	2.15	0.45
1:B:105:MET:O	1:B:135:PRO:HD3	2.16	0.45
1:A:26:ALA:O	1:A:30:MET:HG3	2.16	0.45
1:B:264:ILE:O	1:B:296:SER:HA	2.17	0.45
1:F:236:ARG:NH2	1:F:269:ASN:OD1	2.45	0.45
1:F:29:ARG:NH1	1:F:184:ARG:HG2	2.31	0.45
1:B:258:GLN:H	1:B:314:GLY:HA3	1.80	0.45
1:I:14:ILE:HA	1:I:98:MET:O	2.16	0.45
1:A:29:ARG:HD2	1:A:29:ARG:HA	1.74	0.45
1:E:90:GLU:HG2	1:E:120:ILE:HG23	1.98	0.45
1:F:212:ALA:C	1:F:214:VAL:H	2.20	0.45
1:C:265:THR:HA	1:C:297:VAL:O	2.16	0.45
1:C:162:ILE:HD11	1:C:311:ILE:HD13	1.99	0.45
1:E:187:ASP:OD1	1:E:188:ASN:N	2.50	0.45
1:C:135:PRO:HG2	1:C:144:GLN:NE2	2.32	0.45
1:B:133:THR:HG23	1:B:190:LEU:HD22	1.98	0.45
1:E:41:ILE:HA	1:E:57:VAL:HG13	1.98	0.45
1:E:85:SER:HA	1:E:88:GLN:OE1	2.17	0.45
1:A:200:LEU:HD21	1:A:263:ASN:HD22	1.81	0.45
1:F:264:ILE:CD1	1:F:308:VAL:HG22	2.47	0.45
1:E:264:ILE:HD13	1:E:308:VAL:HG22	1.99	0.45
1:D:40:TYR:O	1:D:57:VAL:HG13	2.16	0.45
1:A:209:LEU:HA	2:J:4:HIS:NE2	2.31	0.45
1:B:245:ILE:HG22	1:B:254:ILE:CD1	2.46	0.45
1:G:226:MET:HB3	1:G:311:ILE:HG12	1.99	0.45
1:E:120:ILE:O	1:E:124:LEU:HD13	2.17	0.45
1:A:90:GLU:HG2	1:A:120:ILE:HG23	1.98	0.45
1:C:93:LEU:HA	1:C:93:LEU:HD23	1.68	0.45
1:C:264:ILE:CD1	1:C:308:VAL:HG22	2.48	0.44
1:D:295:GLY:HA2	2:M:11:VAL:HA	1.98	0.44
1:F:15:LYS:O	1:F:99:VAL:HA	2.17	0.44
1:C:275:VAL:HG12	2:L:23:LEU:HD13	1.99	0.44
1:F:18:GLY:HA2	1:F:102:THR:HG23	1.99	0.44
1:E:78:GLY:HA3	1:E:108:GLY:O	2.17	0.44
1:G:213:ASP:CG	1:G:214:VAL:N	2.71	0.44
1:A:245:ILE:HD13	1:A:281:ILE:HG22	2.00	0.44
1:I:164:ILE:HD13	1:I:189:VAL:HG12	2.00	0.44
1:I:52:LEU:HA	1:I:52:LEU:HD23	1.69	0.44
1:E:295:GLY:CA	2:N:11:VAL:HG22	2.38	0.44
1:B:174:ASP:HB2	1:B:177:THR:HG23	1.99	0.44
1:G:89:ILE:HD13	1:G:117:ILE:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:243:LYS:O	1:E:247:SER:N	2.50	0.44
1:G:59:MET:HE1	1:G:92:ALA:HB3	1.98	0.44
1:D:172:ILE:HG13	1:D:248:PRO:HG2	1.99	0.44
1:C:166:ASN:O	1:C:169:ILE:HG12	2.18	0.44
1:C:190:LEU:HA	1:C:190:LEU:HD12	1.69	0.44
1:C:29:ARG:NH2	1:C:188:ASN:HB2	2.33	0.44
1:I:14:ILE:HG13	1:I:38:VAL:HG12	1.99	0.44
1:A:30:MET:HA	1:A:191:ARG:HG3	2.00	0.44
1:A:24:ASN:OD1	1:A:53:SER:HB2	2.16	0.44
1:C:44:ASN:HB3	1:C:50:LEU:HB2	2.00	0.44
1:D:264:ILE:O	1:D:296:SER:HA	2.18	0.44
1:D:25:ASN:O	1:D:29:ARG:HG2	2.18	0.44
1:H:25:ASN:O	1:H:29:ARG:HG2	2.18	0.44
1:A:74:ASN:ND2	1:G:145:LEU:HD13	2.32	0.44
1:D:245:ILE:CG2	1:D:254:ILE:HD11	2.47	0.44
1:C:74:ASN:HA	1:C:75:PRO:HD3	1.78	0.44
1:H:158:VAL:HG21	1:H:161:LEU:HB2	2.00	0.44
1:C:238:ALA:HA	1:C:281:ILE:HD11	1.98	0.44
1:A:75:PRO:HA	1:A:108:GLY:O	2.18	0.44
1:I:241:ALA:HB2	1:I:278:ALA:HB1	2.00	0.43
1:F:131:VAL:HG12	1:F:190:LEU:HD12	2.00	0.43
1:A:118:ALA:HB1	1:A:158:VAL:HG12	1.98	0.43
1:F:28:ASN:HD22	1:H:52:LEU:HD22	1.83	0.43
1:H:15:LYS:HD3	1:H:41:ILE:HD11	2.00	0.43
1:F:67:ARG:HD2	1:H:138:PHE:O	2.18	0.43
1:E:50:LEU:HG	1:E:58:LYS:HB3	2.00	0.43
1:D:134:ARG:HG3	1:D:135:PRO:HD2	2.00	0.43
1:A:290:VAL:HG12	2:J:16:ALA:HB2	2.00	0.43
1:E:238:ALA:HB1	1:E:281:ILE:HD11	2.00	0.43
1:H:134:ARG:HB3	1:H:165:PRO:HA	2.00	0.43
1:G:17:ILE:HG12	1:G:41:ILE:HB	2.00	0.43
1:I:171:GLU:OE1	1:I:248:PRO:HB3	2.18	0.43
1:F:141:ARG:O	1:F:145:LEU:HG	2.18	0.43
1:F:79:LYS:HE3	1:F:83:GLU:OE2	2.18	0.43
1:C:261:LEU:HA	1:C:293:ILE:O	2.18	0.43
1:B:35:VAL:HG22	1:B:195:GLN:CD	2.39	0.43
1:G:267:GLY:HA2	1:G:299:ASN:O	2.19	0.43
1:E:273:TYR:O	1:E:277:GLU:HB2	2.18	0.43
1:A:250:LEU:HA	1:A:250:LEU:HD12	1.80	0.43
1:D:78:GLY:CA	1:D:108:GLY:O	2.64	0.43
1:H:196:GLY:HA3	1:H:309:THR:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:141:ARG:NE	3:H:402:PO4:O4	2.40	0.43
1:B:287:ASP:O	1:B:290:VAL:HB	2.17	0.43
1:G:131:VAL:O	1:G:190:LEU:HD11	2.19	0.43
1:C:90:GLU:HG2	1:C:120:ILE:CG2	2.49	0.43
1:F:120:ILE:O	1:F:124:LEU:HD13	2.18	0.43
1:A:106:GLY:N	1:A:111:THR:OG1	2.43	0.43
1:D:174:ASP:HB2	1:D:177:THR:HG23	2.01	0.43
1:B:25:ASN:O	1:B:29:ARG:HG2	2.18	0.43
1:B:171:GLU:OE1	1:B:248:PRO:HB3	2.17	0.43
1:A:297:VAL:HG12	2:J:9:GLY:HA3	2.00	0.43
1:D:59:MET:HE1	1:D:92:ALA:CB	2.49	0.43
1:A:94:LYS:HA	1:A:124:LEU:HD23	2.00	0.43
1:D:245:ILE:HG22	1:D:254:ILE:HD11	2.01	0.43
1:D:79:LYS:HE3	1:D:83:GLU:OE2	2.19	0.43
1:G:169:ILE:CD1	1:G:189:VAL:HG21	2.48	0.43
1:G:134:ARG:HB3	1:G:165:PRO:HA	2.01	0.43
1:F:89:ILE:HD13	1:F:117:ILE:HG12	2.00	0.43
1:F:226:MET:HB3	1:F:311:ILE:HG12	2.00	0.43
1:F:247:SER:HA	1:F:248:PRO:HD3	1.92	0.43
1:C:17:ILE:CD1	1:C:93:LEU:HD11	2.49	0.43
1:I:18:GLY:HA2	1:I:102:THR:HG23	1.99	0.43
1:B:290:VAL:O	2:K:16:ALA:HB2	2.18	0.43
1:B:77:VAL:O	1:B:81:ALA:N	2.43	0.43
1:I:13:SER:O	1:I:97:ASP:N	2.52	0.42
1:G:154:MET:O	1:G:158:VAL:HG22	2.19	0.42
1:E:86:LYS:O	1:E:90:GLU:HG3	2.19	0.42
1:H:102:THR:HA	1:H:131:VAL:O	2.19	0.42
1:C:114:ALA:HB3	1:C:115:PRO:HD3	2.01	0.42
1:A:180:LEU:HD12	1:A:180:LEU:HA	1.74	0.42
1:G:85:SER:HB3	1:G:88:GLN:HB2	2.01	0.42
1:C:41:ILE:HD13	1:C:92:ALA:HB1	2.01	0.42
1:A:162:ILE:HD11	1:A:197:ILE:HD11	2.02	0.42
1:I:35:VAL:HB	1:I:40:TYR:OH	2.19	0.42
1:F:35:VAL:HB	1:F:40:TYR:OH	2.19	0.42
1:I:192:GLN:HB3	1:I:228:ILE:CD1	2.49	0.42
1:A:17:ILE:HG21	1:A:17:ILE:HD13	1.72	0.42
1:E:295:GLY:HA3	2:N:11:VAL:CG2	2.38	0.42
1:E:29:ARG:NH2	1:E:188:ASN:HB2	2.34	0.42
1:G:170:LEU:HA	1:G:173:VAL:HG22	2.02	0.42
1:G:30:MET:HE2	1:G:30:MET:HB3	1.78	0.42
1:D:264:ILE:O	1:D:297:VAL:N	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:164:ILE:HD13	1:G:189:VAL:HG12	2.00	0.42
1:G:155:LYS:HD3	1:G:223:SER:HB3	2.01	0.42
1:H:227:GLY:HA3	1:H:244:ALA:O	2.19	0.42
1:G:264:ILE:O	1:G:296:SER:HA	2.20	0.42
1:H:133:THR:HA	1:H:164:ILE:O	2.20	0.42
1:H:141:ARG:O	1:H:145:LEU:HG	2.20	0.42
1:F:265:THR:HG23	1:F:307:VAL:HG13	2.00	0.42
1:H:41:ILE:HG12	1:H:57:VAL:CG1	2.49	0.42
1:G:226:MET:CB	1:G:311:ILE:HG12	2.50	0.42
1:A:265:THR:OG1	1:A:297:VAL:HG23	2.20	0.42
1:B:238:ALA:HB1	1:B:281:ILE:HD11	2.02	0.42
1:D:27:VAL:HG13	1:D:40:TYR:CD1	2.54	0.42
1:B:129:VAL:HG22	1:B:160:THR:HG22	2.01	0.42
1:F:129:VAL:HG13	1:F:160:THR:CG2	2.50	0.42
1:D:226:MET:HA	1:D:310:VAL:O	2.20	0.42
1:F:25:ASN:O	1:F:29:ARG:HG2	2.20	0.42
1:C:18:GLY:HA2	1:C:102:THR:HG23	2.02	0.42
1:B:29:ARG:HD2	1:B:29:ARG:HA	1.61	0.42
1:G:129:VAL:HG22	1:G:160:THR:HG22	2.02	0.42
1:C:128:THR:HG22	1:C:158:VAL:HG12	2.01	0.42
1:F:30:MET:HE2	1:F:40:TYR:CE1	2.55	0.42
1:F:173:VAL:HB	1:F:177:THR:HG21	2.01	0.42
1:F:200:LEU:C	1:F:201:ILE:HG13	2.39	0.42
1:I:17:ILE:HG12	1:I:41:ILE:HB	2.00	0.42
1:B:168:ARG:HB3	1:B:248:PRO:HB2	2.02	0.42
1:G:29:ARG:NH1	1:G:184:ARG:HG2	2.35	0.42
2:O:22:LYS:HE3	2:O:26:TYR:CE2	2.55	0.42
1:C:272:LEU:HD12	1:C:272:LEU:H	1.83	0.42
1:A:166:ASN:O	1:A:169:ILE:N	2.44	0.42
1:G:45:THR:HG22	1:G:61:ILE:O	2.19	0.42
1:A:44:ASN:HB3	1:A:50:LEU:HB2	2.02	0.42
1:A:15:LYS:O	1:A:99:VAL:HA	2.20	0.41
1:B:190:LEU:HD12	1:B:190:LEU:HA	1.89	0.41
1:A:145:LEU:HD13	1:B:74:ASN:ND2	2.35	0.41
2:N:19:ILE:O	2:N:23:LEU:HG	2.20	0.41
1:H:60:GLN:NE2	1:H:68:GLY:HA2	2.35	0.41
1:H:78:GLY:HA3	1:H:108:GLY:O	2.19	0.41
1:E:200:LEU:HD12	1:E:261:LEU:HD21	2.02	0.41
1:C:236:ARG:CZ	1:C:306:ILE:HD12	2.50	0.41
1:I:41:ILE:HG12	1:I:57:VAL:HG11	2.02	0.41
1:C:226:MET:CB	1:C:311:ILE:HG12	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:VAL:HG13	1:A:162:ILE:HB	2.02	0.41
1:A:93:LEU:HD23	1:A:93:LEU:HA	1.69	0.41
1:G:98:MET:HE3	1:G:127:LEU:HD23	2.02	0.41
1:F:90:GLU:O	1:F:94:LYS:N	2.49	0.41
1:A:168:ARG:HD3	1:A:171:GLU:OE2	2.20	0.41
1:D:280:ASP:OD1	2:M:20:ARG:NE	2.47	0.41
1:I:166:ASN:HA	1:I:169:ILE:HG12	2.02	0.41
1:A:263:ASN:HB3	1:A:309:THR:HB	2.02	0.41
1:D:102:THR:HA	1:D:131:VAL:O	2.21	0.41
1:B:143:ARG:HD3	1:B:143:ARG:HA	1.88	0.41
1:I:169:ILE:HD13	1:I:249:LEU:HD21	2.01	0.41
1:E:195:GLN:HA	1:E:198:SER:OG	2.20	0.41
1:D:24:ASN:OD1	1:D:53:SER:HB2	2.20	0.41
1:A:52:LEU:HD23	1:A:52:LEU:HA	1.80	0.41
1:B:128:THR:HG22	1:B:158:VAL:HG12	2.02	0.41
1:C:196:GLY:HA3	1:C:309:THR:HG21	2.02	0.41
1:C:20:GLY:CA	1:C:109:THR:HB	2.50	0.41
1:C:115:PRO:HG3	1:C:154:MET:HG2	2.02	0.41
1:I:60:GLN:HE21	1:I:68:GLY:HA2	1.85	0.41
1:E:93:LEU:HA	1:E:93:LEU:HD23	1.69	0.41
1:B:169:ILE:HD11	1:B:189:VAL:HG21	2.02	0.41
1:A:101:VAL:HG21	1:A:118:ALA:HA	2.02	0.41
1:C:131:VAL:O	1:C:190:LEU:HD11	2.21	0.41
1:A:90:GLU:HG2	1:A:120:ILE:CG2	2.51	0.41
1:F:79:LYS:O	1:F:83:GLU:HG3	2.21	0.41
1:B:128:THR:N	1:B:159:ASP:OD2	2.46	0.41
1:B:18:GLY:HA2	1:B:102:THR:HG23	2.02	0.41
1:E:75:PRO:HG3	1:E:107:GLY:O	2.20	0.41
1:F:41:ILE:HG12	1:F:57:VAL:CG1	2.51	0.41
1:A:192:GLN:OE1	1:A:228:ILE:HD13	2.20	0.41
2:N:12:LEU:HG	2:N:12:LEU:H	1.75	0.41
1:D:266:GLY:HA3	1:D:306:ILE:HG22	2.03	0.41
1:F:241:ALA:HB2	1:F:308:VAL:HG21	2.02	0.41
1:A:143:ARG:HD3	1:A:143:ARG:HA	1.75	0.41
2:J:36:TRP:O	2:J:36:TRP:HD1	2.03	0.41
1:I:136:PHE:CE1	1:I:166:ASN:HB3	2.55	0.41
1:A:275:VAL:HG13	1:A:294:PHE:HZ	1.86	0.41
1:B:105:MET:HG2	1:B:132:VAL:HB	2.03	0.41
1:D:270:LEU:O	2:M:33:VAL:HG23	2.20	0.41
2:N:25:GLU:O	2:N:29:THR:HG22	2.21	0.41
1:C:119:GLN:OE1	1:C:157:ALA:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:111:THR:HG23	1:D:150:GLY:HA3	2.02	0.41
1:E:269:ASN:ND2	1:E:303:LYS:O	2.49	0.41
1:E:272:LEU:H	1:E:272:LEU:HD12	1.86	0.41
1:G:105:MET:O	1:G:135:PRO:HD3	2.21	0.41
1:F:261:LEU:HA	1:F:293:ILE:O	2.21	0.41
1:F:294:PHE:C	1:F:294:PHE:CD2	2.95	0.41
1:F:127:LEU:HD12	1:F:159:ASP:OD2	2.21	0.41
1:E:154:MET:O	1:E:158:VAL:HG22	2.21	0.41
1:I:139:GLU:HB3	1:I:143:ARG:HG3	2.02	0.41
1:A:226:MET:CB	1:A:311:ILE:HG12	2.51	0.41
1:G:35:VAL:HG22	1:G:195:GLN:CD	2.40	0.41
1:F:212:ALA:O	1:F:214:VAL:N	2.54	0.40
1:B:17:ILE:HG12	1:B:41:ILE:HB	2.03	0.40
1:E:263:ASN:OD1	1:E:265:THR:HG22	2.21	0.40
1:F:196:GLY:HA2	1:F:263:ASN:HD22	1.86	0.40
1:G:150:GLY:O	1:G:154:MET:N	2.50	0.40
1:D:241:ALA:HA	1:D:308:VAL:HG11	2.03	0.40
1:G:164:ILE:HG21	1:G:189:VAL:CG1	2.50	0.40
1:H:142:LYS:HE3	1:H:146:GLN:OE1	2.21	0.40
1:G:180:LEU:HA	1:G:180:LEU:HD12	1.88	0.40
1:A:190:LEU:HA	1:A:190:LEU:HD12	1.69	0.40
1:G:245:ILE:HG22	1:G:254:ILE:CD1	2.51	0.40
2:J:12:LEU:CD2	2:J:19:ILE:HG23	2.52	0.40
1:E:200:LEU:CD1	1:E:261:LEU:HD21	2.52	0.40
1:E:261:LEU:HA	1:E:293:ILE:O	2.21	0.40
1:G:294:PHE:C	1:G:294:PHE:CD2	2.94	0.40
1:H:162:ILE:CD1	1:H:197:ILE:HD11	2.50	0.40
1:D:272:LEU:HD13	2:M:30:PHE:O	2.22	0.40
1:B:17:ILE:HA	1:B:41:ILE:O	2.21	0.40
1:B:20:GLY:O	1:B:24:ASN:HB2	2.21	0.40
1:G:275:VAL:HG13	1:G:294:PHE:HZ	1.85	0.40
1:H:101:VAL:O	1:H:130:GLY:HA2	2.20	0.40
1:H:88:GLN:OE1	1:H:88:GLN:N	2.50	0.40
1:F:98:MET:HE3	1:F:127:LEU:HD23	2.04	0.40
1:I:264:ILE:CD1	1:I:308:VAL:HG22	2.50	0.40
1:G:196:GLY:HA3	1:G:309:THR:HG21	2.03	0.40
1:A:169:ILE:HD13	1:A:249:LEU:HD21	2.03	0.40
1:I:100:PHE:CD2	1:I:194:VAL:HG13	2.56	0.40
1:H:272:LEU:HA	1:H:275:VAL:HB	2.04	0.40
1:A:100:PHE:CD2	1:A:194:VAL:HG13	2.57	0.40
1:A:145:LEU:HD21	1:B:77:VAL:HG23	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:LEU:HD23	1:B:124:LEU:HA	1.80	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	288/305 (94%)	283 (98%)	5 (2%)	0	100	100
1	B	281/305 (92%)	276 (98%)	5 (2%)	0	100	100
1	C	280/305 (92%)	273 (98%)	7 (2%)	0	100	100
1	D	268/305 (88%)	266 (99%)	2 (1%)	0	100	100
1	E	276/305 (90%)	271 (98%)	5 (2%)	0	100	100
1	F	274/305 (90%)	270 (98%)	4 (2%)	0	100	100
1	G	269/305 (88%)	265 (98%)	4 (2%)	0	100	100
1	H	253/305 (83%)	247 (98%)	5 (2%)	1 (0%)	39	80
1	I	260/305 (85%)	255 (98%)	4 (2%)	1 (0%)	39	80
2	J	34/60 (57%)	34 (100%)	0	0	100	100
2	K	11/60 (18%)	11 (100%)	0	0	100	100
2	L	28/60 (47%)	27 (96%)	1 (4%)	0	100	100
2	M	19/60 (32%)	19 (100%)	0	0	100	100
2	N	23/60 (38%)	23 (100%)	0	0	100	100
2	O	26/60 (43%)	25 (96%)	1 (4%)	0	100	100
2	P	19/60 (32%)	18 (95%)	1 (5%)	0	100	100
2	Q	23/60 (38%)	22 (96%)	1 (4%)	0	100	100
2	R	16/60 (27%)	15 (94%)	0	1 (6%)	2	13
All	All	2648/3285 (81%)	2600 (98%)	45 (2%)	3 (0%)	56	91

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	R	15	LYS
1	I	222	GLY
1	H	222	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	205/227 (90%)	197 (96%)	8 (4%)	39 78
1	B	174/227 (77%)	169 (97%)	5 (3%)	50 83
1	C	200/227 (88%)	190 (95%)	10 (5%)	30 71
1	D	190/227 (84%)	181 (95%)	9 (5%)	32 73
1	E	187/227 (82%)	175 (94%)	12 (6%)	22 62
1	F	196/227 (86%)	188 (96%)	8 (4%)	37 76
1	G	188/227 (83%)	180 (96%)	8 (4%)	35 75
1	H	173/227 (76%)	167 (96%)	6 (4%)	43 80
1	I	172/227 (76%)	165 (96%)	7 (4%)	37 76
2	J	22/52 (42%)	20 (91%)	2 (9%)	12 42
2	K	2/52 (4%)	0	2 (100%)	0 0
2	L	18/52 (35%)	16 (89%)	2 (11%)	8 32
2	M	5/52 (10%)	4 (80%)	1 (20%)	1 8
2	N	11/52 (21%)	9 (82%)	2 (18%)	2 10
2	O	16/52 (31%)	14 (88%)	2 (12%)	6 26
2	P	11/52 (21%)	9 (82%)	2 (18%)	2 10
2	Q	7/52 (14%)	5 (71%)	2 (29%)	0 1
2	R	5/52 (10%)	5 (100%)	0	100 100
All	All	1782/2511 (71%)	1694 (95%)	88 (5%)	31 72

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	87	GLU
1	A	160	THR
1	A	191	ARG
1	A	286	SER
1	A	290	VAL
1	A	297	VAL
1	A	306	ILE
1	B	48	GLN
1	B	187	ASP
1	B	191	ARG
1	B	219	SER
1	B	297	VAL
1	C	191	ARG
1	C	225	LEU
1	C	260	VAL
1	C	264	ILE
1	C	265	THR
1	C	286	SER
1	C	290	VAL
1	C	297	VAL
1	C	306	ILE
1	C	307	VAL
1	D	48	GLN
1	D	57	VAL
1	D	191	ARG
1	D	260	VAL
1	D	264	ILE
1	D	265	THR
1	D	290	VAL
1	D	304	ASP
1	D	307	VAL
1	E	48	GLN
1	E	141	ARG
1	E	187	ASP
1	E	191	ARG
1	E	219	SER
1	E	255	ASP
1	E	265	THR
1	E	290	VAL
1	E	293	ILE
1	E	297	VAL
1	E	306	ILE

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Mol	Chain	Res	Type
1	E	307	VAL
1	F	48	GLN
1	F	191	ARG
1	F	214	VAL
1	F	223	SER
1	F	255	ASP
1	F	265	THR
1	F	290	VAL
1	F	297	VAL
1	G	87	GLU
1	G	191	ARG
1	G	213	ASP
1	G	219	SER
1	G	225	LEU
1	G	255	ASP
1	G	290	VAL
1	G	297	VAL
1	H	48	GLN
1	H	76	GLU
1	H	187	ASP
1	H	191	ARG
1	H	269	ASN
1	H	286	SER
1	I	76	GLU
1	I	191	ARG
1	I	225	LEU
1	I	255	ASP
1	I	260	VAL
1	I	290	VAL
1	I	307	VAL
2	J	29	THR
2	J	37	ILE
2	K	10	VAL
2	K	17	TRP
2	L	13	VAL
2	L	22	LYS
2	M	29	THR
2	N	12	LEU
2	N	29	THR
2	O	12	LEU
2	O	29	THR
2	P	13	VAL

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Mol	Chain	Res	Type
2	P	29	THR
2	Q	12	LEU
2	Q	33	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	263	ASN
1	B	263	ASN
1	C	144	GLN
1	H	144	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry

16 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	$\#\|Z\| > 2$
3	PO4	A	401	-	4,4,4	0.41	0	6,6,6	0.29	0
3	PO4	A	402	-	4,4,4	0.53	0	6,6,6	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	PO4	B	401	-	4,4,4	0.47	0	6,6,6	0.30	0
3	PO4	B	402	-	4,4,4	0.35	0	6,6,6	0.28	0
3	PO4	C	401	-	4,4,4	0.55	0	6,6,6	0.27	0
3	PO4	C	402	-	4,4,4	0.68	0	6,6,6	0.32	0
3	PO4	D	401	-	4,4,4	0.37	0	6,6,6	0.28	0
3	PO4	D	402	-	4,4,4	0.51	0	6,6,6	0.30	0
3	PO4	E	401	-	4,4,4	0.41	0	6,6,6	0.27	0
3	PO4	F	401	-	4,4,4	0.47	0	6,6,6	0.27	0
3	PO4	G	401	-	4,4,4	0.49	0	6,6,6	0.28	0
3	PO4	G	402	-	4,4,4	0.44	0	6,6,6	0.30	0
3	PO4	H	401	-	4,4,4	0.49	0	6,6,6	0.29	0
3	PO4	H	402	-	4,4,4	0.63	0	6,6,6	0.29	0
3	PO4	I	401	-	4,4,4	0.46	0	6,6,6	0.30	0
3	PO4	I	402	-	4,4,4	0.76	0	6,6,6	0.28	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PO4	A	401	-	-	0/0/0/0	0/0/0/0
3	PO4	A	402	-	-	0/0/0/0	0/0/0/0
3	PO4	B	401	-	-	0/0/0/0	0/0/0/0
3	PO4	B	402	-	-	0/0/0/0	0/0/0/0
3	PO4	C	401	-	-	0/0/0/0	0/0/0/0
3	PO4	C	402	-	-	0/0/0/0	0/0/0/0
3	PO4	D	401	-	-	0/0/0/0	0/0/0/0
3	PO4	D	402	-	-	0/0/0/0	0/0/0/0
3	PO4	E	401	-	-	0/0/0/0	0/0/0/0
3	PO4	F	401	-	-	0/0/0/0	0/0/0/0
3	PO4	G	401	-	-	0/0/0/0	0/0/0/0
3	PO4	G	402	-	-	0/0/0/0	0/0/0/0
3	PO4	H	401	-	-	0/0/0/0	0/0/0/0
3	PO4	H	402	-	-	0/0/0/0	0/0/0/0
3	PO4	I	401	-	-	0/0/0/0	0/0/0/0
3	PO4	I	402	-	-	0/0/0/0	0/0/0/0

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.

11 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	PO4	1	0
3	A	402	PO4	1	0
3	C	401	PO4	1	0
3	C	402	PO4	1	0
3	D	401	PO4	1	0
3	D	402	PO4	1	0
3	E	401	PO4	1	0
3	F	401	PO4	1	0
3	G	401	PO4	1	0
3	H	402	PO4	2	0
3	I	401	PO4	1	0

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, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	294/305 (96%)	0.07	1 (0%) 94 93	43, 72, 125, 180	0
1	B	289/305 (94%)	0.25	12 (4%) 40 26	48, 102, 158, 209	0
1	C	288/305 (94%)	0.11	3 (1%) 84 75	43, 77, 137, 197	0
1	D	280/305 (91%)	0.23	10 (3%) 46 31	50, 83, 153, 193	0
1	E	286/305 (93%)	0.16	9 (3%) 52 38	50, 93, 150, 198	0
1	F	284/305 (93%)	0.20	6 (2%) 67 52	53, 92, 146, 233	0
1	G	279/305 (91%)	0.32	16 (5%) 27 15	50, 93, 151, 229	0
1	H	269/305 (88%)	0.22	11 (4%) 41 27	52, 91, 148, 188	0
1	I	270/305 (88%)	0.36	19 (7%) 19 11	46, 94, 150, 204	0
2	J	36/60 (60%)	-0.01	0 100 100	61, 84, 122, 145	0
2	K	15/60 (25%)	-0.40	0 100 100	84, 101, 118, 130	0
2	L	30/60 (50%)	-0.15	1 (3%) 50 35	62, 97, 119, 170	0
2	M	25/60 (41%)	-0.03	0 100 100	69, 106, 138, 145	0
2	N	27/60 (45%)	-0.15	0 100 100	73, 104, 138, 189	0
2	O	28/60 (46%)	-0.25	0 100 100	65, 89, 127, 161	0
2	P	21/60 (35%)	0.06	0 100 100	63, 90, 113, 158	0
2	Q	27/60 (45%)	-0.42	1 (3%) 45 30	75, 100, 114, 157	0
2	R	18/60 (30%)	0.38	3 (16%) 2 1	81, 105, 141, 184	0
All	All	2766/3285 (84%)	0.18	92 (3%) 50 35	43, 90, 147, 233	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	256	GLY	6.2
1	D	298	ILE	5.2
1	G	267	GLY	5.2

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Mol	Chain	Res	Type	RSRZ
1	G	298	ILE	5.1
1	I	292	MET	4.7
1	D	268	THR	4.4
1	E	241	ALA	4.3
1	I	200	LEU	4.1
1	H	308	VAL	3.7
1	I	255	ASP	3.7
1	G	127	LEU	3.7
1	G	255	ASP	3.5
1	F	300	GLU	3.4
1	G	98	MET	3.3
1	B	294	PHE	3.3
1	E	238	ALA	3.3
1	B	292	MET	3.3
1	I	262	MET	3.3
1	I	39	GLU	3.2
1	I	160	THR	3.1
1	I	98	MET	3.1
1	F	248	PRO	3.1
1	F	269	ASN	3.0
1	I	309	THR	3.0
1	D	275	VAL	3.0
1	B	249	LEU	2.9
1	B	296	SER	2.9
1	D	267	GLY	2.9
1	G	258	GLN	2.9
1	B	262	MET	2.9
1	I	127	LEU	2.9
1	B	313	THR	2.8
1	F	155	LYS	2.8
1	H	157	ALA	2.8
1	E	262	MET	2.8
1	A	268	THR	2.8
1	B	170	LEU	2.7
1	G	290	VAL	2.7
1	G	268	THR	2.7
1	D	272	LEU	2.7
1	G	299	ASN	2.7
1	G	257	ALA	2.7
1	H	262	MET	2.6
1	F	256	GLY	2.6
1	E	258	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	251	GLU	2.6
1	E	264	ILE	2.6
1	G	262	MET	2.5
1	I	254	ILE	2.5
2	R	14	GLY	2.5
1	H	281	ILE	2.5
1	B	158	VAL	2.5
1	D	276	GLN	2.5
1	H	56	GLU	2.4
1	C	237	ALA	2.4
1	E	296	SER	2.4
1	H	35	VAL	2.4
1	D	299	ASN	2.3
1	F	298	ILE	2.3
1	H	287	ASP	2.3
1	I	57	VAL	2.3
1	H	36	GLN	2.3
1	G	264	ILE	2.3
2	R	13	VAL	2.3
1	D	39	GLU	2.2
1	I	228	ILE	2.2
2	Q	23	LEU	2.2
1	H	41	ILE	2.2
1	I	14	ILE	2.2
2	R	11	VAL	2.2
1	I	226	MET	2.2
1	I	199	ASP	2.2
1	B	171	GLU	2.2
1	G	300	GLU	2.2
1	G	160	THR	2.2
1	I	293	ILE	2.2
1	B	160	THR	2.1
1	C	275	VAL	2.1
1	E	313	THR	2.1
2	L	9	GLY	2.1
1	I	159	ASP	2.1
1	G	228	ILE	2.1
1	B	254	ILE	2.1
1	H	160	THR	2.1
1	D	262	MET	2.1
1	H	238	ALA	2.1
1	I	38	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	264	ILE	2.1
1	C	296	SER	2.0
1	E	169	ILE	2.0
1	E	308	VAL	2.0
1	I	291	ASN	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	PO4	C	401	5/5	0.95	0.36	5.30	69,72,74,84	0
3	PO4	I	401	5/5	0.94	0.31	2.10	83,84,85,90	0
3	PO4	D	401	5/5	0.97	0.29	1.42	62,62,68,69	0
3	PO4	G	401	5/5	0.95	0.27	1.34	76,77,82,84	0
3	PO4	H	401	5/5	0.95	0.26	1.11	63,67,74,75	0
3	PO4	B	401	5/5	0.97	0.27	0.92	77,78,83,83	0
3	PO4	H	402	5/5	0.97	0.25	0.36	64,67,72,76	0
3	PO4	A	401	5/5	0.98	0.21	0.24	59,63,65,70	0
3	PO4	F	401	5/5	0.98	0.22	0.22	72,73,79,80	0
3	PO4	E	401	5/5	0.96	0.21	-0.14	72,77,84,87	0
3	PO4	A	402	5/5	0.97	0.21	-0.35	47,55,59,64	0
3	PO4	D	402	5/5	0.95	0.20	-0.39	57,62,68,69	0
3	PO4	C	402	5/5	0.96	0.21	-0.54	60,62,71,73	0
3	PO4	I	402	5/5	0.96	0.20	-0.64	59,63,72,78	0
3	PO4	G	402	5/5	0.98	0.18	-1.88	50,59,62,67	0
3	PO4	B	402	5/5	0.94	0.10	-	120,125,129,132	0

6.5 Other polymers (i)

There are no such residues in this entry.