



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:43 AM GMT

PDB ID : 2B7X
Title : Sequential reorganization of beta-sheet topology by insertion of a single strand
Authors : Sagermann, M.; Matthews, B.W.
Deposited on : 2005-10-05
Resolution : 3.00 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

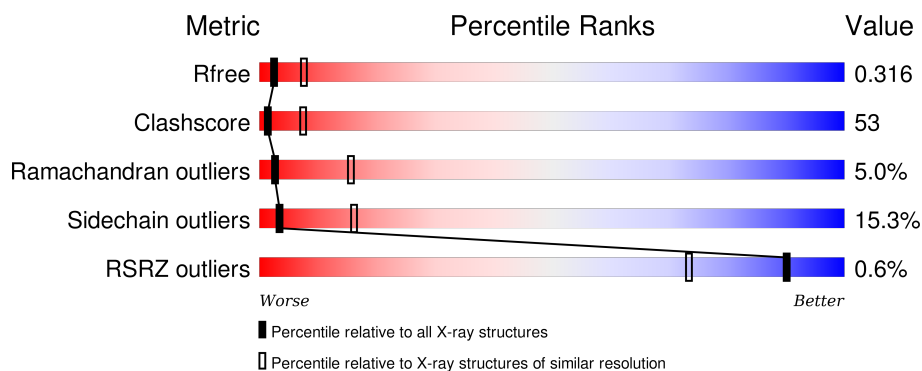
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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 $\leq 5\%$. 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	170	<div> <div></div> <div>27% 47% 14% • 8%</div> </div>
1	B	170	<div> <div></div> <div>32% 46% 10% 5% 8%</div> </div>
1	C	170	<div> <div></div> <div>26% 49% 16% • 8%</div> </div>
1	D	170	<div> <div></div> <div>36% 42% 12% • 6%</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	807	-	-	X	-
2	SO4	D	802	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5085 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 Lysozyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total	C	N	O	S	0	0	0
			1256	791	227	233	5			
1	B	157	Total	C	N	O	S	0	0	0
			1256	791	227	233	5			
1	C	157	Total	C	N	O	S	0	0	0
			1256	791	227	233	5			
1	D	160	Total	C	N	O	S	0	0	0
			1277	805	230	237	5			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	TYR	-	INSERTION	UNP P00720
A	32	THR	-	INSERTION	UNP P00720
A	33	ILE	-	INSERTION	UNP P00720
A	34	GLY	-	INSERTION	UNP P00720
A	35	ILE	-	INSERTION	UNP P00720
A	36	GLY	-	INSERTION	UNP P00720
A	60	THR	CYS	ENGINEERED	UNP P00720
A	103	ALA	CYS	ENGINEERED	UNP P00720
B	25	TYR	-	INSERTION	UNP P00720
B	26	THR	-	INSERTION	UNP P00720
B	27	ILE	-	INSERTION	UNP P00720
B	28	GLY	-	INSERTION	UNP P00720
B	29	ILE	-	INSERTION	UNP P00720
B	30	GLY	-	INSERTION	UNP P00720
B	60	THR	CYS	ENGINEERED	UNP P00720
B	103	ALA	CYS	ENGINEERED	UNP P00720
C	31	TYR	-	INSERTION	UNP P00720
C	32	THR	-	INSERTION	UNP P00720
C	33	ILE	-	INSERTION	UNP P00720
C	34	GLY	-	INSERTION	UNP P00720
C	35	ILE	-	INSERTION	UNP P00720

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Chain	Residue	Modelled	Actual	Comment	Reference
C	36	GLY	-	INSERTION	UNP P00720
C	60	THR	CYS	ENGINEERED	UNP P00720
C	103	ALA	CYS	ENGINEERED	UNP P00720
D	31	TYR	-	INSERTION	UNP P00720
D	32	THR	-	INSERTION	UNP P00720
D	33	ILE	-	INSERTION	UNP P00720
D	34	GLY	-	INSERTION	UNP P00720
D	35	ILE	-	INSERTION	UNP P00720
D	36	GLY	-	INSERTION	UNP P00720
D	60	THR	CYS	ENGINEERED	UNP P00720
D	103	ALA	CYS	ENGINEERED	UNP P00720

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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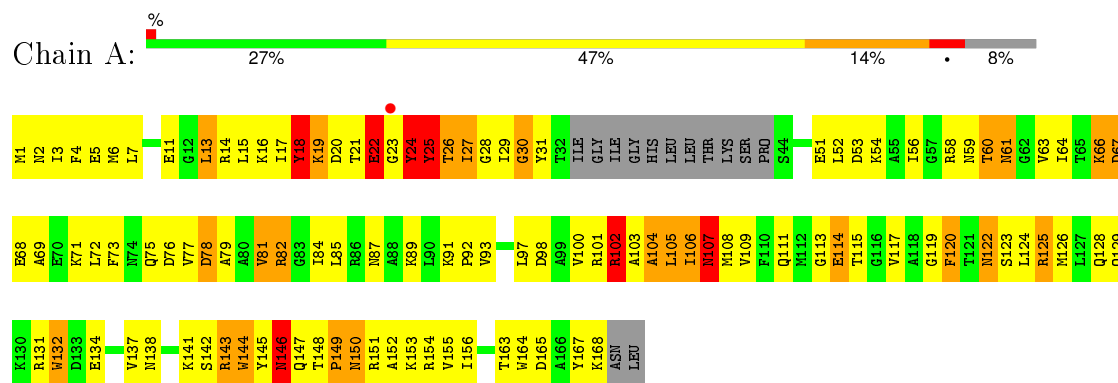
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

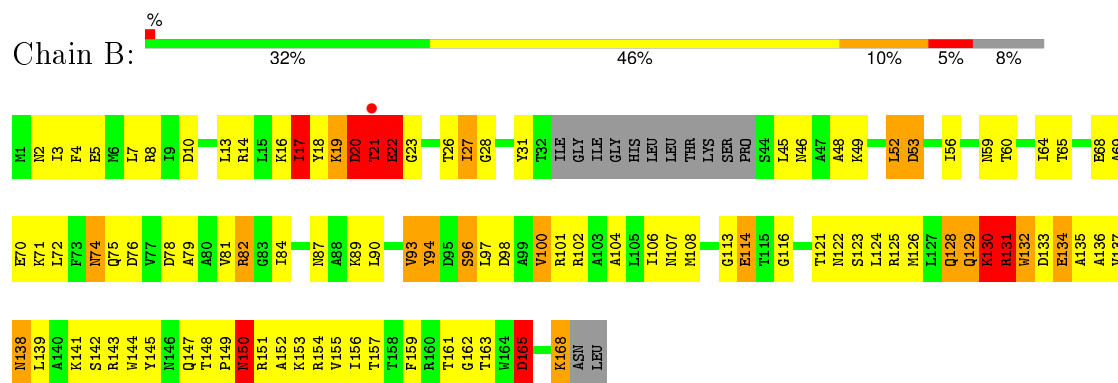
3 Residue-property plots

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.

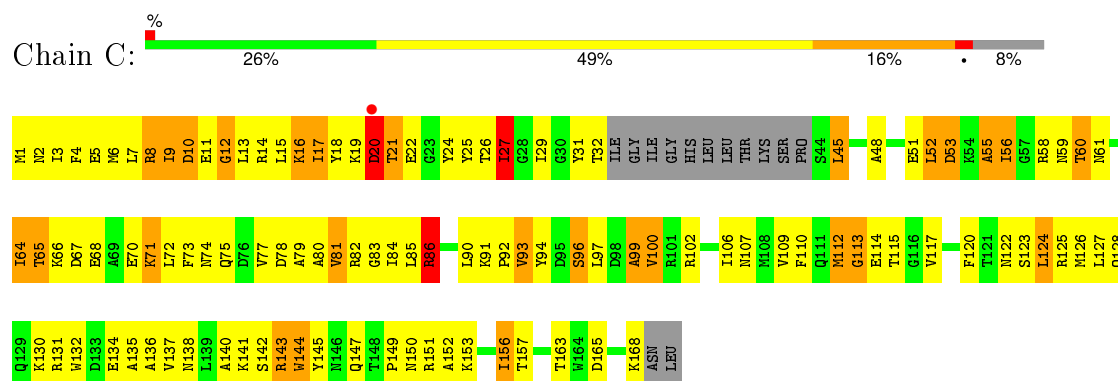
• Molecule 1: Lysozyme



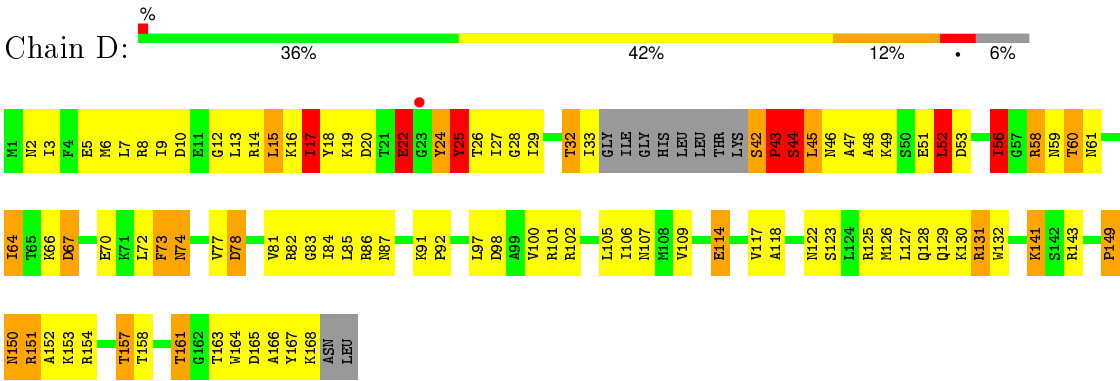
• Molecule 1: Lysozyme



• Molecule 1: Lysozyme



● Molecule 1: Lysozyme



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.38 Å 78.08 Å 143.35 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 20.01 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-3.00) 70.1 (20.01-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 2.41 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.239 , 0.319 0.237 , 0.316	Depositor DCC
R_{free} test set	521 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 19371 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	5085	wwPDB-VP
Average B, all atoms (Å ²)	8.0	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 38.10 % 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 3.8790e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	1.87	22/1274 (1.7%)	2.60	42/1714 (2.5%)
1	B	2.51	18/1274 (1.4%)	2.61	32/1714 (1.9%)
1	C	1.26	5/1274 (0.4%)	1.20	7/1714 (0.4%)
1	D	1.95	10/1296 (0.8%)	1.43	14/1745 (0.8%)
All	All	1.95	55/5118 (1.1%)	2.06	95/6887 (1.4%)

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	A	1	2
1	B	0	6
1	D	1	1
All	All	2	9

All (55) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	21	THR	CB-OG1	64.69	2.72	1.43
1	D	43	PRO	N-CD	31.03	1.91	1.47
1	D	43	PRO	CB-CG	27.65	2.88	1.50
1	D	44	SER	CB-OG	-25.73	1.08	1.42
1	A	60	THR	CB-OG1	-23.03	0.97	1.43
1	B	22	GLU	CB-CG	17.71	1.85	1.52
1	A	147	GLN	CB-CG	-17.56	1.05	1.52
1	A	150	ASN	CB-CG	-17.30	1.11	1.51
1	B	22	GLU	C-N	-17.16	1.02	1.33
1	B	131	ARG	C-N	-16.96	0.95	1.34
1	D	24	TYR	CA-CB	16.35	1.90	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	149	PRO	N-CD	15.98	1.70	1.47
1	C	100	VAL	CB-CG1	15.13	1.84	1.52
1	A	107	ASN	CB-CG	-14.82	1.17	1.51
1	B	19	LYS	CB-CG	14.22	1.91	1.52
1	D	25	TYR	CB-CG	-13.60	1.31	1.51
1	B	17	ILE	C-N	-13.51	1.02	1.34
1	B	132	TRP	C-N	-13.36	1.03	1.34
1	B	20	ASP	C-N	-12.84	1.04	1.34
1	A	106	ILE	CB-CG2	12.66	1.92	1.52
1	A	146	ASN	CB-CG	-10.72	1.26	1.51
1	D	58	ARG	CB-CG	-10.18	1.25	1.52
1	A	148	THR	CB-OG1	-9.88	1.23	1.43
1	A	60	THR	CB-CG2	9.22	1.82	1.52
1	B	131	ARG	CB-CG	-8.98	1.28	1.52
1	D	17	ILE	CB-CG2	8.52	1.79	1.52
1	A	26	THR	CB-OG1	8.41	1.60	1.43
1	A	21	THR	CB-OG1	-8.33	1.26	1.43
1	A	25	TYR	C-N	-8.03	1.15	1.34
1	C	100	VAL	CB-CG2	-8.00	1.36	1.52
1	B	130	LYS	CA-CB	7.99	1.71	1.53
1	B	128	GLN	C-N	-7.92	1.15	1.34
1	A	104	ALA	C-N	7.43	1.51	1.34
1	B	21	THR	C-N	-7.38	1.17	1.34
1	B	20	ASP	CB-CG	-7.00	1.37	1.51
1	A	18	TYR	CE2-CZ	6.99	1.47	1.38
1	D	58	ARG	C-N	6.97	1.50	1.34
1	A	146	ASN	C-N	-6.96	1.18	1.34
1	A	106	ILE	CB-CG1	-6.92	1.34	1.54
1	D	15	LEU	C-N	-6.32	1.19	1.34
1	A	20	ASP	C-N	6.24	1.48	1.34
1	D	42	SER	C-N	-6.19	1.22	1.34
1	B	18	TYR	CD1-CE1	6.07	1.48	1.39
1	B	21	THR	CB-CG2	-5.97	1.32	1.52
1	A	61	ASN	CB-CG	-5.79	1.37	1.51
1	A	149	PRO	CB-CG	-5.53	1.22	1.50
1	B	134	GLU	CG-CD	5.48	1.60	1.51
1	C	100	VAL	C-N	-5.47	1.21	1.34
1	A	102	ARG	CB-CG	-5.36	1.38	1.52
1	A	26	THR	CB-CG2	-5.34	1.34	1.52
1	B	70	GLU	CB-CG	-5.31	1.42	1.52
1	C	24	TYR	CE1-CZ	5.21	1.45	1.38
1	C	99	ALA	C-N	-5.20	1.22	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	24	TYR	CD2-CE2	5.04	1.47	1.39
1	B	18	TYR	CG-CD1	5.04	1.45	1.39

All (95) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	TYR	CB-CG-CD1	47.27	149.36	121.00
1	A	25	TYR	CB-CG-CD2	-46.86	92.88	121.00
1	B	20	ASP	CB-CG-OD1	32.83	147.85	118.30
1	A	24	TYR	CB-CG-CD2	-32.43	101.54	121.00
1	B	20	ASP	CB-CG-OD2	-30.70	90.67	118.30
1	B	132	TRP	CB-CG-CD2	-30.23	87.31	126.60
1	B	132	TRP	CB-CG-CD1	29.00	164.70	127.00
1	A	147	GLN	CA-CB-CG	24.93	168.25	113.40
1	B	22	GLU	O-C-N	-24.18	82.09	123.20
1	B	21	THR	CA-CB-OG1	-20.17	66.64	109.00
1	B	18	TYR	CB-CG-CD2	19.85	132.91	121.00
1	B	21	THR	OG1-CB-CG2	-19.80	64.45	110.00
1	B	21	THR	O-C-N	-19.71	91.16	122.70
1	B	22	GLU	C-N-CA	19.71	163.69	122.30
1	B	22	GLU	CA-C-N	19.39	154.97	116.20
1	B	132	TRP	O-C-N	-18.45	93.18	122.70
1	B	131	ARG	C-N-CA	17.71	165.99	121.70
1	A	24	TYR	CB-CG-CD1	17.66	131.59	121.00
1	A	146	ASN	CB-CG-OD1	-17.53	86.55	121.60
1	B	132	TRP	C-N-CA	16.88	163.89	121.70
1	B	18	TYR	CB-CG-CD1	-16.62	111.03	121.00
1	A	21	THR	CA-CB-CG2	-15.83	90.23	112.40
1	D	43	PRO	CA-CB-CG	-14.94	75.62	104.00
1	B	22	GLU	CB-CG-CD	-14.73	74.44	114.20
1	A	149	PRO	CA-N-CD	-14.47	91.24	111.50
1	A	102	ARG	CA-CB-CG	14.34	144.95	113.40
1	A	146	ASN	CB-CG-ND2	14.25	150.90	116.70
1	A	150	ASN	CA-CB-CG	13.97	144.13	113.40
1	B	20	ASP	CA-CB-CG	13.73	143.61	113.40
1	D	16	LYS	CB-CG-CD	13.53	146.78	111.60
1	D	43	PRO	N-CA-CB	13.15	119.08	103.30
1	B	21	THR	CA-C-N	12.93	145.64	117.20
1	B	131	ARG	CA-CB-CG	12.84	141.64	113.40
1	B	21	THR	C-N-CA	11.96	151.60	121.70
1	B	132	TRP	CA-C-N	11.90	143.38	117.20
1	A	148	THR	CA-CB-CG2	-11.42	96.41	112.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	146	ASN	CA-CB-CG	11.19	138.02	113.40
1	A	106	ILE	CA-CB-CG2	-10.72	89.45	110.90
1	C	97	LEU	CB-CG-CD1	-10.70	92.81	111.00
1	D	56	ILE	CB-CG1-CD1	-10.63	84.15	113.90
1	C	97	LEU	CB-CG-CD2	10.39	128.67	111.00
1	A	60	THR	CA-CB-OG1	10.37	130.77	109.00
1	D	25	TYR	CA-CB-CG	10.19	132.76	113.40
1	A	107	ASN	CA-CB-CG	10.05	135.52	113.40
1	B	131	ARG	O-C-N	-9.78	107.05	122.70
1	D	45	LEU	CB-CG-CD2	-9.77	94.39	111.00
1	D	42	SER	O-C-N	-9.66	102.75	121.10
1	A	22	GLU	CA-CB-CG	8.94	133.07	113.40
1	C	100	VAL	CA-CB-CG1	-8.92	97.53	110.90
1	C	100	VAL	CA-CB-CG2	8.71	123.97	110.90
1	A	107	ASN	CB-CG-ND2	-8.25	96.91	116.70
1	A	150	ASN	CB-CG-OD1	-8.24	105.12	121.60
1	B	53	ASP	CB-CG-OD2	8.12	125.61	118.30
1	D	56	ILE	CA-CB-CG1	8.10	126.38	111.00
1	A	149	PRO	CA-CB-CG	7.79	119.60	104.80
1	A	60	THR	CA-CB-CG2	-7.62	101.73	112.40
1	D	25	TYR	CB-CG-CD2	-7.35	116.59	121.00
1	D	17	ILE	CA-CB-CG1	7.33	124.92	111.00
1	A	21	THR	OG1-CB-CG2	7.03	126.16	110.00
1	B	21	THR	CA-CB-CG2	7.03	122.24	112.40
1	D	52	LEU	CB-CG-CD1	6.99	122.88	111.00
1	A	23	GLY	O-C-N	6.82	133.62	122.70
1	A	107	ASN	CB-CG-OD1	6.78	135.17	121.60
1	A	26	THR	CA-CB-CG2	6.76	121.86	112.40
1	A	102	ARG	CB-CG-CD	6.70	129.02	111.60
1	A	106	ILE	CG1-CB-CG2	-6.69	96.67	111.40
1	D	42	SER	CA-C-N	6.59	135.56	117.10
1	D	16	LYS	CA-CB-CG	6.59	127.89	113.40
1	B	132	TRP	N-CA-CB	6.42	122.16	110.60
1	B	19	LYS	CA-CB-CG	-6.40	99.31	113.40
1	A	26	THR	CA-CB-OG1	-6.35	95.67	109.00
1	A	60	THR	OG1-CB-CG2	6.22	124.32	110.00
1	A	150	ASN	CB-CG-ND2	6.09	131.32	116.70
1	A	21	THR	CA-CB-OG1	-6.08	96.23	109.00
1	B	131	ARG	CB-CG-CD	-6.04	95.90	111.60
1	C	86	ARG	NE-CZ-NH1	6.02	123.31	120.30
1	A	82	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	D	22	GLU	C-N-CA	5.92	134.73	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	TYR	CA-CB-CG	5.88	124.57	113.40
1	C	53	ASP	CB-CG-OD2	5.86	123.58	118.30
1	A	107	ASN	O-C-N	5.84	132.04	122.70
1	A	105	LEU	CB-CG-CD2	-5.84	101.08	111.00
1	A	61	ASN	CB-CG-OD1	-5.76	110.08	121.60
1	B	132	TRP	CB-CA-C	5.69	121.78	110.40
1	B	129	GLN	N-CA-CB	-5.67	100.40	110.60
1	A	25	TYR	CA-C-N	5.54	129.39	117.20
1	A	148	THR	OG1-CB-CG2	5.54	122.75	110.00
1	C	112	MET	CG-SD-CE	5.53	109.06	100.20
1	B	131	ARG	CA-C-N	5.52	129.35	117.20
1	B	129	GLN	CB-CA-C	5.51	121.41	110.40
1	B	22	GLU	CA-CB-CG	-5.47	101.38	113.40
1	A	59	ASN	O-C-N	-5.35	114.14	122.70
1	A	146	ASN	O-C-N	-5.23	114.34	122.70
1	A	106	ILE	CB-CG1-CD1	-5.16	99.46	113.90
1	A	107	ASN	C-N-CA	-5.03	109.13	121.70

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	60	THR	CB
1	D	56	ILE	CB

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	24	TYR	Sidechain
1	A	25	TYR	Mainchain
1	B	132	TRP	Peptide
1	B	20	ASP	Mainchain
1	B	21	THR	Mainchain,Peptide
1	B	22	GLU	Mainchain,Peptide
1	D	25	TYR	Sidechain

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	1256	0	1271	125	0
1	B	1256	0	1266	124	0
1	C	1256	0	1271	139	0
1	D	1277	0	1294	152	0
2	A	10	0	0	3	0
2	C	15	0	0	3	0
2	D	15	0	0	4	0
All	All	5085	0	5102	540	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 53.

All (540) 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:D:17:ILE:CG2	1:D:17:ILE:CB	1.79	1.57
1:A:60:THR:CB	1:A:60:THR:CG2	1.82	1.53
1:C:100:VAL:CG1	1:C:100:VAL:CB	1.84	1.52
1:B:22:GLU:CG	1:B:22:GLU:CB	1.85	1.50
1:D:24:TYR:CB	1:D:24:TYR:CA	1.89	1.49
1:B:19:LYS:CG	1:B:19:LYS:CB	1.90	1.49
1:A:106:ILE:CG2	1:A:106:ILE:CB	1.92	1.48
1:A:149:PRO:N	1:A:149:PRO:CD	1.70	1.43
1:D:26:THR:O	1:D:27:ILE:CD1	1.72	1.38
1:D:43:PRO:CD	1:D:43:PRO:N	1.91	1.34
1:B:22:GLU:CD	1:B:22:GLU:CB	2.06	1.24
1:D:26:THR:C	1:D:27:ILE:HD12	1.59	1.21
1:D:26:THR:O	1:D:27:ILE:HD12	1.04	1.20
1:D:45:LEU:H	1:D:45:LEU:HD23	1.12	1.12
1:B:131:ARG:HE	1:B:131:ARG:HA	1.03	1.11
1:C:71:LYS:HE2	1:C:75:GLN:HE21	1.19	1.04
1:D:87:ASN:HB2	1:D:114:GLU:OE2	1.61	1.01
1:D:25:TYR:CE2	1:D:45:LEU:HB3	1.96	1.00
1:D:53:ASP:O	1:D:56:ILE:O	1.80	0.99
1:C:27:ILE:HD11	1:C:64:ILE:HD11	1.45	0.98
1:C:14:ARG:HE	1:C:19:LYS:HB2	1.28	0.98
1:D:32:THR:O	1:D:33:ILE:HG13	1.64	0.97
1:A:98:ASP:O	1:A:102:ARG:HG2	1.65	0.96
1:D:52:LEU:HG	1:D:60:THR:HG21	1.48	0.94
1:A:106:ILE:CG2	1:A:106:ILE:CA	2.45	0.93
1:A:106:ILE:CG1	1:A:106:ILE:CG2	2.46	0.93
1:B:142:SER:HB2	1:B:145:TYR:H	1.33	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:ARG:HA	1:B:131:ARG:NE	1.86	0.90
1:A:151:ARG:O	1:A:155:VAL:HG12	1.70	0.90
1:D:45:LEU:N	1:D:45:LEU:HD23	1.85	0.89
1:D:43:PRO:HG2	1:D:43:PRO:O	1.71	0.89
1:C:153:LYS:O	1:C:157:THR:HG23	1.71	0.89
1:B:22:GLU:CD	1:B:22:GLU:HB2	1.90	0.88
1:D:33:ILE:HG23	1:D:51:GLU:HG2	1.56	0.88
1:C:52:LEU:HG	1:C:60:THR:HG21	1.53	0.88
1:A:106:ILE:N	1:A:106:ILE:HD12	1.87	0.88
1:D:12:GLY:O	1:D:29:ILE:HA	1.74	0.87
1:D:13:LEU:HD22	1:D:14:ARG:H	1.39	0.87
1:B:21:THR:HG23	1:B:21:THR:OG1	1.74	0.86
1:B:22:GLU:OE1	1:B:22:GLU:CB	2.23	0.86
1:D:43:PRO:CG	1:D:43:PRO:O	2.24	0.86
1:C:1:MET:HG3	1:C:5:GLU:HB2	1.58	0.86
1:C:100:VAL:CG1	1:C:100:VAL:CA	2.55	0.85
1:B:137:VAL:HG12	1:B:141:LYS:NZ	1.91	0.85
1:A:106:ILE:H	1:A:106:ILE:HD12	1.40	0.84
1:D:17:ILE:CG1	1:D:17:ILE:CG2	2.54	0.84
1:C:25:TYR:O	1:C:32:THR:HG23	1.75	0.84
1:C:100:VAL:CG1	1:C:100:VAL:CG2	2.56	0.83
1:B:157:THR:O	1:B:161:THR:HG23	1.80	0.81
1:B:151:ARG:CA	1:B:154:ARG:HH21	1.94	0.81
1:A:138:ASN:OD1	1:A:141:LYS:NZ	2.14	0.80
1:C:10:ASP:OD2	1:C:151:ARG:HG3	1.80	0.80
1:C:86:ARG:HB3	1:C:86:ARG:NH1	1.96	0.80
1:C:18:TYR:HE1	1:C:20:ASP:HA	1.45	0.80
1:C:14:ARG:NE	1:C:19:LYS:HB2	1.95	0.80
1:A:60:THR:CA	1:A:60:THR:CG2	2.60	0.80
1:B:19:LYS:CG	1:B:19:LYS:CA	2.60	0.79
1:D:25:TYR:CZ	1:D:45:LEU:HB3	2.18	0.79
1:D:17:ILE:CA	1:D:17:ILE:CG2	2.61	0.79
1:B:22:GLU:OE1	1:B:22:GLU:HB2	1.82	0.79
1:D:157:THR:CG2	1:D:166:ALA:HB2	2.13	0.79
1:B:137:VAL:HG12	1:B:141:LYS:HZ2	1.48	0.78
1:B:151:ARG:HA	1:B:154:ARG:HH21	1.48	0.78
1:D:151:ARG:HH11	1:D:151:ARG:HG3	1.46	0.78
1:B:10:ASP:HB3	1:B:151:ARG:HD2	1.65	0.78
1:A:145:TYR:OH	1:A:153:LYS:HE3	1.84	0.78
1:C:142:SER:OG	1:C:144:TRP:HB3	1.84	0.77
1:C:27:ILE:CD1	1:C:64:ILE:HD11	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:48:ALA:O	1:D:51:GLU:HG3	1.85	0.76
1:C:52:LEU:HD12	1:C:56:ILE:HG22	1.66	0.76
1:A:111:GLN:HB2	1:A:151:ARG:NH2	2.01	0.75
1:B:139:LEU:O	1:B:142:SER:OG	2.04	0.75
1:B:93:VAL:HA	1:B:128:GLN:OE1	1.86	0.75
1:C:56:ILE:HD13	1:C:68:GLU:CD	2.06	0.74
1:C:72:LEU:O	1:C:73:PHE:C	2.22	0.74
1:D:17:ILE:CG2	1:D:18:TYR:N	2.50	0.74
1:B:22:GLU:CG	1:B:22:GLU:CA	2.66	0.74
1:D:26:THR:O	1:D:27:ILE:CG1	2.36	0.74
1:A:150:ASN:HB2	2:A:807:SO4:O4	1.87	0.74
1:D:15:LEU:O	1:D:64:ILE:HD13	1.86	0.73
1:B:107:ASN:HD21	1:B:151:ARG:HE	1.37	0.73
1:D:8:ARG:NH1	1:D:12:GLY:HA2	2.03	0.73
1:D:64:ILE:HD13	1:D:64:ILE:H	1.55	0.72
1:B:56:ILE:HD11	1:B:68:GLU:HB3	1.70	0.72
1:B:19:LYS:HG2	1:B:19:LYS:H	1.54	0.72
1:C:117:VAL:O	1:C:117:VAL:HG12	1.90	0.71
1:B:107:ASN:ND2	1:B:155:VAL:HG21	2.05	0.71
1:C:93:VAL:HG21	1:C:124:LEU:CD2	2.19	0.71
1:B:98:ASP:O	1:B:102:ARG:HB2	1.89	0.71
1:D:157:THR:HG21	1:D:166:ALA:HB2	1.72	0.71
1:D:74:ASN:O	1:D:77:VAL:HG12	1.89	0.71
1:C:53:ASP:OD1	1:C:59:ASN:HA	1.91	0.71
1:D:91:LYS:HB3	1:D:92:PRO:HD3	1.73	0.70
1:C:5:GLU:O	1:C:9:ILE:HD13	1.90	0.70
1:A:150:ASN:HB2	2:A:807:SO4:S	2.31	0.70
1:C:18:TYR:CE1	1:C:20:ASP:HA	2.27	0.70
1:D:153:LYS:O	1:D:157:THR:HB	1.92	0.70
1:A:29:ILE:O	1:A:30:GLY:C	2.30	0.70
1:B:22:GLU:C	1:B:22:GLU:CG	2.60	0.69
1:D:53:ASP:OD1	1:D:59:ASN:HA	1.90	0.69
1:D:13:LEU:HD22	1:D:14:ARG:N	2.08	0.69
1:A:103:ALA:HA	1:A:106:ILE:HD13	1.74	0.69
1:D:165:ASP:HA	1:D:168:LYS:HE2	1.73	0.69
1:D:161:THR:OG1	1:D:163:THR:OG1	2.09	0.69
1:B:93:VAL:HG21	1:B:124:LEU:HD22	1.73	0.69
1:A:102:ARG:O	1:A:106:ILE:HD12	1.93	0.69
1:A:76:ASP:O	1:A:79:ALA:HB3	1.93	0.68
1:A:104:ALA:HB1	1:A:155:VAL:HG23	1.73	0.68
1:C:143:ARG:NH1	1:C:147:GLN:HB2	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:ALA:HA	1:B:82:ARG:NH1	2.08	0.68
1:B:76:ASP:O	1:B:79:ALA:HB3	1.93	0.68
1:D:167:TYR:O	1:D:168:LYS:C	2.32	0.67
1:D:109:VAL:HA	1:D:117:VAL:HG21	1.75	0.67
1:A:3:ILE:O	1:A:6:MET:HB3	1.94	0.67
1:C:1:MET:CG	1:C:5:GLU:HB2	2.23	0.67
1:C:120:PHE:O	1:C:124:LEU:HB2	1.95	0.67
1:D:149:PRO:O	1:D:152:ALA:N	2.27	0.67
1:A:102:ARG:O	1:A:106:ILE:CD1	2.41	0.67
1:D:42:SER:C	1:D:43:PRO:CD	2.63	0.67
1:B:22:GLU:C	1:B:22:GLU:HG3	2.14	0.67
1:B:79:ALA:HA	1:B:82:ARG:HH12	1.60	0.67
1:B:84:ILE:HD13	1:B:90:LEU:HD13	1.76	0.67
1:C:29:ILE:HD12	1:C:29:ILE:N	2.10	0.66
1:D:122:ASN:HB2	2:D:802:SO4:O2	1.94	0.66
1:C:13:LEU:HD11	1:C:15:LEU:CD1	2.25	0.66
1:D:25:TYR:CE2	1:D:45:LEU:CB	2.75	0.66
1:B:22:GLU:O	1:B:22:GLU:HG3	1.95	0.66
1:B:104:ALA:HB3	1:B:159:PHE:CE1	2.31	0.66
1:A:60:THR:N	1:A:60:THR:CG2	2.58	0.66
1:A:98:ASP:OD2	1:A:98:ASP:C	2.35	0.66
1:C:86:ARG:CZ	1:C:86:ARG:HB3	2.26	0.66
1:C:150:ASN:HB2	2:C:805:SO4:O4	1.95	0.65
1:C:123:SER:OG	1:C:138:ASN:HB3	1.95	0.65
1:C:73:PHE:CE1	1:C:77:VAL:HG23	2.31	0.65
1:B:102:ARG:O	1:B:106:ILE:HD13	1.97	0.65
1:B:22:GLU:O	1:B:22:GLU:CG	2.45	0.65
1:C:107:ASN:O	1:C:110:PHE:HB3	1.97	0.64
1:B:53:ASP:OD1	1:B:60:THR:HG22	1.97	0.64
1:D:157:THR:HG22	1:D:166:ALA:HB2	1.80	0.64
1:D:24:TYR:CE2	1:D:33:ILE:HD11	2.33	0.64
1:C:112:MET:O	1:C:113:GLY:O	2.15	0.64
1:A:56:ILE:HD12	1:A:68:GLU:HB3	1.78	0.64
1:A:60:THR:OG1	1:A:63:VAL:O	2.16	0.64
1:A:14:ARG:HD3	1:A:18:TYR:CD1	2.32	0.63
1:D:19:LYS:NZ	1:D:43:PRO:HB2	2.13	0.63
1:A:18:TYR:O	1:A:25:TYR:HA	1.99	0.63
1:A:152:ALA:O	1:A:156:ILE:HG13	1.99	0.63
1:B:46:ASN:O	1:B:49:LYS:HB3	1.99	0.62
1:D:58:ARG:NH1	1:D:60:THR:HA	2.14	0.62
1:D:32:THR:O	1:D:33:ILE:CG1	2.44	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:144:TRP:CZ3	1:C:156:ILE:HD11	2.33	0.62
1:B:165:ASP:HA	1:B:168:LYS:NZ	2.13	0.62
1:C:4:PHE:HD2	1:C:73:PHE:CE2	2.18	0.62
1:A:69:ALA:O	1:A:72:LEU:HB2	1.99	0.62
1:C:3:ILE:O	1:C:6:MET:HB3	1.99	0.62
1:B:21:THR:CG2	1:B:21:THR:OG1	2.46	0.62
1:A:106:ILE:HG22	1:A:106:ILE:O	1.99	0.62
1:C:14:ARG:HH21	1:C:19:LYS:HB2	1.65	0.62
1:D:123:SER:O	1:D:127:LEU:HG	2.00	0.62
1:C:79:ALA:HA	1:C:82:ARG:NH1	2.15	0.62
1:C:106:ILE:HG22	1:C:106:ILE:O	2.00	0.61
1:D:17:ILE:CG2	1:D:17:ILE:C	2.68	0.61
1:C:25:TYR:OH	1:C:45:LEU:HG	1.99	0.61
1:A:78:ASP:O	1:A:81:VAL:HB	2.00	0.61
1:D:151:ARG:NH1	1:D:151:ARG:HG3	2.16	0.61
1:C:3:ILE:HG23	1:C:4:PHE:N	2.16	0.61
1:C:100:VAL:C	1:C:100:VAL:CG1	2.69	0.61
1:C:126:MET:SD	1:C:138:ASN:ND2	2.74	0.61
1:A:150:ASN:N	2:A:807:SO4:O4	2.33	0.60
1:B:161:THR:OG1	1:B:162:GLY:N	2.32	0.60
1:A:14:ARG:NH1	1:A:18:TYR:CE1	2.68	0.60
1:B:19:LYS:CG	1:B:19:LYS:H	2.14	0.60
1:D:13:LEU:HD11	1:D:15:LEU:HG	1.83	0.60
1:D:122:ASN:HB2	2:D:802:SO4:S	2.41	0.59
1:C:58:ARG:HH12	1:C:60:THR:HB	1.67	0.59
1:A:7:LEU:HD21	1:A:107:ASN:HA	1.83	0.59
1:B:148:THR:N	1:B:149:PRO:CD	2.65	0.59
1:D:13:LEU:HA	1:D:28:GLY:O	2.01	0.59
1:A:106:ILE:CG2	1:A:106:ILE:C	2.70	0.59
1:A:87:ASN:OD1	1:A:89:LYS:N	2.36	0.59
1:D:129:GLN:HB2	1:D:131:ARG:HD3	1.84	0.59
1:A:56:ILE:CD1	1:A:68:GLU:HB3	2.32	0.59
1:B:93:VAL:HG12	1:B:94:TYR:N	2.18	0.59
1:D:58:ARG:HH11	1:D:58:ARG:HG3	1.67	0.59
1:D:33:ILE:HG23	1:D:51:GLU:CG	2.28	0.59
1:B:87:ASN:OD1	1:B:89:LYS:N	2.36	0.59
1:B:150:ASN:ND2	1:B:150:ASN:H	1.99	0.59
1:C:145:TYR:O	1:C:149:PRO:HD3	2.03	0.59
1:A:52:LEU:HD23	1:A:60:THR:CG2	2.32	0.59
1:D:58:ARG:NH1	1:D:58:ARG:HG3	2.17	0.58
1:A:52:LEU:HD23	1:A:60:THR:HG21	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:17:ILE:HG22	1:D:18:TYR:N	2.17	0.58
1:B:138:ASN:HD22	1:B:141:LYS:HE2	1.67	0.58
1:D:3:ILE:HA	1:D:6:MET:HB3	1.84	0.58
1:A:29:ILE:HG21	1:A:73:PHE:CE1	2.38	0.58
1:D:45:LEU:O	1:D:49:LYS:HG3	2.04	0.58
1:C:64:ILE:HA	1:C:68:GLU:OE1	2.03	0.58
1:D:102:ARG:O	1:D:106:ILE:HG13	2.03	0.58
1:B:26:THR:HG23	1:B:31:TYR:O	2.03	0.58
1:B:90:LEU:O	1:B:93:VAL:HB	2.03	0.58
1:C:114:GLU:HG2	1:C:115:THR:N	2.18	0.58
1:C:59:ASN:ND2	1:C:61:ASN:HD21	2.02	0.57
1:B:19:LYS:CG	1:B:19:LYS:N	2.67	0.57
1:C:14:ARG:HE	1:C:19:LYS:CB	2.10	0.57
1:B:129:GLN:O	1:B:130:LYS:HB2	2.04	0.57
1:D:27:ILE:CG2	1:D:28:GLY:N	2.67	0.57
1:A:69:ALA:HA	1:A:72:LEU:HD12	1.87	0.57
1:C:17:ILE:HG22	1:C:18:TYR:N	2.19	0.57
1:A:106:ILE:N	1:A:106:ILE:CD1	2.66	0.57
1:A:81:VAL:O	1:A:84:ILE:HB	2.04	0.57
1:B:81:VAL:O	1:B:84:ILE:HB	2.04	0.57
1:B:16:LYS:O	1:B:17:ILE:HG23	2.04	0.57
1:C:122:ASN:HB2	2:C:806:SO4:O2	2.05	0.57
1:B:161:THR:OG1	1:B:163:THR:N	2.37	0.57
1:C:131:ARG:HH21	1:C:134:GLU:CD	2.09	0.57
1:A:142:SER:OG	1:A:144:TRP:HB3	2.05	0.56
1:B:2:ASN:OD1	1:B:5:GLU:N	2.29	0.56
1:D:13:LEU:HD13	1:D:13:LEU:C	2.26	0.56
1:A:106:ILE:HG22	1:A:106:ILE:C	2.25	0.56
1:C:14:ARG:NH2	1:C:19:LYS:HB2	2.20	0.56
1:B:138:ASN:HD22	1:B:141:LYS:CE	2.18	0.56
1:B:151:ARG:HA	1:B:154:ARG:NH2	2.17	0.56
1:C:93:VAL:HG11	1:C:124:LEU:HD23	1.87	0.56
1:B:82:ARG:HB2	1:B:82:ARG:HH11	1.69	0.56
1:D:7:LEU:HD23	1:D:107:ASN:ND2	2.21	0.56
1:C:90:LEU:HD23	1:C:124:LEU:HD11	1.88	0.56
1:B:150:ASN:O	1:B:153:LYS:HB2	2.06	0.56
1:D:19:LYS:HZ2	1:D:43:PRO:HB2	1.71	0.56
1:C:112:MET:HG3	1:C:117:VAL:HG22	1.87	0.56
1:A:51:GLU:O	1:A:54:LYS:HG3	2.06	0.56
1:A:19:LYS:HB3	1:A:25:TYR:CE2	2.40	0.56
1:C:86:ARG:CB	1:C:86:ARG:CZ	2.83	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:53:ASP:OD1	1:B:59:ASN:HA	2.05	0.56
1:C:93:VAL:HG21	1:C:124:LEU:HD22	1.88	0.56
1:D:13:LEU:HD13	1:D:14:ARG:N	2.21	0.55
1:D:60:THR:O	1:D:61:ASN:HB2	2.06	0.55
1:C:72:LEU:O	1:C:75:GLN:N	2.39	0.55
1:A:97:LEU:O	1:A:102:ARG:NE	2.40	0.55
1:A:120:PHE:CD2	1:A:120:PHE:N	2.74	0.55
1:C:109:VAL:HA	1:C:117:VAL:HG21	1.88	0.55
1:C:117:VAL:CG1	1:C:117:VAL:O	2.53	0.55
1:B:19:LYS:HG2	1:B:19:LYS:N	2.20	0.55
1:B:98:ASP:OD2	1:B:100:VAL:HG12	2.06	0.55
1:C:163:THR:HB	1:C:165:ASP:OD1	2.06	0.55
1:C:14:ARG:CZ	1:C:19:LYS:HB2	2.37	0.55
1:B:151:ARG:HA	1:B:154:ARG:HE	1.72	0.55
1:D:24:TYR:CB	1:D:24:TYR:C	2.71	0.55
1:B:100:VAL:HG11	1:B:162:GLY:C	2.27	0.55
1:D:165:ASP:HA	1:D:168:LYS:CE	2.36	0.55
1:C:143:ARG:HD3	1:C:143:ARG:O	2.06	0.54
1:B:148:THR:N	1:B:149:PRO:HD3	2.22	0.54
1:C:71:LYS:CE	1:C:75:GLN:HE21	2.06	0.54
1:D:24:TYR:CD2	1:D:33:ILE:HD11	2.43	0.54
1:B:84:ILE:HG21	1:B:94:TYR:CD1	2.43	0.54
1:D:157:THR:O	1:D:161:THR:HG23	2.07	0.54
1:C:124:LEU:HA	1:C:127:LEU:HD12	1.90	0.54
1:D:17:ILE:HG12	1:D:27:ILE:HD11	1.90	0.54
1:A:106:ILE:H	1:A:106:ILE:CD1	2.17	0.54
1:D:43:PRO:N	1:D:43:PRO:CG	2.69	0.53
1:C:91:LYS:HB3	1:C:92:PRO:HD3	1.89	0.53
1:A:27:ILE:HG22	1:A:28:GLY:H	1.73	0.53
1:B:131:ARG:HD3	1:B:134:GLU:HG3	1.89	0.53
1:C:144:TRP:HZ3	1:C:156:ILE:HD11	1.73	0.53
1:D:10:ASP:OD1	1:D:154:ARG:NH2	2.41	0.53
1:C:112:MET:O	1:C:117:VAL:HG23	2.08	0.53
1:B:165:ASP:HA	1:B:168:LYS:HZ1	1.72	0.53
1:A:15:LEU:O	1:A:63:VAL:HA	2.09	0.53
1:A:17:ILE:HG22	1:A:18:TYR:N	2.22	0.53
1:C:13:LEU:HD11	1:C:15:LEU:HD11	1.91	0.52
1:B:133:ASP:O	1:B:136:ALA:HB3	2.10	0.52
1:D:27:ILE:HG22	1:D:28:GLY:N	2.23	0.52
1:C:100:VAL:C	1:C:100:VAL:HG12	2.30	0.52
1:A:13:LEU:HD12	1:A:14:ARG:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:ASN:ND2	1:B:155:VAL:CG2	2.73	0.52
1:A:52:LEU:HD21	1:A:64:ILE:HG23	1.91	0.52
1:C:2:ASN:OD1	1:C:4:PHE:HB2	2.09	0.52
1:C:143:ARG:N	2:C:804:SO4:O1	2.42	0.52
1:B:147:GLN:O	1:B:147:GLN:HG3	2.10	0.52
1:B:74:ASN:ND2	1:B:78:ASP:OD1	2.42	0.52
1:D:98:ASP:OD2	1:D:100:VAL:HB	2.10	0.52
1:A:4:PHE:O	1:A:5:GLU:C	2.47	0.52
1:D:43:PRO:CB	1:D:43:PRO:CG	2.88	0.51
1:C:64:ILE:HG22	1:C:68:GLU:OE1	2.09	0.51
1:A:93:VAL:HG21	1:A:124:LEU:HB3	1.91	0.51
1:D:109:VAL:HA	1:D:117:VAL:CG2	2.40	0.51
1:D:17:ILE:HG23	1:D:18:TYR:H	1.75	0.51
1:A:120:PHE:HD2	1:A:120:PHE:N	2.07	0.51
1:A:2:ASN:OD1	1:A:4:PHE:HB2	2.11	0.51
1:A:126:MET:HE3	1:A:138:ASN:HD22	1.75	0.51
1:C:71:LYS:HG3	1:C:75:GLN:NE2	2.25	0.51
1:D:149:PRO:O	1:D:150:ASN:C	2.49	0.51
1:B:27:ILE:CD1	1:B:52:LEU:HD23	2.41	0.51
1:A:151:ARG:HB2	1:A:154:ARG:HH21	1.76	0.50
1:D:17:ILE:HG23	1:D:18:TYR:N	2.25	0.50
1:D:87:ASN:CB	1:D:114:GLU:OE2	2.48	0.50
1:A:143:ARG:HA	1:A:146:ASN:OD1	2.10	0.50
1:D:67:ASP:O	1:D:70:GLU:HB2	2.10	0.50
1:D:49:LYS:O	1:D:53:ASP:OD2	2.30	0.50
1:D:52:LEU:O	1:D:56:ILE:HG12	2.12	0.50
1:B:100:VAL:HG11	1:B:162:GLY:O	2.11	0.50
1:A:17:ILE:CG2	1:A:18:TYR:N	2.75	0.50
1:D:17:ILE:HA	1:D:27:ILE:HG13	1.93	0.50
1:B:107:ASN:HD22	1:B:155:VAL:HG21	1.77	0.50
1:B:49:LYS:HG3	1:B:53:ASP:OD2	2.10	0.50
1:A:53:ASP:HA	1:A:58:ARG:O	2.12	0.50
1:A:16:LYS:HG3	1:A:63:VAL:HG22	1.94	0.50
1:A:60:THR:HG22	1:A:60:THR:N	2.27	0.50
1:A:145:TYR:O	1:A:149:PRO:HD3	2.11	0.50
1:A:76:ASP:O	1:A:79:ALA:N	2.45	0.50
1:C:126:MET:SD	1:C:134:GLU:O	2.70	0.50
1:D:78:ASP:O	1:D:81:VAL:HB	2.12	0.50
1:D:26:THR:C	1:D:27:ILE:CD1	2.50	0.49
1:C:31:TYR:CD1	1:C:72:LEU:HD13	2.47	0.49
1:A:6:MET:SD	1:A:107:ASN:HB2	2.51	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:LEU:O	1:C:56:ILE:HG22	2.12	0.49
1:C:66:LYS:O	1:C:70:GLU:HG3	2.13	0.49
1:D:25:TYR:OH	1:D:45:LEU:HD22	2.13	0.49
1:C:65:THR:O	1:C:68:GLU:N	2.46	0.49
1:D:73:PHE:CD1	1:D:73:PHE:O	2.66	0.49
1:C:94:TYR:CE1	1:C:102:ARG:HB2	2.47	0.49
1:D:43:PRO:CG	1:D:43:PRO:CA	2.91	0.49
1:C:86:ARG:CB	1:C:86:ARG:NH1	2.73	0.49
1:C:16:LYS:HB3	1:C:16:LYS:NZ	2.28	0.49
1:B:53:ASP:O	1:B:56:ILE:HG22	2.12	0.49
1:C:1:MET:HG2	1:C:2:ASN:N	2.28	0.49
1:A:122:ASN:HB3	1:A:138:ASN:ND2	2.28	0.49
1:C:93:VAL:O	1:C:96:SER:HB3	2.12	0.49
1:D:105:LEU:O	1:D:109:VAL:HG23	2.12	0.49
1:D:91:LYS:N	1:D:92:PRO:CD	2.76	0.48
1:B:113:GLY:O	1:B:114:GLU:C	2.52	0.48
1:B:126:MET:HB3	1:B:135:ALA:HB2	1.95	0.48
1:A:126:MET:CE	1:A:138:ASN:ND2	2.76	0.48
1:B:72:LEU:O	1:B:75:GLN:HB2	2.12	0.48
1:D:17:ILE:CG2	1:D:17:ILE:CD1	2.91	0.48
1:D:52:LEU:HD12	1:D:56:ILE:CG1	2.43	0.48
1:C:27:ILE:HG13	1:C:64:ILE:CD1	2.44	0.48
1:A:68:GLU:O	1:A:72:LEU:HG	2.14	0.48
1:B:151:ARG:N	1:B:154:ARG:HH21	2.11	0.48
1:C:27:ILE:HG22	1:C:31:TYR:O	2.14	0.48
1:A:107:ASN:HD22	1:A:107:ASN:C	2.16	0.48
1:B:93:VAL:O	1:B:96:SER:HB3	2.14	0.48
1:C:152:ALA:O	1:C:156:ILE:HD13	2.14	0.48
1:C:59:ASN:ND2	1:C:61:ASN:ND2	2.62	0.48
1:C:135:ALA:O	1:C:136:ALA:C	2.50	0.48
1:A:11:GLU:HB3	1:A:30:GLY:H	1.79	0.47
1:D:125:ARG:O	1:D:128:GLN:HB3	2.14	0.47
1:D:58:ARG:HH12	1:D:60:THR:HA	1.79	0.47
1:C:7:LEU:HG	1:C:107:ASN:ND2	2.29	0.47
1:C:122:ASN:O	1:C:125:ARG:HG2	2.14	0.47
1:B:94:TYR:CE2	1:B:102:ARG:HD3	2.49	0.47
1:B:2:ASN:OD1	1:B:2:ASN:C	2.52	0.47
1:D:17:ILE:HG22	1:D:17:ILE:C	2.34	0.47
1:C:55:ALA:O	1:C:56:ILE:C	2.52	0.47
1:D:126:MET:HG2	1:D:131:ARG:HH21	1.79	0.47
1:D:105:LEU:HD12	1:D:105:LEU:HA	1.73	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:101:ARG:O	1:B:104:ALA:HB3	2.15	0.47
1:D:3:ILE:HD12	1:D:106:ILE:HB	1.97	0.47
1:C:52:LEU:HD12	1:C:56:ILE:CG2	2.39	0.47
1:D:82:ARG:O	1:D:86:ARG:HG3	2.15	0.47
1:A:26:THR:HB	1:A:31:TYR:O	2.15	0.47
1:D:126:MET:HA	1:D:131:ARG:HE	1.78	0.47
1:B:122:ASN:O	1:B:125:ARG:N	2.48	0.47
1:A:126:MET:SD	1:A:134:GLU:HB3	2.54	0.47
1:D:20:ASP:C	1:D:22:GLU:N	2.67	0.47
1:A:64:ILE:HD12	1:A:69:ALA:HA	1.97	0.47
1:C:84:ILE:HD11	1:C:109:VAL:HG21	1.97	0.47
1:C:127:LEU:O	1:C:128:GLN:C	2.50	0.47
1:C:82:ARG:O	1:C:85:LEU:N	2.47	0.47
1:B:104:ALA:O	1:B:108:MET:HG3	2.15	0.47
1:A:1:MET:CE	1:A:167:TYR:HB3	2.45	0.47
1:A:22:GLU:HG3	1:A:24:TYR:CE2	2.48	0.47
1:D:143:ARG:HG2	2:D:801:SO4:O1	2.15	0.47
1:C:73:PHE:CE1	1:C:77:VAL:CG2	2.98	0.46
1:C:53:ASP:OD1	1:C:60:THR:HG22	2.16	0.46
1:C:10:ASP:CG	1:C:151:ARG:HG3	2.34	0.46
1:C:96:SER:OG	1:C:96:SER:O	2.33	0.46
1:D:129:GLN:HB2	1:D:131:ARG:CD	2.46	0.46
1:A:101:ARG:CD	1:A:132:TRP:CH2	2.99	0.46
1:D:33:ILE:CG2	1:D:51:GLU:HG2	2.38	0.46
1:C:143:ARG:CD	1:C:143:ARG:O	2.64	0.46
1:D:18:TYR:CE2	1:D:20:ASP:HB3	2.50	0.46
1:D:18:TYR:O	1:D:25:TYR:HA	2.15	0.46
1:A:104:ALA:O	1:A:108:MET:HG3	2.16	0.46
1:C:126:MET:O	1:C:131:ARG:N	2.44	0.46
1:A:167:TYR:O	1:A:168:LYS:HG2	2.15	0.46
1:D:44:SER:O	1:D:47:ALA:HB3	2.15	0.46
1:C:5:GLU:O	1:C:9:ILE:CD1	2.60	0.46
1:D:158:THR:HG22	1:D:158:THR:O	2.16	0.46
1:A:14:ARG:O	1:A:28:GLY:N	2.46	0.46
1:A:66:LYS:HE2	1:A:67:ASP:OD1	2.15	0.46
1:A:109:VAL:O	1:A:113:GLY:N	2.42	0.46
1:B:133:ASP:O	1:B:136:ALA:N	2.49	0.46
1:C:13:LEU:CD1	1:C:15:LEU:CD1	2.94	0.46
1:B:93:VAL:O	1:B:94:TYR:C	2.54	0.46
1:C:109:VAL:HG13	1:C:114:GLU:HA	1.97	0.46
1:B:72:LEU:HA	1:B:75:GLN:NE2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3:ILE:CG2	1:C:4:PHE:N	2.78	0.45
1:C:74:ASN:O	1:C:77:VAL:HB	2.16	0.45
1:C:82:ARG:O	1:C:83:GLY:C	2.53	0.45
1:A:101:ARG:NE	1:A:132:TRP:CZ2	2.84	0.45
1:A:109:VAL:HG13	1:A:114:GLU:N	2.31	0.45
1:B:142:SER:CB	1:B:144:TRP:HB3	2.47	0.45
1:B:10:ASP:HB3	1:B:151:ARG:CD	2.42	0.45
1:D:7:LEU:CD2	1:D:107:ASN:CG	2.85	0.45
1:B:142:SER:CB	1:B:144:TRP:H	2.29	0.45
1:A:117:VAL:C	1:A:119:GLY:N	2.70	0.45
1:A:85:LEU:N	1:A:85:LEU:HD12	2.30	0.45
1:D:52:LEU:HD12	1:D:56:ILE:HG12	1.97	0.45
1:C:99:ALA:HA	1:C:102:ARG:HG2	1.98	0.45
1:A:29:ILE:CG2	1:A:73:PHE:CE1	2.99	0.45
1:C:48:ALA:O	1:C:51:GLU:N	2.50	0.45
1:B:93:VAL:O	1:B:96:SER:N	2.48	0.45
1:C:163:THR:CB	1:C:165:ASP:OD1	2.64	0.45
1:B:113:GLY:O	1:B:116:GLY:N	2.49	0.45
1:C:21:THR:OG1	1:C:22:GLU:N	2.48	0.45
1:A:14:ARG:NH1	1:A:18:TYR:CZ	2.85	0.45
1:D:7:LEU:HD21	1:D:107:ASN:CG	2.36	0.45
1:D:150:ASN:O	1:D:154:ARG:HG3	2.16	0.45
1:D:2:ASN:O	1:D:6:MET:N	2.40	0.45
1:A:31:TYR:CD2	1:A:31:TYR:C	2.90	0.45
1:A:101:ARG:CZ	1:A:132:TRP:CZ2	2.99	0.45
1:A:150:ASN:O	1:A:154:ARG:HG3	2.17	0.45
1:C:3:ILE:HG23	1:C:4:PHE:H	1.82	0.45
1:C:165:ASP:HA	1:C:168:LYS:HG2	1.97	0.45
1:D:66:LYS:O	1:D:70:GLU:HG3	2.16	0.45
1:D:58:ARG:CG	1:D:58:ARG:HH11	2.28	0.44
1:C:14:ARG:HH21	1:C:19:LYS:CB	2.27	0.44
1:D:18:TYR:HE2	1:D:20:ASP:HB3	1.82	0.44
1:D:49:LYS:HA	1:D:52:LEU:HB3	1.98	0.44
1:A:124:LEU:O	1:A:125:ARG:C	2.54	0.44
1:C:80:ALA:O	1:C:81:VAL:C	2.53	0.44
1:D:27:ILE:HG21	1:D:64:ILE:HD12	1.98	0.44
1:A:120:PHE:HB3	1:A:123:SER:HB2	1.99	0.44
1:C:140:ALA:HA	1:C:145:TYR:CD1	2.52	0.44
1:B:64:ILE:CD1	1:B:69:ALA:HB2	2.48	0.44
1:B:138:ASN:HA	1:B:141:LYS:HE2	1.99	0.44
1:C:81:VAL:O	1:C:82:ARG:C	2.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:86:ARG:HB2	1:D:86:ARG:CZ	2.48	0.44
1:C:26:THR:O	1:C:27:ILE:HB	2.18	0.44
1:A:126:MET:HE3	1:A:138:ASN:ND2	2.33	0.44
1:D:150:ASN:O	1:D:151:ARG:C	2.55	0.44
1:C:126:MET:HB3	1:C:131:ARG:HB2	1.99	0.44
1:B:72:LEU:HD23	1:B:75:GLN:NE2	2.33	0.44
1:D:58:ARG:CZ	1:D:60:THR:HA	2.48	0.44
1:B:26:THR:HG22	1:B:27:ILE:N	2.32	0.44
1:A:100:VAL:HG22	1:A:164:TRP:CE2	2.52	0.44
1:B:98:ASP:O	1:B:102:ARG:N	2.44	0.43
1:B:17:ILE:HD12	1:B:17:ILE:O	2.18	0.43
1:D:129:GLN:O	1:D:130:LYS:C	2.56	0.43
1:D:45:LEU:CD2	1:D:45:LEU:H	2.03	0.43
1:C:71:LYS:HE3	1:C:71:LYS:HA	1.99	0.43
1:C:72:LEU:HD23	1:C:72:LEU:HA	1.67	0.43
1:B:16:LYS:HG3	1:B:17:ILE:N	2.33	0.43
1:B:27:ILE:HD12	1:B:52:LEU:HD23	2.00	0.43
1:A:14:ARG:NH1	1:A:18:TYR:CD1	2.86	0.43
1:D:98:ASP:OD2	1:D:101:ARG:HG3	2.18	0.43
1:A:98:ASP:C	1:A:102:ARG:HG2	2.35	0.43
1:B:53:ASP:CA	1:B:56:ILE:HG22	2.49	0.43
1:D:12:GLY:O	1:D:29:ILE:HG23	2.18	0.43
1:C:130:LYS:HA	1:C:132:TRP:CH2	2.53	0.43
1:A:7:LEU:O	1:A:11:GLU:N	2.52	0.43
1:B:53:ASP:C	1:B:56:ILE:HG22	2.39	0.43
1:D:154:ARG:O	1:D:158:THR:OG1	2.20	0.43
1:A:51:GLU:HA	1:A:54:LYS:HG2	2.00	0.43
1:A:117:VAL:C	1:A:119:GLY:H	2.22	0.43
1:B:13:LEU:HD12	1:B:14:ARG:H	1.83	0.43
1:D:3:ILE:CD1	1:D:106:ILE:CG2	2.97	0.42
1:A:2:ASN:OD1	1:A:2:ASN:C	2.56	0.42
1:C:65:THR:OG1	1:C:67:ASP:HB2	2.18	0.42
1:D:91:LYS:CB	1:D:92:PRO:HD3	2.42	0.42
1:A:76:ASP:O	1:A:79:ALA:CB	2.64	0.42
1:A:81:VAL:HG12	1:A:82:ARG:N	2.34	0.42
1:B:22:GLU:HG3	1:B:23:GLY:N	2.32	0.42
1:D:150:ASN:HA	1:D:153:LYS:HD2	2.01	0.42
1:D:7:LEU:HD23	1:D:7:LEU:HA	1.86	0.42
1:A:66:LYS:HD2	1:A:67:ASP:N	2.34	0.42
1:A:19:LYS:O	1:A:19:LYS:HD3	2.19	0.42
1:D:132:TRP:HA	1:D:132:TRP:CE3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:ARG:O	1:A:132:TRP:C	2.58	0.42
1:D:151:ARG:NH1	1:D:151:ARG:CG	2.83	0.42
1:C:11:GLU:HB2	1:C:29:ILE:CG2	2.49	0.42
1:D:123:SER:N	2:D:802:SO4:O3	2.49	0.42
1:C:91:LYS:O	1:C:94:TYR:HB3	2.19	0.42
1:B:71:LYS:O	1:B:75:GLN:HG3	2.19	0.42
1:D:52:LEU:CD1	1:D:56:ILE:CG1	2.98	0.42
1:D:64:ILE:HD13	1:D:64:ILE:N	2.27	0.42
1:A:11:GLU:CD	1:A:151:ARG:HH12	2.22	0.42
1:D:17:ILE:HG21	1:D:17:ILE:CD1	2.49	0.42
1:C:16:LYS:O	1:C:17:ILE:C	2.58	0.42
1:B:16:LYS:O	1:B:27:ILE:CG2	2.68	0.42
1:D:84:ILE:C	1:D:86:ARG:H	2.22	0.42
1:A:71:LYS:O	1:A:75:GLN:HG3	2.20	0.42
1:D:52:LEU:CG	1:D:60:THR:HG21	2.36	0.42
1:A:98:ASP:O	1:A:102:ARG:CG	2.54	0.42
1:B:53:ASP:OD1	1:B:60:THR:N	2.53	0.42
1:B:152:ALA:O	1:B:156:ILE:HG13	2.19	0.42
1:D:17:ILE:HA	1:D:27:ILE:CG1	2.50	0.41
1:C:11:GLU:O	1:C:12:GLY:C	2.58	0.41
1:A:27:ILE:N	1:A:27:ILE:HD12	2.34	0.41
1:A:82:ARG:C	1:A:84:ILE:H	2.24	0.41
1:A:113:GLY:O	1:A:117:VAL:HG23	2.20	0.41
1:A:102:ARG:O	1:A:105:LEU:HB3	2.20	0.41
1:B:26:THR:HA	1:B:31:TYR:O	2.20	0.41
1:C:13:LEU:HD11	1:C:15:LEU:HD12	2.01	0.41
1:D:131:ARG:O	1:D:132:TRP:C	2.58	0.41
1:D:84:ILE:O	1:D:86:ARG:N	2.53	0.41
1:A:91:LYS:O	1:A:92:PRO:C	2.53	0.41
1:C:1:MET:HG3	1:C:5:GLU:CB	2.38	0.41
1:A:108:MET:HE1	1:A:144:TRP:CZ3	2.56	0.41
1:B:147:GLN:O	1:B:147:GLN:CG	2.68	0.41
1:A:167:TYR:C	1:A:168:LYS:HG2	2.40	0.41
1:B:107:ASN:CG	1:B:151:ARG:HH21	2.24	0.41
1:B:52:LEU:HD12	1:B:60:THR:HG21	2.02	0.41
1:D:130:LYS:HD2	1:D:132:TRP:CH2	2.55	0.41
1:D:97:LEU:HD22	1:D:101:ARG:CB	2.51	0.41
1:B:3:ILE:HG23	1:B:4:PHE:CD1	2.56	0.41
1:D:165:ASP:CA	1:D:168:LYS:HE2	2.46	0.41
1:A:52:LEU:HD23	1:A:60:THR:HG23	2.01	0.41
1:B:82:ARG:CB	1:B:82:ARG:HH11	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:LYS:CB	1:A:25:TYR:CE2	3.03	0.41
1:D:82:ARG:O	1:D:83:GLY:C	2.58	0.41
1:A:60:THR:CG2	1:A:60:THR:H	2.31	0.41
1:B:27:ILE:HB	1:B:28:GLY:H	1.68	0.41
1:B:16:LYS:HG3	1:B:17:ILE:H	1.86	0.41
1:C:137:VAL:HG12	1:C:141:LYS:NZ	2.35	0.41
1:B:45:LEU:HD12	1:B:48:ALA:HB3	2.02	0.41
1:C:52:LEU:C	1:C:52:LEU:HD12	2.41	0.41
1:B:98:ASP:HA	1:B:102:ARG:HH21	1.86	0.41
1:A:124:LEU:C	1:A:126:MET:N	2.72	0.41
1:B:5:GLU:O	1:B:8:ARG:HB3	2.21	0.41
1:D:86:ARG:HB2	1:D:86:ARG:NH1	2.36	0.41
1:C:8:ARG:HH21	1:C:13:LEU:HD23	1.86	0.40
1:B:7:LEU:O	1:B:8:ARG:C	2.57	0.40
1:C:53:ASP:OD1	1:C:60:THR:N	2.54	0.40
1:A:120:PHE:O	1:A:124:LEU:HG	2.21	0.40
1:D:164:TRP:O	1:D:168:LYS:HG3	2.21	0.40
1:C:100:VAL:HG12	1:C:100:VAL:O	2.21	0.40
1:C:27:ILE:CG1	1:C:64:ILE:HD11	2.51	0.40
1:B:133:ASP:O	1:B:137:VAL:HG23	2.22	0.40
1:D:5:GLU:O	1:D:9:ILE:HG12	2.21	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	153/170 (90%)	124 (81%)	22 (14%)	7 (5%)	3	18
1	B	153/170 (90%)	119 (78%)	27 (18%)	7 (5%)	3	18
1	C	153/170 (90%)	112 (73%)	31 (20%)	10 (6%)	1	8
1	D	156/170 (92%)	119 (76%)	30 (19%)	7 (4%)	3	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	615/680 (90%)	474 (77%)	110 (18%)	31 (5%)	3	15

All (31) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	17	ILE
1	C	113	GLY
1	D	43	PRO
1	D	118	ALA
1	A	30	GLY
1	A	81	VAL
1	A	132	TRP
1	B	93	VAL
1	C	20	ASP
1	C	144	TRP
1	D	149	PRO
1	A	13	LEU
1	A	144	TRP
1	B	17	ILE
1	B	150	ASN
1	B	165	ASP
1	C	21	THR
1	C	55	ALA
1	C	93	VAL
1	D	22	GLU
1	D	150	ASN
1	B	97	LEU
1	C	12	GLY
1	C	27	ILE
1	C	81	VAL
1	D	141	LYS
1	B	94	TYR
1	B	114	GLU
1	D	85	LEU
1	A	165	ASP
1	A	77	VAL

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	130/141 (92%)	107 (82%)	23 (18%)	2	11
1	B	130/141 (92%)	112 (86%)	18 (14%)	4	20
1	C	130/141 (92%)	111 (85%)	19 (15%)	4	18
1	D	133/141 (94%)	113 (85%)	20 (15%)	3	17
All	All	523/564 (93%)	443 (85%)	80 (15%)	3	16

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	TYR
1	A	19	LYS
1	A	22	GLU
1	A	24	TYR
1	A	25	TYR
1	A	27	ILE
1	A	61	ASN
1	A	66	LYS
1	A	67	ASP
1	A	78	ASP
1	A	102	ARG
1	A	107	ASN
1	A	114	GLU
1	A	115	THR
1	A	120	PHE
1	A	122	ASN
1	A	125	ARG
1	A	128	GLN
1	A	129	GLN
1	A	137	VAL
1	A	143	ARG
1	A	146	ASN
1	A	163	THR
1	B	20	ASP
1	B	22	GLU
1	B	27	ILE
1	B	52	LEU
1	B	65	THR
1	B	74	ASN
1	B	82	ARG

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Mol	Chain	Res	Type
1	B	96	SER
1	B	100	VAL
1	B	121	THR
1	B	123	SER
1	B	130	LYS
1	B	131	ARG
1	B	138	ASN
1	B	143	ARG
1	B	150	ASN
1	B	165	ASP
1	B	168	LYS
1	C	8	ARG
1	C	9	ILE
1	C	10	ASP
1	C	16	LYS
1	C	20	ASP
1	C	27	ILE
1	C	45	LEU
1	C	52	LEU
1	C	56	ILE
1	C	60	THR
1	C	64	ILE
1	C	65	THR
1	C	71	LYS
1	C	78	ASP
1	C	86	ARG
1	C	96	SER
1	C	124	LEU
1	C	143	ARG
1	C	156	ILE
1	D	17	ILE
1	D	32	THR
1	D	43	PRO
1	D	44	SER
1	D	46	ASN
1	D	52	LEU
1	D	56	ILE
1	D	60	THR
1	D	64	ILE
1	D	67	ASP
1	D	72	LEU
1	D	73	PHE

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Mol	Chain	Res	Type
1	D	74	ASN
1	D	78	ASP
1	D	114	GLU
1	D	131	ARG
1	D	141	LYS
1	D	151	ARG
1	D	157	THR
1	D	161	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	107	ASN
1	A	129	GLN
1	A	147	GLN
1	B	74	ASN
1	B	75	GLN
1	B	107	ASN
1	B	138	ASN
1	B	146	ASN
1	B	150	ASN
1	C	59	ASN
1	C	75	GLN
1	D	74	ASN
1	D	147	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

8 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	$\# Z > 2$
2	SO4	A	807	-	4,4,4	0.51	0	6,6,6	0.93	0
2	SO4	A	808	-	4,4,4	0.36	0	6,6,6	0.42	0
2	SO4	C	804	-	4,4,4	0.20	0	6,6,6	0.57	0
2	SO4	C	805	-	4,4,4	0.41	0	6,6,6	0.46	0
2	SO4	C	806	-	4,4,4	0.56	0	6,6,6	0.70	0
2	SO4	D	801	-	4,4,4	0.74	0	6,6,6	0.75	0
2	SO4	D	802	-	4,4,4	0.20	0	6,6,6	0.26	0
2	SO4	D	803	-	4,4,4	0.42	0	6,6,6	0.56	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
2	SO4	A	807	-	-	0/0/0/0	0/0/0/0
2	SO4	A	808	-	-	0/0/0/0	0/0/0/0
2	SO4	C	804	-	-	0/0/0/0	0/0/0/0
2	SO4	C	805	-	-	0/0/0/0	0/0/0/0
2	SO4	C	806	-	-	0/0/0/0	0/0/0/0
2	SO4	D	801	-	-	0/0/0/0	0/0/0/0
2	SO4	D	802	-	-	0/0/0/0	0/0/0/0
2	SO4	D	803	-	-	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.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	807	SO4	3	0
2	C	804	SO4	1	0
2	C	805	SO4	1	0
2	C	806	SO4	1	0
2	D	801	SO4	1	0
2	D	802	SO4	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	157/170 (92%)	-0.79	1 (0%) 90 73	2, 7, 15, 20	0
1	B	157/170 (92%)	-0.77	1 (0%) 90 73	1, 7, 19, 36	0
1	C	157/170 (92%)	-0.82	1 (0%) 90 73	2, 7, 20, 37	0
1	D	160/170 (94%)	-0.77	1 (0%) 90 73	1, 6, 24, 35	0
All	All	631/680 (92%)	-0.79	4 (0%) 90 73	1, 7, 19, 37	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	20	ASP	2.2
1	B	21	THR	2.1
1	D	23	GLY	2.0
1	A	23	GLY	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, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	SO4	C	806	5/5	0.93	0.17	0.33	29,33,34,36	0
2	SO4	D	803	5/5	0.92	0.15	0.30	37,37,39,41	0
2	SO4	D	801	5/5	0.98	0.13	-0.75	13,15,19,19	0
2	SO4	A	808	5/5	0.94	0.14	-0.80	30,31,32,34	0
2	SO4	C	805	5/5	0.98	0.12	-1.17	21,25,26,33	0
2	SO4	C	804	5/5	0.97	0.12	-1.29	14,14,22,26	0
2	SO4	A	807	5/5	0.95	0.12	-1.36	20,20,24,26	0
2	SO4	D	802	5/5	0.97	0.10	-2.20	37,38,41,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.