



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 08:08 pm BST

PDB ID : 1FXI
Title : STRUCTURE OF THE [2FE-2S] FERREDOXIN I FROM THE BLUE-GREEN ALGA APHANOTHECE SACRUM AT 2.2 ANGSTROMS RESOLUTION
Authors : Tsukihara, T.
Deposited on : 1990-08-28
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

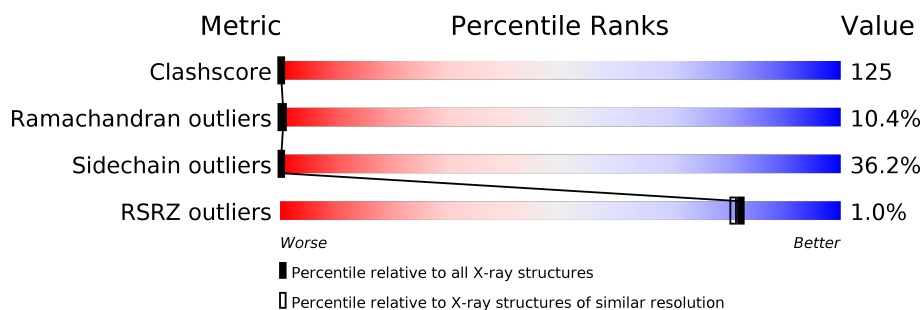
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	96	<div> <div>2%</div> <div>7% 28% 45% 20%</div> </div>
1	B	96	<div> <div>2%</div> <div>6% 35% 33% 25%</div> </div>
1	C	96	<div> <div>7% 33% 40% 20%</div> </div>
1	D	96	<div> <div>10% 35% 27% 27%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FES	A	97	-	-	X	-
2	FES	B	97	-	-	X	-
2	FES	C	97	-	-	X	-
2	FES	D	97	-	-	X	-

2 Entry composition [i](#)

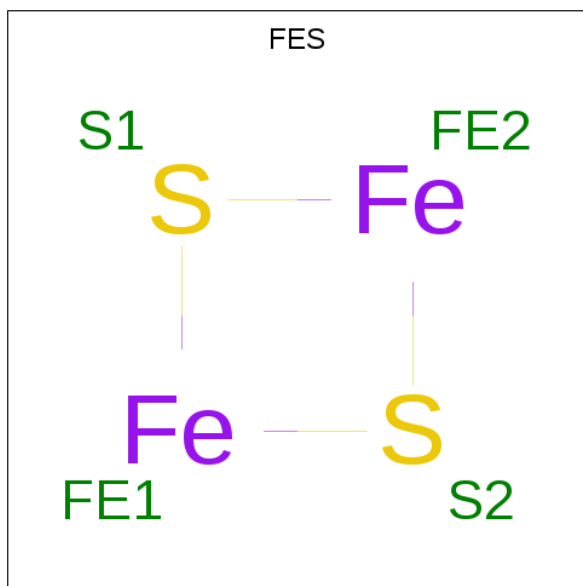
There are 3 unique types of molecules in this entry. The entry contains 3058 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FERREDOXIN I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	96	Total	C	N	O	S	0	0	0
			721	448	109	159	5			
1	B	96	Total	C	N	O	S	0	0	0
			721	448	109	159	5			
1	C	96	Total	C	N	O	S	0	0	0
			721	448	109	159	5			
1	D	96	Total	C	N	O	S	0	0	0
			721	448	109	159	5			

- Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			4	2	2		
2	B	1	Total	Fe	S	0	0
			4	2	2		

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

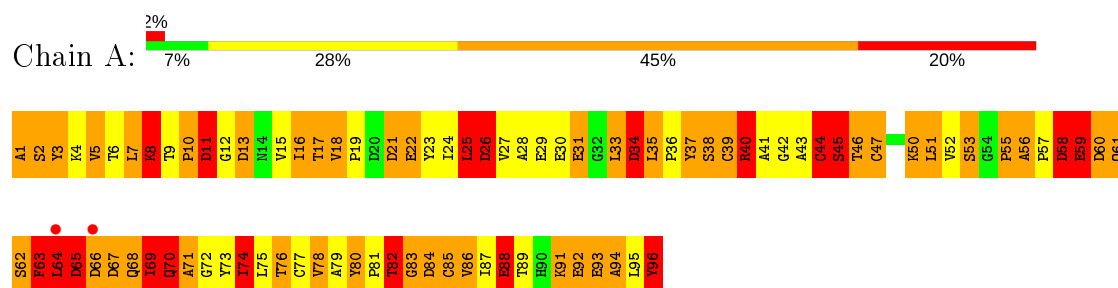
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	33	Total 33	O 33	0	0
3	B	42	Total 42	O 42	0	0
3	C	52	Total 52	O 52	0	0
3	D	31	Total 31	O 31	0	0

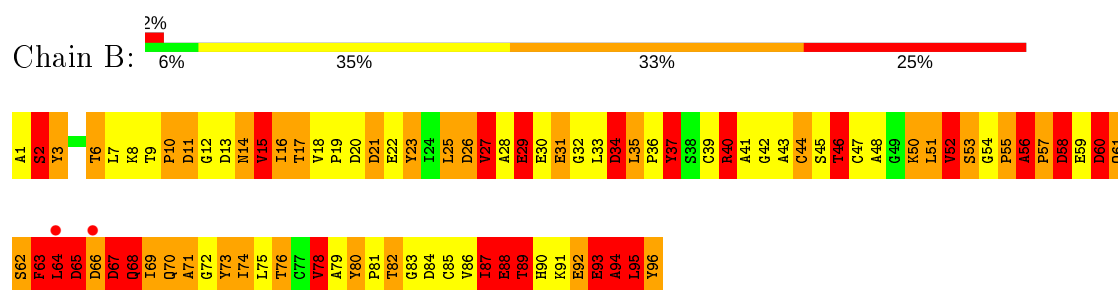
3 Residue-property plots [i](#)

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

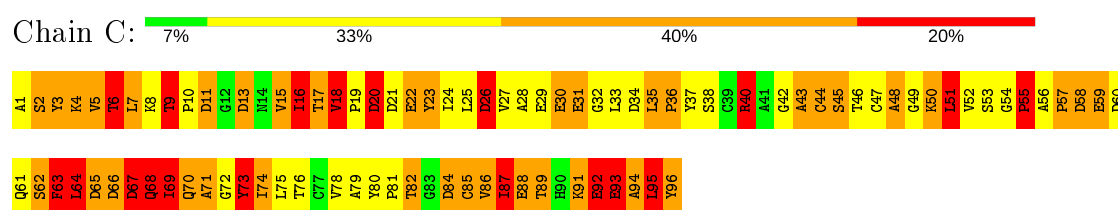
• Molecule 1: FERREDOXIN I



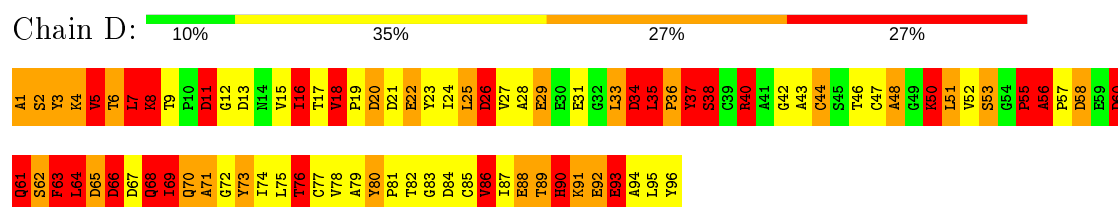
• Molecule 1: FERREDOXIN I



• Molecule 1: FERREDOXIN I



• Molecule 1: FERREDOXIN I



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	92.20 Å 92.20 Å 47.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.20 6.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (6.00-2.20) 61.9 (6.00-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.230 , (Not available) 0.224 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	15.3	Xtriage
Anisotropy	0.436	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.58 , 188.8	EDS
L-test for twinning ¹	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.087 for h,-k,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	3058	wwPDB-VP
Average B, all atoms (Å ²)	13.0	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 21.62 % 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 6.7569e-03.*

¹Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	1.14	1/734 (0.1%)	3.20	99/1002 (9.9%)
1	B	1.17	0/734	3.35	117/1002 (11.7%)
1	C	1.11	0/734	3.12	100/1002 (10.0%)
1	D	1.14	0/734	3.41	105/1002 (10.5%)
All	All	1.14	1/2936 (0.0%)	3.27	421/4008 (10.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	59	GLU	CD-OE1	-5.11	1.20	1.25

All (421) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	40	ARG	NE-CZ-NH1	24.09	132.34	120.30
1	B	13	ASP	CB-CG-OD1	21.05	137.25	118.30
1	B	58	ASP	CB-CG-OD1	20.71	136.94	118.30
1	D	73	TYR	CB-CG-CD1	-20.17	108.90	121.00
1	D	73	TYR	CB-CG-CD2	17.47	131.48	121.00
1	D	65	ASP	CB-CG-OD2	16.32	132.99	118.30
1	A	67	ASP	CA-CB-CG	15.79	148.14	113.40
1	A	34	ASP	CB-CG-OD1	-14.17	105.55	118.30
1	A	84	ASP	CB-CG-OD2	13.70	130.63	118.30
1	C	40	ARG	NE-CZ-NH2	13.56	127.08	120.30
1	C	65	ASP	CB-CG-OD2	13.51	130.46	118.30
1	B	63	PHE	CB-CG-CD1	-13.50	111.35	120.80
1	D	69	ILE	O-C-N	13.29	143.96	122.70
1	B	69	ILE	C-N-CA	12.99	154.16	121.70
1	D	65	ASP	CB-CG-OD1	-12.87	106.71	118.30
1	B	11	ASP	CA-CB-CG	12.49	140.87	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	88	GLU	OE1-CD-OE2	12.49	138.28	123.30
1	A	93	GLU	CA-CB-CG	12.31	140.49	113.40
1	D	73	TYR	N-CA-CB	12.07	132.32	110.60
1	A	63	PHE	CB-CG-CD1	-12.01	112.39	120.80
1	C	35	LEU	N-CA-CB	11.84	134.08	110.40
1	A	93	GLU	CB-CG-CD	11.72	145.84	114.20
1	D	22	GLU	OE1-CD-OE2	11.70	137.34	123.30
1	A	67	ASP	CB-CG-OD1	11.56	128.71	118.30
1	C	58	ASP	CA-CB-CG	11.51	138.73	113.40
1	A	59	GLU	OE1-CD-OE2	-11.44	109.57	123.30
1	D	34	ASP	CA-C-O	11.41	144.06	120.10
1	D	64	LEU	CB-CA-C	11.07	131.23	110.20
1	D	96	TYR	CB-CG-CD2	-11.01	114.39	121.00
1	A	69	ILE	O-C-N	10.99	140.29	122.70
1	A	58	ASP	CB-CG-OD1	-10.90	108.49	118.30
1	A	40	ARG	NE-CZ-NH1	10.75	125.68	120.30
1	D	66	ASP	CB-CG-OD2	-10.67	108.70	118.30
1	B	80	TYR	CA-CB-CG	10.64	133.62	113.40
1	D	96	TYR	CB-CG-CD1	10.61	127.37	121.00
1	D	16	ILE	CB-CA-C	10.61	132.82	111.60
1	C	67	ASP	CA-CB-CG	10.34	136.14	113.40
1	C	28	ALA	CB-CA-C	10.32	125.58	110.10
1	B	73	TYR	C-N-CA	10.21	147.22	121.70
1	C	69	ILE	C-N-CA	10.17	147.13	121.70
1	C	69	ILE	CB-CA-C	10.16	131.93	111.60
1	D	66	ASP	CB-CA-C	10.11	130.61	110.40
1	D	66	ASP	CA-CB-CG	-10.06	91.26	113.40
1	D	29	GLU	OE1-CD-OE2	10.03	135.33	123.30
1	B	66	ASP	CA-C-O	10.01	141.12	120.10
1	D	63	PHE	CB-CG-CD1	-9.97	113.82	120.80
1	A	88	GLU	CA-CB-CG	9.94	135.26	113.40
1	A	63	PHE	CA-CB-CG	-9.93	90.08	113.90
1	B	70	GLN	CB-CA-C	-9.87	90.66	110.40
1	B	92	GLU	CG-CD-OE2	-9.85	98.60	118.30
1	B	96	TYR	CB-CG-CD2	-9.84	115.10	121.00
1	B	21	ASP	CB-CG-OD1	-9.82	109.47	118.30
1	A	63	PHE	CB-CG-CD2	9.69	127.58	120.80
1	D	11	ASP	CB-CG-OD2	9.66	127.00	118.30
1	D	93	GLU	CA-CB-CG	9.63	134.58	113.40
1	B	63	PHE	CA-CB-CG	-9.61	90.83	113.90
1	C	26	ASP	CB-CG-OD2	9.55	126.90	118.30
1	C	65	ASP	N-CA-CB	9.38	127.48	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	63	PHE	CA-C-N	9.34	137.76	117.20
1	D	55	PRO	N-CD-CG	-9.34	89.20	103.20
1	B	70	GLN	CB-CG-CD	9.33	135.85	111.60
1	B	73	TYR	O-C-N	-9.31	107.80	122.70
1	A	13	ASP	CB-CG-OD1	-9.26	109.97	118.30
1	C	71	ALA	N-CA-CB	9.24	123.03	110.10
1	A	56	ALA	N-CA-CB	9.21	122.99	110.10
1	D	34	ASP	CA-C-N	-9.11	97.15	117.20
1	B	92	GLU	C-N-CA	9.08	144.40	121.70
1	A	60	ASP	CB-CG-OD1	-9.06	110.15	118.30
1	B	31	GLU	CG-CD-OE2	-9.05	100.21	118.30
1	B	23	TYR	CB-CG-CD2	9.00	126.40	121.00
1	A	93	GLU	N-CA-CB	8.98	126.76	110.60
1	C	68	GLN	CA-C-O	8.97	138.94	120.10
1	C	73	TYR	CB-CG-CD2	-8.96	115.62	121.00
1	B	84	ASP	CB-CG-OD1	8.96	126.36	118.30
1	B	31	GLU	OE1-CD-OE2	8.95	134.04	123.30
1	B	13	ASP	OD1-CG-OD2	-8.94	106.31	123.30
1	C	60	ASP	CB-CG-OD1	-8.82	110.36	118.30
1	C	34	ASP	CB-CG-OD2	8.81	126.23	118.30
1	C	66	ASP	CB-CA-C	8.81	128.02	110.40
1	C	92	GLU	CG-CD-OE2	-8.72	100.85	118.30
1	A	74	ILE	CB-CA-C	-8.71	94.18	111.60
1	B	65	ASP	CB-CA-C	8.65	127.71	110.40
1	B	95	LEU	CA-CB-CG	8.65	135.20	115.30
1	C	82	THR	C-N-CA	8.65	140.46	122.30
1	D	88	GLU	CA-CB-CG	8.64	132.42	113.40
1	A	21	ASP	CB-CA-C	8.62	127.65	110.40
1	C	51	LEU	O-C-N	8.62	136.49	122.70
1	B	94	ALA	CB-CA-C	8.62	123.03	110.10
1	A	11	ASP	CB-CG-OD1	-8.60	110.56	118.30
1	A	96	TYR	CB-CG-CD1	8.60	126.16	121.00
1	B	92	GLU	CA-C-O	8.58	138.12	120.10
1	C	66	ASP	C-N-CA	8.57	143.13	121.70
1	D	69	ILE	C-N-CA	8.50	142.95	121.70
1	A	34	ASP	OD1-CG-OD2	8.49	139.44	123.30
1	C	60	ASP	O-C-N	8.47	136.26	122.70
1	A	80	TYR	CB-CG-CD2	-8.47	115.92	121.00
1	C	68	GLN	CA-C-N	-8.46	98.59	117.20
1	B	62	SER	C-N-CA	-8.42	100.64	121.70
1	A	34	ASP	CA-C-O	8.42	137.78	120.10
1	D	88	GLU	CG-CD-OE2	-8.40	101.49	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	34	ASP	CB-CG-OD2	-8.40	110.74	118.30
1	C	35	LEU	CA-CB-CG	8.38	134.58	115.30
1	C	3	TYR	CA-C-O	8.36	137.66	120.10
1	C	43	ALA	CB-CA-C	8.36	122.63	110.10
1	C	73	TYR	CB-CG-CD1	8.33	126.00	121.00
1	B	93	GLU	N-CA-CB	8.31	125.56	110.60
1	C	84	ASP	CB-CG-OD1	8.23	125.71	118.30
1	D	2	SER	N-CA-CB	-8.22	98.16	110.50
1	C	65	ASP	C-N-CA	8.22	142.24	121.70
1	B	2	SER	N-CA-CB	8.18	122.76	110.50
1	D	73	TYR	C-N-CA	8.15	142.07	121.70
1	B	65	ASP	CA-C-O	8.03	136.95	120.10
1	B	16	ILE	CB-CA-C	8.02	127.64	111.60
1	D	26	ASP	CB-CG-OD1	8.00	125.50	118.30
1	A	33	LEU	CA-C-O	7.99	136.87	120.10
1	A	1	ALA	CB-CA-C	7.98	122.07	110.10
1	C	60	ASP	CB-CG-OD2	-7.96	111.14	118.30
1	B	40	ARG	NE-CZ-NH1	-7.96	116.32	120.30
1	C	64	LEU	CB-CA-C	7.94	125.29	110.20
1	C	60	ASP	OD1-CG-OD2	7.93	138.36	123.30
1	D	93	GLU	CG-CD-OE1	7.91	134.11	118.30
1	A	26	ASP	CB-CG-OD2	-7.90	111.19	118.30
1	D	60	ASP	O-C-N	7.89	135.32	122.70
1	D	90	HIS	CA-CB-CG	7.89	127.01	113.60
1	C	92	GLU	OE1-CD-OE2	7.88	132.76	123.30
1	A	59	GLU	CG-CD-OE1	7.86	134.01	118.30
1	B	70	GLN	O-C-N	7.80	135.18	122.70
1	B	29	GLU	OE1-CD-OE2	7.74	132.59	123.30
1	D	17	THR	N-CA-CB	7.74	125.01	110.30
1	A	59	GLU	CA-CB-CG	7.74	130.43	113.40
1	A	80	TYR	CB-CG-CD1	7.71	125.63	121.00
1	A	66	ASP	CB-CA-C	7.71	125.82	110.40
1	D	63	PHE	CA-CB-CG	-7.70	95.41	113.90
1	B	26	ASP	CB-CG-OD2	7.67	125.20	118.30
1	B	65	ASP	C-N-CA	7.67	140.88	121.70
1	B	66	ASP	CB-CG-OD2	-7.66	111.41	118.30
1	D	40	ARG	NH1-CZ-NH2	-7.64	110.99	119.40
1	D	84	ASP	CB-CG-OD1	7.56	125.11	118.30
1	B	16	ILE	N-CA-CB	-7.56	93.42	110.80
1	A	46	THR	CA-CB-OG1	-7.53	93.18	109.00
1	D	76	THR	CA-CB-CG2	7.51	122.92	112.40
1	C	79	ALA	CA-C-O	7.49	135.82	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	13	ASP	CB-CG-OD1	-7.47	111.58	118.30
1	B	93	GLU	CA-CB-CG	7.46	129.82	113.40
1	A	62	SER	O-C-N	7.44	134.60	122.70
1	B	63	PHE	CB-CA-C	7.42	125.23	110.40
1	D	29	GLU	O-C-N	7.40	134.54	122.70
1	B	16	ILE	CA-CB-CG2	7.40	125.69	110.90
1	A	11	ASP	CA-CB-CG	-7.39	97.13	113.40
1	A	67	ASP	OD1-CG-OD2	-7.39	109.25	123.30
1	D	37	TYR	CA-CB-CG	7.38	127.42	113.40
1	D	40	ARG	NE-CZ-NH2	-7.38	116.61	120.30
1	C	59	GLU	CG-CD-OE2	-7.38	103.55	118.30
1	D	68	GLN	CA-C-N	-7.37	101.00	117.20
1	D	13	ASP	CB-CG-OD2	7.35	124.91	118.30
1	A	34	ASP	C-N-CA	7.34	140.05	121.70
1	C	38	SER	N-CA-CB	7.33	121.49	110.50
1	B	88	GLU	CG-CD-OE1	7.32	132.93	118.30
1	B	29	GLU	CG-CD-OE2	-7.31	103.68	118.30
1	A	63	PHE	CB-CA-C	7.25	124.91	110.40
1	C	66	ASP	O-C-N	-7.23	111.13	122.70
1	B	92	GLU	O-C-N	-7.22	111.16	122.70
1	C	58	ASP	CB-CG-OD1	7.22	124.80	118.30
1	A	63	PHE	CA-C-O	-7.21	104.97	120.10
1	C	62	SER	CA-C-O	7.19	135.20	120.10
1	A	30	GLU	OE1-CD-OE2	-7.17	114.70	123.30
1	A	37	TYR	CA-CB-CG	-7.15	99.81	113.40
1	D	5	VAL	CA-CB-CG1	-7.15	100.18	110.90
1	D	7	LEU	CA-CB-CG	7.12	131.67	115.30
1	C	31	GLU	CG-CD-OE2	-7.11	104.08	118.30
1	B	58	ASP	CB-CG-OD2	-7.08	111.93	118.30
1	B	63	PHE	CB-CG-CD2	7.07	125.75	120.80
1	B	23	TYR	CB-CG-CD1	-7.07	116.76	121.00
1	D	93	GLU	OE1-CD-OE2	-7.05	114.84	123.30
1	D	70	GLN	OE1-CD-NE2	-7.03	105.72	121.90
1	C	95	LEU	CB-CA-C	7.01	123.52	110.20
1	B	11	ASP	N-CA-CB	6.96	123.14	110.60
1	C	57	PRO	CB-CA-C	6.96	129.40	112.00
1	C	74	ILE	CB-CA-C	-6.96	97.68	111.60
1	A	51	LEU	CA-CB-CG	6.96	131.31	115.30
1	B	73	TYR	CA-C-O	6.95	134.69	120.10
1	D	20	ASP	CB-CG-OD2	-6.94	112.05	118.30
1	B	34	ASP	CA-C-O	6.94	134.67	120.10
1	B	51	LEU	N-CA-CB	6.92	124.25	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	96	TYR	CB-CG-CD1	6.92	125.15	121.00
1	D	83	GLY	CA-C-O	-6.88	108.22	120.60
1	D	80	TYR	CB-CG-CD2	-6.87	116.88	121.00
1	C	55	PRO	CA-N-CD	-6.85	101.90	111.50
1	B	17	THR	N-CA-CB	6.84	123.29	110.30
1	D	13	ASP	O-C-N	6.84	133.64	122.70
1	B	6	THR	CA-CB-CG2	6.83	121.97	112.40
1	B	66	ASP	N-CA-C	6.82	129.42	111.00
1	C	63	PHE	CB-CG-CD1	-6.81	116.03	120.80
1	D	62	SER	N-CA-CB	6.80	120.71	110.50
1	C	29	GLU	CG-CD-OE1	6.79	131.89	118.30
1	C	15	VAL	CB-CA-C	-6.79	98.50	111.40
1	B	12	GLY	N-CA-C	6.77	130.03	113.10
1	D	16	ILE	N-CA-CB	-6.76	95.26	110.80
1	C	66	ASP	CA-C-O	6.74	134.26	120.10
1	B	80	TYR	CB-CG-CD2	6.74	125.04	121.00
1	D	26	ASP	O-C-N	6.72	133.45	122.70
1	B	44	CYS	CA-CB-SG	-6.69	101.96	114.00
1	B	70	GLN	N-CA-CB	6.68	122.62	110.60
1	D	73	TYR	CA-C-O	6.68	134.12	120.10
1	D	92	GLU	CG-CD-OE1	6.63	131.57	118.30
1	D	69	ILE	CA-C-N	-6.63	102.61	117.20
1	B	66	ASP	C-N-CA	6.62	138.25	121.70
1	B	56	ALA	O-C-N	6.62	133.67	121.10
1	D	70	GLN	CB-CG-CD	6.58	128.71	111.60
1	C	62	SER	CA-C-N	-6.58	102.73	117.20
1	A	39	CYS	O-C-N	6.56	133.19	122.70
1	C	67	ASP	CB-CG-OD1	6.54	124.19	118.30
1	D	55	PRO	CA-N-CD	-6.54	102.34	111.50
1	A	25	LEU	CA-CB-CG	6.53	130.32	115.30
1	D	38	SER	CB-CA-C	6.52	122.48	110.10
1	D	40	ARG	CA-CB-CG	6.51	127.73	113.40
1	A	92	GLU	CA-CB-CG	6.49	127.68	113.40
1	D	22	GLU	CG-CD-OE2	-6.47	105.36	118.30
1	D	18	VAL	CB-CA-C	6.47	123.69	111.40
1	D	84	ASP	OD1-CG-OD2	-6.46	111.03	123.30
1	C	96	TYR	N-CA-CB	6.45	122.21	110.60
1	A	56	ALA	O-C-N	6.44	133.34	121.10
1	C	88	GLU	CB-CA-C	6.43	123.27	110.40
1	B	58	ASP	OD1-CG-OD2	-6.42	111.11	123.30
1	C	88	GLU	CG-CD-OE1	6.42	131.13	118.30
1	A	12	GLY	O-C-N	6.40	132.94	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	84	ASP	OD1-CG-OD2	-6.40	111.14	123.30
1	C	93	GLU	OE1-CD-OE2	6.38	130.95	123.30
1	A	80	TYR	N-CA-CB	6.37	122.06	110.60
1	B	2	SER	CA-CB-OG	6.34	128.31	111.20
1	C	18	VAL	CA-CB-CG1	6.34	120.41	110.90
1	B	60	ASP	CB-CG-OD2	-6.33	112.60	118.30
1	B	69	ILE	O-C-N	6.33	132.84	122.70
1	D	96	TYR	CA-C-O	-6.33	106.81	120.10
1	A	88	GLU	CG-CD-OE2	-6.32	105.67	118.30
1	A	17	THR	CB-CA-C	6.31	128.63	111.60
1	C	31	GLU	CG-CD-OE1	6.30	130.91	118.30
1	C	84	ASP	OD1-CG-OD2	-6.30	111.33	123.30
1	A	60	ASP	CA-CB-CG	-6.29	99.57	113.40
1	B	92	GLU	OE1-CD-OE2	6.29	130.84	123.30
1	C	35	LEU	O-C-N	6.27	133.02	121.10
1	D	68	GLN	CA-C-O	6.27	133.27	120.10
1	D	62	SER	O-C-N	6.25	132.70	122.70
1	D	70	GLN	CG-CD-OE1	6.23	134.05	121.60
1	A	8	LYS	CA-CB-CG	6.22	127.09	113.40
1	D	72	GLY	C-N-CA	-6.20	106.21	121.70
1	D	3	TYR	CB-CG-CD1	-6.18	117.29	121.00
1	D	84	ASP	CB-CG-OD2	6.17	123.86	118.30
1	A	65	ASP	CB-CA-C	6.17	122.74	110.40
1	C	29	GLU	CA-CB-CG	6.16	126.95	113.40
1	B	89	THR	CA-C-O	-6.15	107.19	120.10
1	A	83	GLY	O-C-N	6.13	132.51	122.70
1	B	52	VAL	CB-CA-C	6.13	123.05	111.40
1	B	67	ASP	CA-CB-CG	-6.13	99.91	113.40
1	B	92	GLU	CG-CD-OE1	6.12	130.53	118.30
1	C	55	PRO	N-CD-CG	-6.11	94.03	103.20
1	C	21	ASP	CB-CG-OD1	-6.11	112.80	118.30
1	B	74	ILE	CB-CA-C	-6.11	99.39	111.60
1	A	62	SER	C-N-CA	-6.09	106.47	121.70
1	B	52	VAL	CA-CB-CG2	6.08	120.02	110.90
1	B	66	ASP	O-C-N	-6.07	112.99	122.70
1	C	38	SER	O-C-N	6.05	132.38	122.70
1	A	71	ALA	CA-C-O	6.05	132.80	120.10
1	A	70	GLN	CA-CB-CG	6.03	126.67	113.40
1	D	92	GLU	CG-CD-OE2	-6.02	106.25	118.30
1	D	11	ASP	CA-CB-CG	6.02	126.65	113.40
1	D	8	LYS	N-CA-CB	6.01	121.43	110.60
1	B	3	TYR	CB-CG-CD2	-6.00	117.40	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	48	ALA	C-N-CA	5.99	134.88	122.30
1	A	93	GLU	OE1-CD-OE2	-5.98	116.12	123.30
1	A	96	TYR	CB-CG-CD2	-5.97	117.42	121.00
1	B	58	ASP	O-C-N	5.97	132.25	122.70
1	B	68	GLN	CB-CA-C	5.94	122.27	110.40
1	A	62	SER	CA-C-O	-5.93	107.64	120.10
1	C	60	ASP	CA-C-O	-5.92	107.68	120.10
1	A	31	GLU	CG-CD-OE1	5.91	130.12	118.30
1	D	93	GLU	N-CA-CB	5.90	121.22	110.60
1	C	11	ASP	CB-CG-OD1	5.89	123.60	118.30
1	B	88	GLU	CG-CD-OE2	-5.89	106.53	118.30
1	C	65	ASP	OD1-CG-OD2	-5.87	112.14	123.30
1	B	88	GLU	C-N-CA	5.86	136.35	121.70
1	D	34	ASP	CB-CG-OD1	-5.86	113.03	118.30
1	A	40	ARG	NE-CZ-NH2	-5.85	117.38	120.30
1	D	71	ALA	N-CA-CB	5.85	118.28	110.10
1	D	69	ILE	CA-CB-CG1	-5.84	99.90	111.00
1	B	10	PRO	CA-C-N	5.83	130.02	117.20
1	C	1	ALA	N-CA-CB	5.81	118.23	110.10
1	C	93	GLU	CA-C-O	5.79	132.27	120.10
1	C	16	ILE	CB-CA-C	5.79	123.17	111.60
1	D	16	ILE	CA-CB-CG1	5.77	121.97	111.00
1	D	36	PRO	N-CA-C	-5.76	97.12	112.10
1	D	11	ASP	OD1-CG-OD2	-5.75	112.37	123.30
1	B	63	PHE	N-CA-CB	5.74	120.93	110.60
1	A	25	LEU	CB-CA-C	5.74	121.10	110.20
1	A	92	GLU	OE1-CD-OE2	5.74	130.18	123.30
1	A	95	LEU	CA-C-N	-5.73	104.59	117.20
1	A	91	LYS	N-CA-C	5.73	126.47	111.00
1	C	89	THR	N-CA-C	5.72	126.44	111.00
1	A	35	LEU	N-CA-C	-5.72	95.56	111.00
1	C	13	ASP	CA-C-O	-5.72	108.09	120.10
1	C	21	ASP	CA-C-O	-5.70	108.14	120.10
1	D	80	TYR	CB-CG-CD1	5.69	124.41	121.00
1	A	96	TYR	CB-CA-C	5.69	121.77	110.40
1	A	5	VAL	C-N-CA	5.68	135.91	121.70
1	A	84	ASP	CB-CA-C	5.67	121.74	110.40
1	C	71	ALA	CB-CA-C	-5.67	101.60	110.10
1	A	44	CYS	CA-CB-SG	-5.64	103.84	114.00
1	A	65	ASP	CA-CB-CG	-5.64	101.00	113.40
1	B	78	VAL	CA-CB-CG2	-5.63	102.45	110.90
1	C	94	ALA	N-CA-CB	5.62	117.97	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	11	ASP	CB-CG-OD1	5.62	123.36	118.30
1	D	62	SER	C-N-CA	-5.60	107.71	121.70
1	C	23	TYR	CB-CG-CD2	5.59	124.36	121.00
1	B	68	GLN	CA-C-N	-5.59	104.90	117.20
1	C	17	THR	N-CA-C	-5.59	95.91	111.00
1	A	35	LEU	O-C-N	5.57	131.68	121.10
1	C	36	PRO	CA-C-N	5.56	129.44	117.20
1	A	82	THR	CA-CB-CG2	5.56	120.19	112.40
1	A	58	ASP	OD1-CG-OD2	5.56	133.86	123.30
1	B	78	VAL	C-N-CA	5.56	135.59	121.70
1	A	47	CYS	CA-CB-SG	-5.54	104.03	114.00
1	B	37	TYR	CB-CA-C	5.54	121.48	110.40
1	B	29	GLU	O-C-N	5.53	131.55	122.70
1	A	46	THR	N-CA-CB	-5.53	99.80	110.30
1	A	74	ILE	O-C-N	-5.52	113.87	122.70
1	B	74	ILE	N-CA-C	5.52	125.89	111.00
1	B	71	ALA	CB-CA-C	5.51	118.37	110.10
1	D	88	GLU	CB-CA-C	-5.51	99.38	110.40
1	A	34	ASP	CA-C-N	-5.49	105.12	117.20
1	A	58	ASP	CB-CA-C	5.49	121.37	110.40
1	D	48	ALA	C-N-CA	5.49	133.82	122.30
1	B	65	ASP	CA-C-N	-5.48	105.14	117.20
1	B	66	ASP	CB-CG-OD1	5.48	123.23	118.30
1	C	85	CYS	O-C-N	5.47	131.46	122.70
1	A	40	ARG	CA-CB-CG	5.46	125.42	113.40
1	D	29	GLU	CG-CD-OE2	-5.45	107.39	118.30
1	C	15	VAL	CA-CB-CG2	5.44	119.06	110.90
1	C	20	ASP	CB-CG-OD1	5.44	123.20	118.30
1	C	40	ARG	CB-CA-C	-5.44	99.52	110.40
1	B	15	VAL	CG1-CB-CG2	-5.43	102.20	110.90
1	A	66	ASP	CB-CG-OD2	5.43	123.18	118.30
1	C	29	GLU	CG-CD-OE2	-5.42	107.45	118.30
1	C	71	ALA	N-CA-C	-5.42	96.36	111.00
1	A	70	GLN	CG-CD-OE1	5.42	132.43	121.60
1	C	22	GLU	CG-CD-OE2	5.42	129.13	118.30
1	D	82	THR	CA-CB-OG1	-5.40	97.66	109.00
1	B	46	THR	CB-CA-C	5.40	126.18	111.60
1	A	78	VAL	N-CA-CB	-5.40	99.63	111.50
1	C	63	PHE	N-CA-CB	-5.39	100.90	110.60
1	B	16	ILE	O-C-N	-5.38	114.08	122.70
1	C	54	GLY	O-C-N	5.38	131.33	121.10
1	B	73	TYR	CB-CA-C	5.36	121.12	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	58	ASP	CA-CB-CG	-5.35	101.62	113.40
1	B	11	ASP	OD1-CG-OD2	-5.35	113.14	123.30
1	B	27	VAL	O-C-N	5.35	131.26	122.70
1	C	9	THR	CA-CB-CG2	5.35	119.89	112.40
1	A	34	ASP	CA-CB-CG	-5.34	101.64	113.40
1	D	60	ASP	CB-CG-OD1	5.33	123.10	118.30
1	C	34	ASP	C-N-CA	5.32	134.99	121.70
1	B	88	GLU	CB-CG-CD	5.31	128.55	114.20
1	C	88	GLU	CG-CD-OE2	-5.31	107.69	118.30
1	D	76	THR	N-CA-CB	-5.31	100.22	110.30
1	D	86	VAL	CA-CB-CG2	-5.31	102.94	110.90
1	A	39	CYS	CA-C-O	-5.30	108.96	120.10
1	A	45	SER	CA-CB-OG	-5.30	96.89	111.20
1	D	1	ALA	CA-C-O	5.30	131.23	120.10
1	C	82	THR	CA-CB-CG2	5.30	119.81	112.40
1	B	15	VAL	C-N-CA	5.29	134.94	121.70
1	B	82	THR	O-C-N	5.28	132.18	123.20
1	B	70	GLN	OE1-CD-NE2	-5.28	109.76	121.90
1	A	41	ALA	CA-C-N	5.27	126.75	116.20
1	B	87	ILE	CB-CA-C	5.27	122.14	111.60
1	D	56	ALA	CA-C-O	-5.26	109.05	120.10
1	C	6	THR	CA-CB-CG2	5.25	119.74	112.40
1	C	67	ASP	N-CA-CB	-5.23	101.18	110.60
1	A	92	GLU	CG-CD-OE2	-5.23	107.84	118.30
1	B	68	GLN	CA-C-O	5.22	131.07	120.10
1	B	70	GLN	CA-C-N	-5.22	105.71	117.20
1	D	37	TYR	N-CA-CB	-5.21	101.22	110.60
1	C	26	ASP	O-C-N	5.21	131.03	122.70
1	B	69	ILE	CB-CA-C	5.20	122.00	111.60
1	A	69	ILE	CA-C-O	-5.20	109.19	120.10
1	B	67	ASP	O-C-N	5.19	131.00	122.70
1	C	93	GLU	CB-CA-C	5.18	120.77	110.40
1	C	87	ILE	CA-CB-CG1	5.18	120.85	111.00
1	A	50	LYS	CB-CG-CD	5.18	125.07	111.60
1	C	70	GLN	O-C-N	-5.18	114.41	122.70
1	B	65	ASP	CB-CG-OD1	5.17	122.95	118.30
1	D	60	ASP	CA-C-O	-5.17	109.25	120.10
1	A	13	ASP	CA-CB-CG	5.17	124.76	113.40
1	B	66	ASP	CA-C-N	-5.16	105.86	117.20
1	A	3	TYR	CB-CG-CD2	-5.15	117.91	121.00
1	A	69	ILE	C-N-CA	5.15	134.57	121.70
1	B	52	VAL	CG1-CB-CG2	-5.14	102.68	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	16	ILE	CA-CB-CG1	-5.13	101.25	111.00
1	B	26	ASP	CA-CB-CG	5.12	124.68	113.40
1	B	15	VAL	N-CA-CB	5.11	122.74	111.50
1	B	12	GLY	C-N-CA	5.11	134.47	121.70
1	C	95	LEU	C-N-CA	5.10	134.44	121.70
1	C	17	THR	O-C-N	5.09	130.85	122.70
1	C	62	SER	CB-CA-C	5.09	119.77	110.10
1	D	96	TYR	CB-CA-C	-5.08	100.24	110.40
1	B	53	SER	CA-C-O	5.07	130.76	120.10
1	A	11	ASP	N-CA-C	5.05	124.65	111.00
1	B	94	ALA	CA-C-O	5.05	130.70	120.10
1	D	35	LEU	O-C-N	5.05	130.69	121.10
1	A	85	CYS	CA-CB-SG	5.04	123.08	114.00
1	D	93	GLU	O-C-N	5.04	130.76	122.70
1	A	72	GLY	C-N-CA	-5.04	109.10	121.70
1	C	79	ALA	O-C-N	-5.03	114.65	122.70
1	C	45	SER	N-CA-CB	-5.03	102.96	110.50
1	D	58	ASP	CB-CG-OD2	-5.03	113.77	118.30
1	D	83	GLY	O-C-N	5.03	130.74	122.70
1	D	16	ILE	CA-CB-CG2	-5.02	100.86	110.90
1	D	66	ASP	N-CA-CB	-5.02	101.56	110.60
1	D	70	GLN	CA-C-O	-5.02	109.56	120.10
1	D	63	PHE	CB-CG-CD2	5.01	124.31	120.80
1	D	50	LYS	CG-CD-CE	5.01	126.94	111.90
1	B	57	PRO	N-CD-CG	-5.01	95.69	103.20
1	B	65	ASP	N-CA-C	-5.00	97.49	111.00
1	B	7	LEU	CB-CA-C	5.00	119.70	110.20

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	721	0	670	186	13
1	B	721	0	670	178	38

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	721	0	670	159	11
1	D	721	0	670	177	27
2	A	4	0	0	3	0
2	B	4	0	0	2	0
2	C	4	0	0	4	0
2	D	4	0	0	3	0
3	A	33	0	0	11	7
3	B	42	0	0	16	16
3	C	52	0	0	11	14
3	D	31	0	0	10	7
All	All	3058	0	2680	696	78

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 125.

All (696) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:42:GLY:HA2	2:C:97:FES:S2	1.50	1.48
1:B:62:SER:OG	1:B:78:VAL:HG11	1.15	1.31
1:B:39:CYS:O	1:B:40:ARG:HG3	1.27	1.28
1:B:48:ALA:CB	1:B:95:LEU:HD11	1.64	1.26
1:C:63:PHE:O	1:C:65:ASP:N	1.69	1.25
1:B:35:LEU:HD13	1:B:36:PRO:O	1.37	1.24
1:D:63:PHE:O	1:D:65:ASP:N	1.74	1.19
1:D:25:LEU:HD22	1:D:76:THR:HG22	1.26	1.17
1:B:9:THR:HA	1:B:89:THR:CG2	1.75	1.16
1:C:42:GLY:CA	2:C:97:FES:S2	2.33	1.16
1:D:35:LEU:HG	1:D:76:THR:HG21	1.17	1.16
1:A:62:SER:OG	1:A:78:VAL:CG1	1.93	1.15
1:B:67:ASP:O	1:B:68:GLN:HG2	1.44	1.14
1:B:48:ALA:HB2	1:B:95:LEU:HD11	1.14	1.14
1:B:35:LEU:CD1	1:B:36:PRO:O	1.96	1.12
1:A:7:LEU:HG	3:A:117:HOH:O	1.50	1.12
1:A:62:SER:CB	1:A:78:VAL:HG11	1.80	1.12
1:D:18:VAL:HG22	1:D:81:PRO:HG3	1.23	1.10
1:D:35:LEU:HG	1:D:76:THR:CG2	1.81	1.10
1:D:7:LEU:HD21	1:D:16:ILE:HG12	1.19	1.09
1:A:9:THR:HB	1:A:10:PRO:HD2	1.29	1.09
1:B:42:GLY:HA2	2:B:97:FES:S2	1.92	1.09
1:A:64:LEU:O	1:A:64:LEU:HG	1.38	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:LEU:HD22	1:A:36:PRO:HD2	1.35	1.08
1:B:62:SER:OG	1:B:78:VAL:CG1	2.01	1.07
1:C:30:GLU:HB2	3:C:143:HOH:O	1.52	1.06
1:D:1:ALA:O	1:D:19:PRO:HA	1.55	1.06
1:A:3:TYR:CD1	1:A:83:GLY:HA2	1.90	1.06
1:A:25:LEU:CD2	1:A:77:CYS:HA	1.85	1.05
1:C:5:VAL:HG13	1:C:16:ILE:HD13	1.36	1.05
1:B:63:PHE:CE1	1:B:75:LEU:HD23	1.92	1.04
1:B:29:GLU:HG2	3:B:121:HOH:O	1.55	1.03
1:A:62:SER:OG	1:A:78:VAL:HB	1.59	1.03
1:C:53:SER:HB3	3:C:131:HOH:O	1.58	1.03
1:D:22:GLU:HG2	3:D:147:HOH:O	1.58	1.03
1:A:62:SER:O	1:A:63:PHE:CD1	2.11	1.02
1:D:63:PHE:CE2	1:D:65:ASP:O	2.13	1.02
1:C:5:VAL:HG13	1:C:16:ILE:CD1	1.89	1.02
1:B:63:PHE:C	1:B:64:LEU:HD12	1.81	1.01
1:A:62:SER:OG	1:A:78:VAL:HG11	1.57	1.00
1:B:62:SER:HG	1:B:78:VAL:HG11	1.21	1.00
1:D:34:ASP:O	1:D:35:LEU:HB2	1.61	1.00
1:D:70:GLN:O	1:D:70:GLN:HG3	1.60	1.00
1:D:22:GLU:CG	3:D:148:HOH:O	2.09	1.00
1:C:35:LEU:HD11	1:C:47:CYS:HB2	1.44	1.00
1:A:52:VAL:HB	1:A:86:VAL:CG2	1.93	0.99
1:A:23:TYR:OH	1:A:61:GLN:OE1	1.81	0.98
1:D:68:GLN:NE2	1:D:68:GLN:HA	1.77	0.98
1:A:17:THR:HG22	1:D:92:GLU:OE1	1.61	0.98
1:B:63:PHE:CE2	1:B:65:ASP:O	2.16	0.97
1:C:8:LYS:HG2	1:C:13:ASP:OD1	1.65	0.97
1:A:62:SER:CA	1:A:78:VAL:HG11	1.94	0.97
1:B:39:CYS:C	1:B:40:ARG:HG3	1.83	0.97
1:B:48:ALA:CB	1:B:95:LEU:CD1	2.42	0.96
1:A:62:SER:OG	1:A:78:VAL:CB	2.15	0.95
1:C:58:ASP:OD1	1:C:80:TYR:HB2	1.66	0.95
1:A:35:LEU:HD11	1:A:47:CYS:HA	1.49	0.95
1:A:61:GLN:HB3	1:A:78:VAL:HG13	1.49	0.94
1:C:51:LEU:CD2	1:C:87:ILE:HD13	1.98	0.94
1:A:17:THR:CG2	1:D:92:GLU:OE1	2.15	0.94
1:B:63:PHE:CZ	1:B:65:ASP:O	2.20	0.94
1:A:18:VAL:HG22	1:A:81:PRO:HG3	1.50	0.93
1:A:38:SER:OG	1:A:46:THR:HG21	1.67	0.93
1:B:16:ILE:HD12	1:B:31:GLU:HG3	1.50	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:LYS:NZ	1:A:71:ALA:O	2.02	0.93
1:D:60:ASP:O	1:D:60:ASP:CG	2.08	0.91
1:D:42:GLY:HA3	1:D:62:SER:OG	1.68	0.91
1:A:16:ILE:HG23	1:A:31:GLU:HG3	1.50	0.91
1:D:7:LEU:CD2	1:D:16:ILE:HG12	2.00	0.90
1:A:58:ASP:OD1	1:A:60:ASP:OD1	1.87	0.90
1:B:93:GLU:O	1:B:94:ALA:HB2	1.70	0.90
1:D:58:ASP:C	1:D:58:ASP:OD1	2.08	0.90
1:B:36:PRO:HD3	1:B:90:HIS:CD2	2.07	0.89
1:D:35:LEU:CG	1:D:76:THR:HG21	2.00	0.89
1:C:68:GLN:OE1	1:C:68:GLN:HA	1.70	0.89
1:D:35:LEU:HD13	1:D:36:PRO:CD	2.03	0.89
1:C:92:GLU:O	1:C:93:GLU:HB3	1.71	0.89
1:A:25:LEU:HD22	1:A:77:CYS:HA	1.55	0.89
1:A:52:VAL:HB	1:A:86:VAL:HG23	1.53	0.89
1:B:1:ALA:O	3:B:98:HOH:O	1.90	0.89
1:D:52:VAL:HB	1:D:86:VAL:CG2	2.03	0.88
1:A:9:THR:CB	1:A:10:PRO:HD2	2.03	0.88
1:D:63:PHE:CE2	1:D:69:ILE:HD11	2.09	0.88
1:D:35:LEU:HD13	1:D:36:PRO:HD2	1.56	0.88
1:A:35:LEU:HD11	1:A:47:CYS:CA	2.04	0.87
1:A:9:THR:HB	1:A:10:PRO:CD	2.04	0.87
1:C:35:LEU:HD11	1:C:47:CYS:CB	2.04	0.87
1:B:9:THR:CA	1:B:89:THR:CG2	2.51	0.87
1:B:9:THR:HA	1:B:89:THR:HG21	1.54	0.86
1:A:62:SER:CB	1:A:78:VAL:CG1	2.48	0.86
1:D:63:PHE:C	1:D:65:ASP:H	1.78	0.86
1:A:39:CYS:SG	1:A:43:ALA:HB3	2.15	0.86
1:A:60:ASP:O	1:A:60:ASP:CG	2.13	0.86
1:B:48:ALA:HB2	1:B:95:LEU:CD1	2.02	0.86
1:B:9:THR:CA	1:B:89:THR:HG21	2.06	0.86
1:D:63:PHE:CD2	1:D:69:ILE:HD11	2.10	0.86
1:D:51:LEU:HG	3:D:138:HOH:O	1.76	0.85
1:A:64:LEU:O	1:A:64:LEU:CG	2.25	0.85
1:A:57:PRO:HA	1:A:80:TYR:O	1.77	0.85
1:A:35:LEU:CD2	1:A:89:THR:O	2.25	0.85
1:D:8:LYS:CE	1:D:86:VAL:HB	2.06	0.85
1:A:9:THR:HG22	1:A:89:THR:OG1	1.78	0.84
1:C:50:LYS:HD2	1:C:91:LYS:HD3	1.57	0.84
1:B:62:SER:O	1:B:63:PHE:HD1	1.59	0.84
1:B:63:PHE:CE1	1:B:75:LEU:CD2	2.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:LEU:HD13	1:A:36:PRO:O	1.79	0.83
1:A:62:SER:N	1:A:78:VAL:HG11	1.94	0.83
1:A:18:VAL:HB	1:A:27:VAL:HG21	1.58	0.82
1:C:23:TYR:OH	1:C:61:GLN:NE2	2.12	0.82
1:D:48:ALA:HB1	1:D:95:LEU:HD11	1.60	0.82
1:A:51:LEU:HD23	1:A:87:ILE:HG22	1.61	0.82
1:A:18:VAL:CG2	1:A:81:PRO:HG3	2.09	0.82
1:B:18:VAL:HG13	1:B:27:VAL:HG21	1.60	0.82
1:D:6:THR:HB	1:D:15:VAL:HG22	1.60	0.81
1:D:70:GLN:O	1:D:70:GLN:CG	2.28	0.81
1:D:37:TYR:CE2	1:D:40:ARG:HG2	2.16	0.81
1:B:63:PHE:N	1:B:64:LEU:HD12	1.94	0.81
1:A:55:PRO:HB2	1:A:82:THR:HG22	1.62	0.81
1:A:55:PRO:CB	1:A:82:THR:HG22	2.11	0.81
1:B:39:CYS:C	1:B:40:ARG:CG	2.49	0.81
1:C:74:ILE:HD13	1:C:87:ILE:HG21	1.63	0.81
1:A:94:ALA:O	1:A:96:TYR:CE2	2.34	0.80
1:B:42:GLY:CA	2:B:97:FES:S2	2.69	0.80
1:C:63:PHE:C	1:C:65:ASP:H	1.83	0.80
1:A:42:GLY:HA2	2:A:97:FES:S2	2.22	0.79
1:A:57:PRO:CA	1:A:80:TYR:O	2.30	0.79
1:D:35:LEU:HD12	1:D:36:PRO:O	1.81	0.79
1:A:58:ASP:C	1:A:58:ASP:OD1	2.19	0.79
1:A:50:LYS:HB2	1:A:91:LYS:CD	2.13	0.79
1:B:21:ASP:HB3	3:B:103:HOH:O	1.81	0.79
1:A:23:TYR:HE1	1:A:80:TYR:CE1	2.00	0.79
1:B:34:ASP:N	1:B:34:ASP:OD2	2.10	0.79
1:C:73:TYR:CD2	1:C:95:LEU:HD21	2.18	0.79
1:B:63:PHE:CZ	1:B:75:LEU:HD23	2.18	0.79
1:B:39:CYS:O	1:B:40:ARG:CG	2.22	0.78
1:C:63:PHE:O	1:C:64:LEU:C	2.22	0.78
1:A:25:LEU:HD23	1:A:77:CYS:HA	1.65	0.78
1:B:94:ALA:N	1:B:96:TYR:CE2	2.52	0.78
1:D:15:VAL:C	1:D:16:ILE:CG2	2.50	0.78
1:A:69:ILE:H	1:A:69:ILE:HD13	1.46	0.78
1:D:44:CYS:SG	1:D:46:THR:OG1	2.39	0.78
1:A:7:LEU:HB3	1:A:89:THR:HG21	1.66	0.78
1:A:73:TYR:OH	1:A:94:ALA:HB1	1.83	0.78
1:B:9:THR:CB	1:B:89:THR:HG21	2.13	0.78
1:D:19:PRO:HG2	1:D:22:GLU:HB2	1.63	0.78
1:B:48:ALA:HB1	1:B:95:LEU:HD11	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:GLU:OE2	1:A:74:ILE:HA	1.84	0.77
1:C:51:LEU:HD23	1:C:87:ILE:HD13	1.65	0.77
1:A:52:VAL:HB	1:A:86:VAL:HG22	1.65	0.77
1:C:5:VAL:CG1	1:C:18:VAL:HG13	2.15	0.77
1:D:52:VAL:HB	1:D:86:VAL:HG23	1.66	0.77
1:D:62:SER:CB	1:D:78:VAL:HG11	2.15	0.76
1:C:59:GLU:OE1	1:C:69:ILE:HD12	1.84	0.76
1:C:35:LEU:HD11	1:C:47:CYS:CA	2.16	0.76
1:C:70:GLN:C	1:C:72:GLY:N	2.37	0.76
1:A:22:GLU:OE1	1:A:26:ASP:HB3	1.84	0.76
1:B:50:LYS:N	1:B:87:ILE:CD1	2.48	0.76
1:C:63:PHE:C	1:C:65:ASP:N	2.40	0.76
1:C:69:ILE:O	1:C:73:TYR:N	2.19	0.75
1:A:68:GLN:HG3	1:A:71:ALA:HB2	1.69	0.75
1:B:52:VAL:HG23	1:B:86:VAL:O	1.87	0.75
1:C:92:GLU:HG3	1:C:92:GLU:O	1.86	0.75
1:B:9:THR:HB	3:B:131:HOH:O	1.86	0.75
1:B:23:TYR:CD2	3:B:137:HOH:O	2.38	0.74
1:B:63:PHE:CZ	1:B:75:LEU:CD2	2.71	0.74
1:D:37:TYR:CE2	1:D:40:ARG:CG	2.70	0.74
1:A:35:LEU:HD21	1:A:89:THR:O	1.88	0.74
1:B:35:LEU:C	1:B:35:LEU:HD13	2.08	0.74
1:B:67:ASP:O	1:B:68:GLN:CG	2.33	0.74
1:C:35:LEU:CD1	1:C:47:CYS:HB2	2.18	0.73
1:A:59:GLU:OE2	1:A:74:ILE:HG23	1.88	0.73
1:D:63:PHE:CZ	1:D:65:ASP:O	2.41	0.73
1:B:74:ILE:HD12	1:B:87:ILE:HD13	1.69	0.73
1:C:69:ILE:HA	1:C:73:TYR:O	1.89	0.73
1:A:3:TYR:HB3	1:A:83:GLY:C	2.09	0.73
1:C:63:PHE:CE1	1:C:65:ASP:O	2.42	0.73
1:A:50:LYS:HB2	1:A:91:LYS:HD2	1.71	0.73
1:A:22:GLU:OE2	3:A:104:HOH:O	2.07	0.72
1:D:23:TYR:O	1:D:27:VAL:HG23	1.89	0.72
1:D:8:LYS:HE3	1:D:86:VAL:HB	1.71	0.72
1:A:42:GLY:HA3	1:A:62:SER:CB	2.19	0.72
1:B:55:PRO:O	1:B:56:ALA:HB2	1.89	0.72
1:C:61:GLN:OE1	3:C:130:HOH:O	2.07	0.72
1:C:73:TYR:OH	1:C:94:ALA:HB3	1.90	0.72
1:A:51:LEU:HD23	1:A:87:ILE:CG2	2.20	0.72
1:D:22:GLU:HG2	3:D:148:HOH:O	1.83	0.72
1:B:56:ALA:HB1	3:B:113:HOH:O	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:35:LEU:CD1	1:D:36:PRO:O	2.37	0.72
1:D:62:SER:HB2	1:D:78:VAL:HG11	1.70	0.72
1:D:62:SER:HB3	1:D:78:VAL:HG21	1.72	0.71
1:A:45:SER:HB2	1:A:92:GLU:OE2	1.90	0.71
1:A:23:TYR:CE1	1:A:80:TYR:CZ	2.78	0.71
1:B:9:THR:HA	1:B:89:THR:HG23	1.69	0.71
1:C:73:TYR:CG	1:C:95:LEU:HD21	2.26	0.71
1:B:25:LEU:HD13	1:B:76:THR:HG22	1.72	0.71
1:B:27:VAL:O	1:B:30:GLU:HB3	1.91	0.71
1:B:62:SER:HB3	1:B:78:VAL:HG21	1.71	0.71
1:D:69:ILE:O	1:D:73:TYR:O	2.07	0.71
1:B:25:LEU:O	1:B:29:GLU:HB2	1.91	0.70
1:C:51:LEU:HD13	1:C:53:SER:O	1.91	0.70
1:D:25:LEU:HD22	1:D:76:THR:CG2	2.15	0.70
1:B:6:THR:OG1	1:B:15:VAL:HG23	1.90	0.70
1:B:76:THR:O	1:B:76:THR:CG2	2.39	0.70
1:C:23:TYR:HB2	1:C:26:ASP:OD2	1.91	0.70
1:B:50:LYS:C	1:B:87:ILE:HD12	2.12	0.69
1:A:10:PRO:HG2	1:A:11:ASP:OD1	1.92	0.69
1:B:16:ILE:CD1	1:B:31:GLU:HG3	2.20	0.69
1:B:14:ASN:N	1:B:14:ASN:HD22	1.90	0.69
1:B:64:LEU:N	1:B:64:LEU:HD12	2.07	0.69
1:D:63:PHE:C	1:D:65:ASP:N	2.29	0.69
1:A:35:LEU:CD2	1:A:36:PRO:HD2	2.19	0.69
1:B:45:SER:HB2	1:B:95:LEU:HD13	1.74	0.69
1:B:88:GLU:OE1	1:B:91:LYS:NZ	2.20	0.69
1:C:18:VAL:HG22	1:C:81:PRO:HG2	1.74	0.69
1:B:9:THR:CB	3:B:131:HOH:O	2.41	0.69
1:B:44:CYS:SG	1:B:46:THR:HG23	2.33	0.69
1:A:23:TYR:HA	1:A:79:ALA:O	1.93	0.69
1:B:15:VAL:O	1:B:15:VAL:CG1	2.41	0.68
1:B:50:LYS:O	1:B:87:ILE:HD12	1.92	0.68
1:A:42:GLY:HA3	1:A:62:SER:HB3	1.76	0.68
1:A:51:LEU:HD22	1:A:53:SER:O	1.92	0.68
1:B:15:VAL:HG12	1:B:15:VAL:O	1.94	0.68
1:C:4:LYS:CG	1:C:84:ASP:OD2	2.41	0.68
1:A:25:LEU:HD22	1:A:77:CYS:CA	2.22	0.68
1:A:56:ALA:O	1:A:82:THR:HB	1.94	0.68
1:A:52:VAL:CB	1:A:86:VAL:CG2	2.71	0.68
1:D:55:PRO:HD3	1:D:85:CYS:HB3	1.76	0.68
1:A:62:SER:O	1:A:63:PHE:HD1	1.61	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:TYR:HB3	1:A:83:GLY:O	1.94	0.68
1:B:25:LEU:CD1	1:B:76:THR:HG22	2.23	0.68
1:D:42:GLY:HA3	1:D:62:SER:CB	2.23	0.68
1:B:52:VAL:HG23	1:B:86:VAL:C	2.15	0.67
1:D:36:PRO:O	1:D:36:PRO:HG2	1.94	0.67
1:D:43:ALA:O	1:D:44:CYS:HB3	1.94	0.67
1:B:52:VAL:HG23	1:B:87:ILE:HA	1.77	0.67
1:D:51:LEU:CD2	1:D:57:PRO:HD3	2.24	0.67
1:C:78:VAL:O	3:C:117:HOH:O	2.12	0.67
1:A:62:SER:N	1:A:78:VAL:CG1	2.58	0.67
1:D:44:CYS:N	2:D:97:FES:S2	2.67	0.67
1:C:35:LEU:HD11	1:C:47:CYS:HA	1.76	0.67
1:B:23:TYR:OH	1:B:61:GLN:OE1	2.12	0.66
1:B:62:SER:CB	1:B:78:VAL:HG21	2.25	0.66
1:B:50:LYS:N	1:B:87:ILE:HD12	2.10	0.66
1:B:93:GLU:O	1:B:94:ALA:CB	2.43	0.66
1:C:73:TYR:CE2	1:C:95:LEU:HD21	2.29	0.66
1:A:50:LYS:HG3	1:A:91:LYS:HZ2	1.59	0.66
1:A:50:LYS:HB2	1:A:91:LYS:HD3	1.77	0.66
1:D:74:ILE:HD11	3:D:151:HOH:O	1.93	0.66
1:D:42:GLY:CA	1:D:62:SER:OG	2.43	0.66
1:C:4:LYS:HG2	1:C:84:ASP:CG	2.16	0.66
1:B:2:SER:HB3	3:B:98:HOH:O	1.94	0.66
1:C:67:ASP:O	1:C:68:GLN:OE1	2.14	0.66
3:A:130:HOH:O	1:C:82:THR:HG23	1.95	0.66
1:A:35:LEU:CD1	1:A:36:PRO:O	2.44	0.65
1:A:55:PRO:HD2	3:A:125:HOH:O	1.95	0.65
1:C:51:LEU:HA	1:C:87:ILE:HG23	1.78	0.65
1:A:62:SER:H	1:A:78:VAL:CG1	2.09	0.65
1:D:88:GLU:CB	1:D:91:LYS:HD2	2.27	0.65
1:A:17:THR:HG21	1:D:92:GLU:OE1	1.96	0.65
1:A:11:ASP:OD1	1:A:11:ASP:N	2.11	0.65
1:D:34:ASP:O	1:D:35:LEU:CB	2.42	0.65
1:D:63:PHE:O	1:D:64:LEU:C	2.35	0.65
1:A:35:LEU:CD1	1:A:47:CYS:HA	2.23	0.65
1:A:52:VAL:CB	1:A:86:VAL:HG23	2.25	0.65
1:A:7:LEU:HB3	1:A:89:THR:CG2	2.27	0.65
1:B:57:PRO:O	3:B:112:HOH:O	2.14	0.65
1:D:38:SER:HB3	1:D:46:THR:HG21	1.79	0.65
1:D:7:LEU:HD23	1:D:16:ILE:HG21	1.79	0.64
1:A:42:GLY:CA	2:A:97:FES:S2	2.85	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:GLN:HG2	1:B:71:ALA:N	1.99	0.64
1:B:50:LYS:C	1:B:87:ILE:CD1	2.65	0.64
1:B:36:PRO:CD	1:B:90:HIS:CD2	2.78	0.64
1:D:5:VAL:HG23	1:D:87:ILE:HD12	1.78	0.64
1:C:30:GLU:O	1:C:31:GLU:C	2.35	0.64
1:C:73:TYR:OH	1:C:94:ALA:CB	2.46	0.64
1:C:35:LEU:HD13	1:C:36:PRO:O	1.98	0.64
1:C:5:VAL:HG22	1:C:7:LEU:CD2	2.27	0.64
1:C:74:ILE:CD1	1:C:87:ILE:HG21	2.28	0.64
1:D:25:LEU:O	1:D:28:ALA:N	2.30	0.64
1:D:52:VAL:HB	1:D:86:VAL:HG22	1.79	0.64
1:B:23:TYR:HD2	3:B:137:HOH:O	1.76	0.64
1:B:63:PHE:HE1	1:B:75:LEU:CD2	2.09	0.64
1:D:67:ASP:C	1:D:67:ASP:OD2	2.36	0.64
1:B:55:PRO:HG2	1:B:83:GLY:HA3	1.80	0.64
1:C:62:SER:OG	1:C:78:VAL:HG21	1.98	0.64
1:A:25:LEU:CD2	1:A:77:CYS:CA	2.70	0.64
1:C:52:VAL:HB	1:C:86:VAL:HG23	1.79	0.63
1:D:37:TYR:HE2	1:D:40:ARG:CG	2.08	0.63
1:A:16:ILE:HG23	1:A:31:GLU:CG	2.27	0.63
1:A:9:THR:O	1:A:10:PRO:C	2.35	0.63
1:B:9:THR:HG22	1:B:89:THR:HG21	1.80	0.63
1:A:23:TYR:HE1	1:A:80:TYR:CZ	2.17	0.63
1:C:5:VAL:HG11	1:C:18:VAL:HG13	1.80	0.63
1:D:66:ASP:N	1:D:66:ASP:OD2	2.32	0.63
1:B:35:LEU:HD11	1:B:36:PRO:O	1.96	0.63
1:D:9:THR:OG1	1:D:12:GLY:O	2.17	0.63
1:A:86:VAL:O	1:A:87:ILE:CG2	2.47	0.63
1:D:67:ASP:HB2	3:D:141:HOH:O	1.99	0.63
1:D:63:PHE:CE2	1:D:69:ILE:CD1	2.81	0.62
1:A:50:LYS:HB3	1:A:88:GLU:HG3	1.79	0.62
1:A:51:LEU:HD13	3:A:123:HOH:O	1.98	0.62
1:B:63:PHE:HE1	1:B:75:LEU:HD23	1.61	0.62
1:A:57:PRO:HG3	1:A:74:ILE:HG21	1.82	0.62
1:D:68:GLN:NE2	1:D:68:GLN:CA	2.54	0.62
1:B:35:LEU:HD13	1:B:36:PRO:C	2.16	0.62
1:B:63:PHE:N	1:B:64:LEU:CD1	2.62	0.62
1:B:10:PRO:HD3	1:B:89:THR:HG23	1.82	0.62
1:C:74:ILE:CD1	1:C:87:ILE:CG2	2.78	0.62
1:D:42:GLY:HA2	2:D:97:FES:S2	2.40	0.61
1:B:47:CYS:SG	1:B:75:LEU:HD12	2.39	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:53:SER:O	1:B:85:CYS:HA	2.00	0.61
1:C:35:LEU:CD1	1:C:47:CYS:HA	2.30	0.61
1:D:58:ASP:OD1	1:D:60:ASP:HB3	2.00	0.61
1:C:4:LYS:HG3	1:C:84:ASP:OD2	1.99	0.61
1:D:6:THR:CB	1:D:15:VAL:HG22	2.30	0.61
1:D:47:CYS:O	1:D:76:THR:HB	2.00	0.61
1:D:7:LEU:CD2	1:D:16:ILE:HG21	2.30	0.61
1:D:60:ASP:OD2	1:D:60:ASP:O	2.17	0.61
1:A:59:GLU:OE1	1:A:69:ILE:HB	2.01	0.61
1:B:14:ASN:N	1:B:14:ASN:ND2	2.48	0.61
1:D:86:VAL:C	1:D:87:ILE:HG13	2.20	0.60
1:A:69:ILE:CD1	1:A:69:ILE:H	2.14	0.60
1:A:62:SER:HG	1:A:78:VAL:HB	1.64	0.60
1:D:35:LEU:HD11	1:D:47:CYS:HA	1.82	0.60
1:D:48:ALA:CB	1:D:95:LEU:CD1	2.79	0.60
1:C:62:SER:CB	1:C:78:VAL:HG11	2.32	0.60
1:D:50:LYS:HB3	1:D:88:GLU:CG	2.31	0.60
1:D:74:ILE:CD1	3:D:151:HOH:O	2.48	0.60
1:C:59:GLU:OE1	1:C:69:ILE:CD1	2.49	0.60
1:A:62:SER:C	1:A:63:PHE:HD1	2.02	0.60
1:B:40:ARG:HD2	3:B:136:HOH:O	2.00	0.60
1:D:35:LEU:HG	1:D:76:THR:HG22	1.81	0.60
1:D:52:VAL:CB	1:D:86:VAL:HG23	2.32	0.60
1:A:69:ILE:HA	1:A:73:TYR:O	2.02	0.60
1:B:3:TYR:CD1	1:B:83:GLY:HA2	2.37	0.60
1:B:70:GLN:CG	1:B:70:GLN:O	2.46	0.60
1:A:3:TYR:CB	1:A:83:GLY:O	2.50	0.60
1:C:55:PRO:HD3	1:C:85:CYS:HB3	1.83	0.60
1:B:62:SER:O	1:B:63:PHE:CD1	2.49	0.59
1:C:88:GLU:HB3	1:C:91:LYS:HD2	1.84	0.59
1:B:40:ARG:NE	3:B:135:HOH:O	2.35	0.59
1:B:42:GLY:HA3	1:B:62:SER:CB	2.33	0.59
1:C:50:LYS:HG2	1:C:88:GLU:HB2	1.83	0.59
1:C:55:PRO:HD2	1:C:56:ALA:N	2.17	0.59
1:D:50:LYS:HB3	1:D:88:GLU:HG3	1.84	0.59
1:B:76:THR:O	1:B:76:THR:HG23	2.02	0.59
1:D:62:SER:O	1:D:63:PHE:HD1	1.84	0.59
1:A:86:VAL:O	1:A:87:ILE:HG22	2.02	0.59
1:A:94:ALA:O	1:A:96:TYR:CZ	2.55	0.59
1:B:63:PHE:CA	1:B:64:LEU:HD12	2.33	0.59
1:B:46:THR:HG22	3:B:128:HOH:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:9:THR:CG2	1:B:89:THR:HG21	2.33	0.59
1:A:60:ASP:N	1:A:60:ASP:OD1	2.36	0.59
1:C:64:LEU:HD22	1:C:64:LEU:H	1.68	0.59
1:D:35:LEU:HD13	1:D:36:PRO:CG	2.32	0.59
1:A:6:THR:OG1	1:A:15:VAL:HG13	2.03	0.59
1:D:48:ALA:HB1	1:D:95:LEU:CD1	2.32	0.59
1:B:96:TYR:CD2	1:B:96:TYR:N	2.69	0.58
1:D:15:VAL:C	1:D:16:ILE:HG22	2.22	0.58
1:C:51:LEU:HD23	1:C:87:ILE:HG23	1.84	0.58
1:D:65:ASP:O	1:D:66:ASP:C	2.39	0.58
1:A:50:LYS:HG3	1:A:91:LYS:NZ	2.18	0.58
1:B:34:ASP:O	3:B:124:HOH:O	2.16	0.58
1:A:47:CYS:O	1:A:76:THR:OG1	2.16	0.58
1:D:51:LEU:HD23	1:D:57:PRO:CD	2.34	0.58
1:A:73:TYR:CE2	1:A:91:LYS:NZ	2.72	0.58
1:D:60:ASP:OD2	1:D:60:ASP:C	2.42	0.58
1:D:23:TYR:CE1	1:D:80:TYR:CE1	2.92	0.57
1:B:35:LEU:HG	1:B:76:THR:HG21	1.86	0.57
1:D:68:GLN:CA	1:D:68:GLN:HE21	2.16	0.57
1:D:51:LEU:HD11	1:D:53:SER:O	2.05	0.57
1:B:50:LYS:N	1:B:87:ILE:HD11	2.18	0.57
1:D:15:VAL:C	1:D:16:ILE:HG23	2.10	0.57
1:B:35:LEU:HD13	1:B:36:PRO:N	2.19	0.57
1:C:4:LYS:HG2	1:C:84:ASP:OD2	2.03	0.57
1:B:55:PRO:HG2	1:B:83:GLY:CA	2.34	0.57
1:C:59:GLU:HB2	1:C:69:ILE:CD1	2.34	0.57
1:A:9:THR:O	1:A:10:PRO:O	2.21	0.57
1:C:35:LEU:CD1	1:C:47:CYS:CB	2.78	0.57
1:C:50:LYS:CD	1:C:91:LYS:HD3	2.33	0.57
1:A:58:ASP:N	1:A:80:TYR:O	2.38	0.57
1:D:23:TYR:HE1	1:D:80:TYR:CE1	2.23	0.57
1:D:52:VAL:CB	1:D:86:VAL:CG2	2.80	0.57
1:A:34:ASP:N	1:A:34:ASP:OD2	2.38	0.56
1:B:9:THR:HG22	1:B:89:THR:CG2	2.35	0.56
1:C:35:LEU:HD11	1:C:76:THR:OG1	2.05	0.56
1:A:3:TYR:CD1	1:A:83:GLY:CA	2.78	0.56
1:D:22:GLU:CD	3:D:148:HOH:O	2.34	0.56
1:C:70:GLN:C	1:C:72:GLY:H	2.00	0.56
1:D:50:LYS:HB2	1:D:91:LYS:HD3	1.87	0.56
1:B:61:GLN:HG2	1:B:78:VAL:HG22	1.88	0.56
1:D:48:ALA:CB	1:D:95:LEU:HD11	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:9:THR:CG2	1:D:89:THR:HG21	2.35	0.56
1:A:35:LEU:HD11	1:A:47:CYS:CB	2.35	0.56
1:B:62:SER:OG	1:B:78:VAL:CB	2.53	0.56
1:C:23:TYR:CE1	1:C:61:GLN:NE2	2.74	0.56
1:A:42:GLY:HA2	1:A:75:LEU:HD13	1.87	0.56
1:B:52:VAL:CG2	1:B:87:ILE:HA	2.35	0.56
1:B:25:LEU:HB2	1:B:76:THR:O	2.06	0.56
1:B:35:LEU:C	1:B:35:LEU:CD1	2.74	0.56
1:B:51:LEU:HG	1:B:74:ILE:HD11	1.88	0.56
1:C:73:TYR:CD1	1:C:95:LEU:HD21	2.41	0.56
1:B:51:LEU:HD11	1:B:56:ALA:HA	1.87	0.56
1:A:50:LYS:CG	1:A:91:LYS:NZ	2.69	0.55
1:C:2:SER:HA	1:C:19:PRO:HA	1.87	0.55
1:D:6:THR:CG2	1:D:15:VAL:HG22	2.35	0.55
1:A:78:VAL:O	1:A:78:VAL:CG1	2.54	0.55
1:B:42:GLY:HA3	1:B:62:SER:HB2	1.88	0.55
1:B:63:PHE:CZ	1:B:75:LEU:HD21	2.41	0.55
1:C:18:VAL:HG22	1:C:81:PRO:CG	2.37	0.55
1:C:92:GLU:O	1:C:92:GLU:CG	2.52	0.55
1:C:22:GLU:HG3	3:C:127:HOH:O	2.06	0.55
1:C:58:ASP:OD1	1:C:80:TYR:CB	2.50	0.55
1:A:68:GLN:HA	1:A:68:GLN:OE1	2.07	0.55
1:A:24:ILE:HD12	1:A:79:ALA:HB3	1.88	0.55
1:D:35:LEU:HD11	1:D:47:CYS:CA	2.36	0.55
1:D:9:THR:HG23	1:D:89:THR:HG21	1.88	0.55
1:A:1:ALA:O	1:A:19:PRO:HA	2.07	0.55
1:B:55:PRO:O	1:B:56:ALA:CB	2.53	0.55
1:B:95:LEU:O	1:B:96:TYR:CG	2.60	0.55
1:B:70:GLN:O	1:B:70:GLN:HG2	1.81	0.55
1:D:1:ALA:H1	1:D:20:ASP:CG	2.10	0.55
1:A:25:LEU:HA	1:A:28:ALA:HB3	1.87	0.55
1:B:61:GLN:HA	1:B:61:GLN:HE21	1.72	0.55
1:D:1:ALA:N	1:D:20:ASP:CG	2.60	0.55
1:A:61:GLN:HB3	1:A:78:VAL:CG1	2.32	0.55
1:D:35:LEU:CD1	1:D:47:CYS:HA	2.37	0.55
1:A:24:ILE:HD12	1:A:79:ALA:CB	2.37	0.54
1:C:35:LEU:CD1	1:C:76:THR:OG1	2.55	0.54
1:D:25:LEU:O	1:D:26:ASP:C	2.46	0.54
1:A:50:LYS:HG2	1:A:91:LYS:HZ3	1.71	0.54
1:D:6:THR:HB	1:D:15:VAL:CG2	2.33	0.54
1:B:36:PRO:HD3	1:B:90:HIS:NE2	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:25:LEU:CD1	1:D:35:LEU:HB3	2.38	0.54
1:D:38:SER:CB	1:D:46:THR:HG21	2.38	0.54
1:C:64:LEU:CD2	1:C:64:LEU:H	2.20	0.54
1:A:62:SER:C	1:A:63:PHE:CD1	2.78	0.54
1:B:52:VAL:HG23	1:B:87:ILE:CA	2.37	0.54
1:D:44:CYS:CA	1:D:65:ASP:OD1	2.56	0.54
1:A:63:PHE:CZ	1:A:69:ILE:HG23	2.43	0.54
1:A:70:GLN:HE21	1:A:70:GLN:C	2.11	0.54
1:A:4:LYS:HB2	1:A:84:ASP:OD2	2.08	0.53
1:D:58:ASP:O	1:D:58:ASP:OD1	2.26	0.53
1:C:37:TYR:HE1	3:C:147:HOH:O	1.91	0.53
1:D:20:ASP:N	1:D:20:ASP:OD2	2.40	0.53
1:D:62:SER:HB3	1:D:78:VAL:HG11	1.89	0.53
1:D:69:ILE:O	1:D:73:TYR:N	2.41	0.53
1:A:63:PHE:CE2	1:A:69:ILE:HD12	2.44	0.53
1:C:9:THR:CG2	1:C:89:THR:OG1	2.57	0.53
1:C:88:GLU:CB	1:C:91:LYS:HD2	2.39	0.53
1:D:18:VAL:CG2	1:D:81:PRO:HG3	2.17	0.53
1:B:35:LEU:HD22	1:B:36:PRO:HD2	1.91	0.52
1:C:51:LEU:CD2	1:C:87:ILE:HG23	2.39	0.52
1:B:33:LEU:C	1:B:34:ASP:OD2	2.48	0.52
1:C:62:SER:N	1:C:78:VAL:HG11	2.24	0.52
1:D:42:GLY:CA	2:D:97:FES:S2	2.97	0.52
1:D:44:CYS:C	1:D:65:ASP:OD1	2.48	0.52
1:D:52:VAL:CG1	1:D:86:VAL:CG2	2.87	0.52
1:D:88:GLU:HB3	1:D:91:LYS:HD2	1.92	0.52
1:D:25:LEU:O	1:D:28:ALA:HB3	2.10	0.52
1:D:88:GLU:HB2	1:D:91:LYS:HD2	1.92	0.52
1:D:5:VAL:CG1	1:D:18:VAL:HG13	2.40	0.52
1:A:38:SER:HG	1:A:46:THR:HG21	1.72	0.52
1:C:18:VAL:HB	1:C:27:VAL:HG21	1.92	0.52
1:C:4:LYS:O	1:C:84:ASP:HB3	2.10	0.52
1:C:73:TYR:CD1	1:C:95:LEU:CD2	2.93	0.52
1:A:38:SER:O	3:A:121:HOH:O	2.19	0.51
1:A:58:ASP:O	1:A:58:ASP:OD1	2.28	0.51
1:B:42:GLY:HA3	1:B:62:SER:OG	2.10	0.51
1:B:67:ASP:C	1:B:67:ASP:OD2	2.49	0.51
1:C:51:LEU:HD22	1:C:86:VAL:O	2.11	0.51
1:B:25:LEU:HD12	1:B:76:THR:CG2	2.40	0.51
1:B:21:ASP:HA	1:B:80:TYR:CD2	2.45	0.51
1:C:59:GLU:CB	1:C:69:ILE:HD13	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:22:GLU:CD	1:C:27:VAL:HG22	2.31	0.51
1:D:89:THR:HG1	1:D:90:HIS:HD1	1.55	0.51
1:A:59:GLU:O	1:A:61:GLN:N	2.43	0.51
1:B:30:GLU:O	1:B:31:GLU:C	2.49	0.51
1:D:51:LEU:CD1	1:D:53:SER:O	2.59	0.51
1:B:50:LYS:H	1:B:87:ILE:HD12	1.71	0.50
1:A:6:THR:C	3:A:117:HOH:O	2.50	0.50
1:B:93:GLU:HA	1:B:96:TYR:HE2	1.75	0.50
1:D:51:LEU:HD23	1:D:57:PRO:HD3	1.92	0.50
1:A:19:PRO:HD2	1:A:22:GLU:HB2	1.94	0.50
1:A:35:LEU:HD23	1:A:89:THR:O	2.08	0.50
1:C:3:TYR:HD1	1:C:84:ASP:OD1	1.93	0.50
1:C:91:LYS:NZ	1:C:91:LYS:HB3	2.26	0.50
1:D:36:PRO:CG	1:D:36:PRO:O	2.60	0.50
1:C:68:GLN:CA	1:C:68:GLN:OE1	2.52	0.50
1:D:35:LEU:HD13	1:D:36:PRO:HG2	1.93	0.50
1:B:36:PRO:O	1:B:37:TYR:HB3	2.12	0.50
1:B:62:SER:OG	1:B:78:VAL:HG21	2.12	0.50
1:D:51:LEU:HD23	1:D:57:PRO:HD2	1.92	0.50
1:C:59:GLU:HB2	1:C:69:ILE:HD13	1.93	0.50
1:A:35:LEU:HD13	1:A:36:PRO:N	2.27	0.50
1:D:7:LEU:CD2	1:D:16:ILE:CG2	2.90	0.50
1:D:8:LYS:HE3	1:D:86:VAL:CB	2.39	0.50
1:B:94:ALA:N	1:B:96:TYR:HE2	2.10	0.49
1:C:73:TYR:CZ	1:C:95:LEU:HD21	2.47	0.49
1:D:5:VAL:HA	1:D:85:CYS:O	2.11	0.49
1:C:51:LEU:HD21	1:C:87:ILE:HD13	1.91	0.49
1:A:31:GLU:OE2	1:A:31:GLU:HA	2.11	0.49
1:B:46:THR:HB	1:B:92:GLU:OE1	2.11	0.49
1:A:44:CYS:SG	1:A:45:SER:N	2.85	0.49
1:D:68:GLN:H	1:D:69:ILE:HD12	1.77	0.49
1:C:51:LEU:O	3:C:115:HOH:O	2.19	0.49
1:A:37:TYR:CD2	1:A:37:TYR:C	2.85	0.49
1:B:23:TYR:HA	1:B:79:ALA:O	2.11	0.49
1:B:45:SER:HB3	1:B:95:LEU:HD22	1.95	0.49
1:C:68:GLN:C	1:C:70:GLN:N	2.64	0.49
1:A:11:ASP:O	1:C:70:GLN:NE2	2.46	0.49
1:C:58:ASP:N	1:C:80:TYR:O	2.34	0.49
1:A:69:ILE:N	1:A:69:ILE:HD13	2.23	0.49
1:C:45:SER:HA	1:C:75:LEU:HD21	1.95	0.49
1:A:59:GLU:OE2	1:A:74:ILE:CA	2.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:27:VAL:O	1:B:28:ALA:C	2.51	0.49
1:C:22:GLU:OE2	1:C:27:VAL:HG22	2.13	0.49
1:C:9:THR:HB	1:C:10:PRO:HD2	1.95	0.49
1:D:24:ILE:HD12	1:D:79:ALA:O	2.13	0.49
1:B:63:PHE:HZ	1:B:75:LEU:HD21	1.77	0.49
1:C:23:TYR:CZ	1:C:61:GLN:NE2	2.81	0.49
1:C:52:VAL:HB	1:C:86:VAL:CG2	2.41	0.49
1:A:55:PRO:HB2	1:A:82:THR:CG2	2.37	0.48
1:A:62:SER:OG	1:A:78:VAL:HG12	2.05	0.48
1:C:68:GLN:O	1:C:69:ILE:C	2.52	0.48
1:D:31:GLU:HB3	3:D:149:HOH:O	2.13	0.48
1:A:60:ASP:O	1:A:60:ASP:OD1	2.31	0.48
1:B:63:PHE:HZ	1:B:75:LEU:CD2	2.24	0.48
1:C:5:VAL:CG1	1:C:16:ILE:CD1	2.77	0.48
1:A:42:GLY:CA	1:A:62:SER:HB3	2.41	0.48
1:A:50:LYS:CG	1:A:91:LYS:HZ3	2.26	0.48
1:B:93:GLU:CA	1:B:96:TYR:HE2	2.27	0.48
1:C:4:LYS:CG	1:C:84:ASP:CG	2.81	0.48
1:D:63:PHE:HE2	1:D:67:ASP:HA	1.79	0.48
1:C:23:TYR:HB2	1:C:26:ASP:CG	2.34	0.48
1:C:20:ASP:HB2	3:C:126:HOH:O	2.14	0.48
1:C:40:ARG:HD3	3:C:112:HOH:O	2.12	0.48
1:C:64:LEU:CD2	1:C:64:LEU:N	2.77	0.48
1:C:6:THR:HG23	1:C:15:VAL:HG22	1.96	0.48
1:A:42:GLY:HA3	1:A:62:SER:OG	2.13	0.48
1:B:67:ASP:C	1:B:68:GLN:HG2	2.29	0.48
1:A:51:LEU:HA	1:A:87:ILE:HG22	1.95	0.48
1:D:37:TYR:CE2	1:D:40:ARG:HG3	2.47	0.48
1:D:50:LYS:HB3	1:D:88:GLU:HB2	1.96	0.48
1:A:63:PHE:CZ	1:A:65:ASP:O	2.67	0.48
1:B:55:PRO:HB2	1:B:82:THR:HG22	1.95	0.47
1:A:84:ASP:O	1:A:85:CYS:HB3	2.13	0.47
1:C:61:GLN:HB3	3:C:117:HOH:O	2.13	0.47
1:C:92:GLU:O	1:C:93:GLU:CB	2.49	0.47
1:D:33:LEU:H	1:D:33:LEU:HG	1.34	0.47
1:C:42:GLY:C	2:C:97:FES:S2	2.91	0.47
1:B:55:PRO:CG	1:B:83:GLY:HA3	2.45	0.47
1:C:68:GLN:O	1:C:73:TYR:HB2	2.14	0.47
1:D:58:ASP:CG	1:D:58:ASP:O	2.51	0.47
1:C:43:ALA:N	2:C:97:FES:S2	2.88	0.47
1:A:7:LEU:N	3:A:117:HOH:O	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:VAL:C	1:A:87:ILE:CG2	2.83	0.47
1:B:48:ALA:HB1	1:B:95:LEU:CD1	2.30	0.47
1:D:52:VAL:HG11	1:D:86:VAL:HG21	1.97	0.47
1:A:63:PHE:HE2	1:A:69:ILE:HD12	1.78	0.47
1:D:8:LYS:HE2	1:D:86:VAL:HB	1.91	0.47
1:D:25:LEU:HD13	1:D:35:LEU:HB3	1.98	0.46
1:C:62:SER:O	1:C:63:PHE:HB2	2.14	0.46
1:D:9:THR:HG23	1:D:89:THR:CG2	2.45	0.46
1:C:59:GLU:CB	1:C:69:ILE:CD1	2.93	0.46
1:D:57:PRO:HG2	1:D:74:ILE:CG1	2.45	0.46
1:D:5:VAL:HG11	1:D:18:VAL:HG13	1.96	0.46
1:A:23:TYR:OH	1:A:61:GLN:CD	2.53	0.46
1:B:76:THR:O	1:B:76:THR:HG22	2.13	0.46
1:A:86:VAL:C	1:A:87:ILE:HG23	2.35	0.46
1:A:5:VAL:HG23	3:A:117:HOH:O	2.15	0.46
1:A:60:ASP:O	1:A:60:ASP:OD2	2.34	0.46
1:B:23:TYR:CE2	3:B:137:HOH:O	2.64	0.46
1:C:16:ILE:HD13	1:C:16:ILE:C	2.36	0.46
1:A:22:GLU:OE1	1:A:26:ASP:CB	2.60	0.46
1:C:9:THR:HG22	1:C:89:THR:OG1	2.15	0.46
1:D:7:LEU:HB3	1:D:89:THR:CG2	2.46	0.46
1:B:18:VAL:HA	1:B:19:PRO:HD3	1.69	0.46
1:C:5:VAL:CG1	1:C:18:VAL:CG1	2.90	0.45
1:C:5:VAL:HG22	1:C:7:LEU:HD23	1.94	0.45
1:A:73:TYR:OH	1:A:94:ALA:CB	2.59	0.45
1:B:56:ALA:HA	1:B:57:PRO:HD3	1.67	0.45
1:D:7:LEU:O	1:D:12:GLY:O	2.34	0.45
1:B:23:TYR:O	1:B:27:VAL:HG23	2.16	0.45
1:B:35:LEU:HD11	1:B:47:CYS:CB	2.46	0.45
1:D:78:VAL:HG23	1:D:78:VAL:O	2.17	0.45
1:B:95:LEU:O	1:B:96:TYR:CB	2.65	0.45
1:A:63:PHE:CE2	1:A:69:ILE:HG23	2.52	0.45
1:A:94:ALA:O	1:A:96:TYR:CD2	2.69	0.45
1:C:73:TYR:CG	1:C:95:LEU:CD2	2.99	0.45
1:A:53:SER:HB2	1:A:86:VAL:HG13	1.99	0.45
1:B:95:LEU:C	1:B:96:TYR:CG	2.89	0.45
1:D:55:PRO:HD2	1:D:56:ALA:H	1.82	0.45
1:B:63:PHE:C	1:B:64:LEU:CD1	2.69	0.45
1:B:68:GLN:HA	1:B:68:GLN:OE1	2.17	0.45
1:B:58:ASP:OD2	1:B:80:TYR:HD1	2.00	0.45
1:D:60:ASP:O	1:D:61:GLN:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:23:TYR:HE1	1:C:61:GLN:NE2	2.14	0.45
1:D:51:LEU:CD2	1:D:57:PRO:CD	2.93	0.45
1:D:52:VAL:HB	1:D:86:VAL:O	2.17	0.45
1:B:40:ARG:CD	3:B:135:HOH:O	2.64	0.44
1:C:70:GLN:O	1:C:71:ALA:C	2.54	0.44
1:A:45:SER:CB	1:A:92:GLU:OE2	2.64	0.44
1:B:50:LYS:C	1:B:87:ILE:HD13	2.37	0.44
1:C:93:GLU:O	1:C:93:GLU:HG3	2.16	0.44
1:B:70:GLN:C	1:B:72:GLY:N	2.67	0.44
1:C:3:TYR:O	1:C:17:THR:HA	2.18	0.44
1:C:9:THR:HG23	1:C:89:THR:OG1	2.17	0.44
1:B:20:ASP:OD2	1:B:21:ASP:N	2.50	0.44
1:D:48:ALA:CB	1:D:95:LEU:HD12	2.47	0.44
1:B:45:SER:CB	1:B:95:LEU:HD22	2.48	0.44
1:C:57:PRO:HA	1:C:80:TYR:O	2.18	0.44
1:A:62:SER:HB3	1:A:75:LEU:HD12	2.00	0.44
1:B:6:THR:HA	1:B:15:VAL:HA	1.99	0.44
1:B:51:LEU:CD2	1:B:85:CYS:HB2	2.48	0.44
1:C:50:LYS:HE2	1:C:50:LYS:HB2	1.78	0.44
1:D:25:LEU:HD11	1:D:35:LEU:HB3	1.99	0.44
1:C:44:CYS:SG	1:C:46:THR:HG23	2.58	0.43
1:C:63:PHE:HE2	1:C:69:ILE:CG2	2.31	0.43
1:D:71:ALA:HA	3:D:142:HOH:O	2.17	0.43
1:C:63:PHE:HA	1:C:63:PHE:HD1	1.47	0.43
1:C:8:LYS:HZ2	1:C:86:VAL:HG21	1.83	0.43
1:A:36:PRO:O	1:A:47:CYS:HA	2.17	0.43
1:B:16:ILE:HD12	1:B:31:GLU:CG	2.33	0.43
1:C:48:ALA:HB1	1:C:95:LEU:CD1	2.49	0.43
1:C:53:SER:H	1:C:86:VAL:HG22	1.83	0.43
1:C:62:SER:O	1:C:63:PHE:CB	2.64	0.43
1:A:57:PRO:CB	1:A:80:TYR:O	2.66	0.43
1:A:55:PRO:HD3	1:A:84:ASP:O	2.18	0.43
1:A:38:SER:HB2	1:A:39:CYS:H	1.58	0.43
1:D:9:THR:CG2	1:D:89:THR:CG2	2.97	0.43
1:A:59:GLU:OE2	1:A:74:ILE:CG2	2.62	0.43
1:B:91:LYS:HA	1:B:91:LYS:HD3	1.85	0.43
1:A:62:SER:CB	1:A:78:VAL:HG12	2.43	0.43
1:A:87:ILE:HD12	1:A:88:GLU:O	2.19	0.43
1:B:50:LYS:HE2	1:B:73:TYR:CZ	2.54	0.43
1:C:4:LYS:HB2	1:C:84:ASP:HB3	2.00	0.43
1:D:4:LYS:HE2	1:D:4:LYS:HB2	1.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ILE:CG2	1:A:31:GLU:CG	2.96	0.43
1:B:52:VAL:CG2	1:B:86:VAL:HG12	2.48	0.43
1:C:16:ILE:CD1	1:C:18:VAL:HG12	2.49	0.43
3:A:130:HOH:O	1:C:82:THR:CG2	2.61	0.43
1:B:18:VAL:CG1	1:B:81:PRO:HG2	2.49	0.42
1:C:35:LEU:HD22	1:C:36:PRO:HG2	2.01	0.42
1:D:1:ALA:HA	1:D:20:ASP:OD2	2.19	0.42
1:D:6:THR:HG22	1:D:15:VAL:HG22	2.00	0.42
1:C:49:GLY:HA2	1:C:88:GLU:O	2.20	0.42
1:D:57:PRO:HG2	1:D:74:ILE:HG13	2.01	0.42
1:A:2:SER:HA	1:A:18:VAL:O	2.19	0.42
1:A:3:TYR:N	1:A:3:TYR:CD2	2.86	0.42
1:B:25:LEU:CD1	1:B:76:THR:CG2	2.93	0.42
1:A:52:VAL:CG1	1:A:86:VAL:CG2	2.98	0.42
1:D:63:PHE:HE1	1:D:75:LEU:HD22	1.85	0.42
1:A:16:ILE:HG12	1:A:16:ILE:H	1.59	0.42
1:B:93:GLU:HA	1:B:96:TYR:CE2	2.54	0.42
1:B:25:LEU:HD11	1:B:35:LEU:HD12	2.02	0.42
1:B:92:GLU:HA	1:B:95:LEU:HD12	2.02	0.42
1:C:72:GLY:HA3	3:C:115:HOH:O	2.19	0.42
1:C:8:LYS:CG	1:C:13:ASP:OD1	2.52	0.41
1:C:78:VAL:CG1	1:C:78:VAL:O	2.68	0.41
1:D:77:CYS:SG	1:D:78:VAL:HG13	2.60	0.41
1:D:26:ASP:O	1:D:29:GLU:HB2	2.20	0.41
1:D:1:ALA:N	1:D:3:TYR:CE2	2.88	0.41
1:D:8:LYS:HE3	1:D:86:VAL:CG2	2.50	0.41
1:D:35:LEU:HA	1:D:36:PRO:HD2	1.67	0.41
1:D:52:VAL:HG11	1:D:86:VAL:CG2	2.50	0.41
1:C:48:ALA:HB1	1:C:95:LEU:HD11	2.03	0.41
1:B:50:LYS:CA	1:B:87:ILE:CD1	2.98	0.41
1:A:73:TYR:CZ	1:A:91:LYS:NZ	2.89	0.41
1:C:5:VAL:HG11	1:C:18:VAL:CG1	2.46	0.41
1:C:7:LEU:N	1:C:7:LEU:HD23	2.35	0.41
1:A:29:GLU:HG2	3:A:106:HOH:O	2.21	0.41
1:A:8:LYS:HB3	1:A:13:ASP:OD2	2.21	0.41
1:B:54:GLY:HA3	1:B:55:PRO:HD3	1.76	0.41
1:C:5:VAL:HG21	1:C:24:ILE:HD13	2.03	0.41
1:C:62:SER:OG	1:C:78:VAL:HG11	2.21	0.41
1:C:52:VAL:HG23	1:C:88:GLU:HG3	2.02	0.41
1:D:21:ASP:O	1:D:80:TYR:HE2	2.03	0.41
1:D:52:VAL:CG1	1:D:86:VAL:HG21	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:PRO:HG3	1:A:74:ILE:CG2	2.50	0.41
1:A:63:PHE:CZ	1:A:69:ILE:CG2	3.04	0.41
1:B:74:ILE:HG22	1:B:74:ILE:O	2.21	0.41
1:C:30:GLU:O	1:C:32:GLY:N	2.53	0.41
1:C:4:LYS:H	1:C:4:LYS:HG2	1.29	0.41
1:D:18:VAL:HB	1:D:27:VAL:HG11	2.01	0.41
1:D:1:ALA:H2	1:D:20:ASP:HB3	1.86	0.41
1:A:35:LEU:HD11	1:A:47:CYS:HB2	2.03	0.41
1:B:71:ALA:HB3	1:B:73:TYR:CD1	2.56	0.41
1:B:9:THR:CA	1:B:89:THR:HG22	2.45	0.41
1:C:16:ILE:HD11	1:C:18:VAL:CG1	2.51	0.41
1:C:59:GLU:HB2	1:C:69:ILE:HD11	2.02	0.41
1:D:21:ASP:OD2	1:D:21:ASP:N	2.54	0.40
1:A:23:TYR:CD2	1:A:77:CYS:O	2.74	0.40
1:A:37:TYR:HB2	2:A:97:FES:S1	2.62	0.40
1:C:18:VAL:HA	1:C:19:PRO:HD3	1.72	0.40
1:C:56:ALA:HA	1:C:57:PRO:HD3	1.83	0.40

All (78) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:ARG:NH2	1:B:58:ASP:CB[3_755]	0.67	1.53
3:C:107:HOH:O	3:D:137:HOH:O[3_655]	0.88	1.32
1:B:55:PRO:O	1:C:93:GLU:OE1[1_554]	0.89	1.31
1:D:60:ASP:CA	3:C:112:HOH:O[3_755]	0.94	1.26
1:B:39:CYS:O	3:B:114:HOH:O[3_755]	0.99	1.21
1:B:93:GLU:OE1	1:D:55:PRO:O[1_554]	1.03	1.17
1:A:60:ASP:CA	3:A:109:HOH:O[4_564]	1.06	1.14
1:D:60:ASP:C	3:C:112:HOH:O[3_755]	1.11	1.09
1:A:40:ARG:CD	1:A:60:ASP:OD2[3_655]	1.12	1.08
1:A:40:ARG:CD	1:A:60:ASP:CG[3_655]	1.16	1.04
1:D:51:LEU:CG	3:B:138:HOH:O[1_556]	1.21	0.99
1:C:40:ARG:CD	1:D:58:ASP:OD1[4_574]	1.26	0.94
1:B:93:GLU:CD	1:D:55:PRO:O[1_554]	1.30	0.90
1:B:40:ARG:CZ	1:B:58:ASP:CG[3_755]	1.31	0.89
1:B:40:ARG:NE	1:B:58:ASP:CG[3_755]	1.32	0.88
1:C:40:ARG:NE	1:D:58:ASP:OD2[4_574]	1.32	0.88
1:B:60:ASP:N	3:B:136:HOH:O[4_574]	1.35	0.85
1:B:40:ARG:CD	1:B:58:ASP:OD1[3_755]	1.37	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:40:ARG:CD	1:D:58:ASP:CG[4_574]	1.41	0.79
1:B:40:ARG:NE	1:B:58:ASP:OD1[3_755]	1.42	0.78
1:B:40:ARG:CZ	1:B:58:ASP:CB[3_755]	1.44	0.76
1:D:60:ASP:O	3:C:112:HOH:O[3_755]	1.48	0.72
1:B:93:GLU:OE2	3:D:138:HOH:O[1_554]	1.48	0.72
1:C:40:ARG:NH2	1:D:60:ASP:O[4_574]	1.52	0.68
1:A:40:ARG:NH2	3:A:127:HOH:O[3_655]	1.52	0.68
1:B:58:ASP:OD1	3:B:135:HOH:O[4_574]	1.53	0.67
1:B:59:GLU:C	3:B:136:HOH:O[4_574]	1.55	0.65
1:D:60:ASP:N	3:C:112:HOH:O[3_755]	1.59	0.61
3:B:111:HOH:O	3:C:137:HOH:O[1_554]	1.59	0.61
1:D:60:ASP:CB	3:C:112:HOH:O[3_755]	1.60	0.60
3:C:144:HOH:O	3:D:136:HOH:O[3_655]	1.62	0.58
1:D:60:ASP:OD1	3:C:113:HOH:O[3_755]	1.62	0.58
3:B:99:HOH:O	3:D:157:HOH:O[1_554]	1.63	0.57
1:B:40:ARG:NH2	1:B:58:ASP:CG[3_755]	1.64	0.56
1:B:40:ARG:O	1:B:60:ASP:OD2[3_755]	1.65	0.55
1:B:40:ARG:CZ	1:B:58:ASP:OD2[3_755]	1.67	0.53
3:C:114:HOH:O	3:D:151:HOH:O[4_574]	1.68	0.52
3:B:138:HOH:O	3:D:138:HOH:O[1_554]	1.72	0.48
1:B:64:LEU:CD2	1:B:67:ASP:OD1[3_755]	1.73	0.47
1:B:93:GLU:OE1	1:D:55:PRO:C[1_554]	1.74	0.46
1:A:60:ASP:C	3:A:109:HOH:O[4_564]	1.75	0.45
1:C:40:ARG:CD	1:D:58:ASP:OD2[4_574]	1.77	0.43
1:B:70:GLN:O	1:C:96:TYR:OH[1_554]	1.77	0.43
1:A:40:ARG:NE	1:A:60:ASP:OD2[3_655]	1.82	0.38
3:B:110:HOH:O	3:C:122:HOH:O[1_554]	1.83	0.37
1:B:40:ARG:CD	1:B:58:ASP:CG[3_755]	1.85	0.35
1:D:60:ASP:CG	3:C:113:HOH:O[3_755]	1.86	0.34
1:B:59:GLU:CA	3:B:136:HOH:O[4_574]	1.88	0.32
1:B:40:ARG:NH2	1:B:58:ASP:CA[3_755]	1.89	0.31
1:D:51:LEU:CB	3:B:138:HOH:O[1_556]	1.90	0.30
1:A:40:ARG:CD	1:A:60:ASP:OD1[3_655]	1.91	0.29
1:B:93:GLU:OE2	1:D:55:PRO:O[1_554]	1.91	0.29
1:A:82:THR:OG1	3:A:121:HOH:O[4_564]	1.91	0.29
1:B:60:ASP:O	3:B:135:HOH:O[4_574]	1.94	0.26
1:B:43:ALA:CB	1:B:69:ILE:CD1[3_755]	1.97	0.23
1:C:40:ARG:NE	1:D:58:ASP:CG[4_574]	2.01	0.19
1:B:40:ARG:NH2	1:B:58:ASP:OD2[3_755]	2.03	0.17
1:B:55:PRO:O	1:C:93:GLU:CD[1_554]	2.04	0.16
1:B:93:GLU:OE1	1:D:56:ALA:CB[1_554]	2.04	0.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:ARG:NE	1:B:58:ASP:CB[3_755]	2.04	0.16
1:A:40:ARG:NH2	1:A:60:ASP:OD2[3_655]	2.05	0.15
1:A:60:ASP:N	3:A:109:HOH:O[4_564]	2.06	0.14
1:B:55:PRO:C	1:C:93:GLU:OE1[1_554]	2.07	0.13
1:D:8:LYS:NZ	3:B:100:HOH:O[1_556]	2.08	0.12
1:D:51:LEU:CD1	3:B:138:HOH:O[1_556]	2.09	0.11
1:D:60:ASP:OD2	3:C:113:HOH:O[3_755]	2.09	0.11
1:D:74:ILE:CD1	3:C:114:HOH:O[3_755]	2.11	0.09
1:B:39:CYS:C	3:B:114:HOH:O[3_755]	2.11	0.09
1:B:91:LYS:CE	1:D:52:VAL:O[1_554]	2.13	0.07
1:B:40:ARG:O	1:B:60:ASP:CG[3_755]	2.14	0.06
1:B:59:GLU:N	3:B:136:HOH:O[4_574]	2.14	0.06
1:C:40:ARG:CB	1:D:60:ASP:CB[4_574]	2.15	0.05
1:B:41:ALA:CA	1:B:60:ASP:OD2[3_755]	2.15	0.05
1:B:8:LYS:O	3:D:157:HOH:O[1_554]	2.15	0.05
1:A:61:GLN:N	3:A:109:HOH:O[4_564]	2.16	0.04
1:A:59:GLU:O	3:A:109:HOH:O[4_564]	2.18	0.02
1:B:93:GLU:OE1	1:D:56:ALA:N[1_554]	2.19	0.01
1:A:40:ARG:NE	1:A:60:ASP:CG[3_655]	2.19	0.01

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	94/96 (98%)	74 (79%)	11 (12%)	9 (10%)	0	0
1	B	94/96 (98%)	67 (71%)	16 (17%)	11 (12%)	0	0
1	C	94/96 (98%)	66 (70%)	19 (20%)	9 (10%)	0	0
1	D	94/96 (98%)	68 (72%)	16 (17%)	10 (11%)	0	0
All	All	376/384 (98%)	275 (73%)	62 (16%)	39 (10%)	0	0

All (39) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	PRO
1	A	64	LEU
1	A	67	ASP
1	A	93	GLU
1	B	55	PRO
1	B	56	ALA
1	B	66	ASP
1	B	67	ASP
1	B	68	GLN
1	B	93	GLU
1	B	94	ALA
1	C	55	PRO
1	C	64	LEU
1	C	67	ASP
1	C	93	GLU
1	D	35	LEU
1	D	55	PRO
1	D	56	ALA
1	D	61	GLN
1	D	64	LEU
1	D	68	GLN
1	D	93	GLU
1	A	66	ASP
1	C	20	ASP
1	C	66	ASP
1	A	10	PRO
1	A	76	THR
1	B	95	LEU
1	C	2	SER
1	C	63	PHE
1	A	94	ALA
1	B	76	THR
1	D	11	ASP
1	D	66	ASP
1	D	94	ALA
1	B	64	LEU
1	C	30	GLU
1	A	58	ASP
1	B	32	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	80/80 (100%)	49 (61%)	31 (39%)	0	0
1	B	80/80 (100%)	53 (66%)	27 (34%)	0	0
1	C	80/80 (100%)	54 (68%)	26 (32%)	0	0
1	D	80/80 (100%)	48 (60%)	32 (40%)	0	0
All	All	320/320 (100%)	204 (64%)	116 (36%)	0	0

All (116) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	7	LEU
1	A	8	LYS
1	A	11	ASP
1	A	16	ILE
1	A	18	VAL
1	A	21	ASP
1	A	22	GLU
1	A	25	LEU
1	A	26	ASP
1	A	33	LEU
1	A	34	ASP
1	A	38	SER
1	A	40	ARG
1	A	44	CYS
1	A	45	SER
1	A	53	SER
1	A	58	ASP
1	A	59	GLU
1	A	61	GLN
1	A	63	PHE
1	A	64	LEU
1	A	65	ASP
1	A	68	GLN

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Mol	Chain	Res	Type
1	A	69	ILE
1	A	70	GLN
1	A	74	ILE
1	A	82	THR
1	A	86	VAL
1	A	88	GLU
1	A	96	TYR
1	B	2	SER
1	B	11	ASP
1	B	14	ASN
1	B	15	VAL
1	B	17	THR
1	B	22	GLU
1	B	25	LEU
1	B	26	ASP
1	B	27	VAL
1	B	29	GLU
1	B	34	ASP
1	B	35	LEU
1	B	37	TYR
1	B	40	ARG
1	B	46	THR
1	B	50	LYS
1	B	52	VAL
1	B	58	ASP
1	B	60	ASP
1	B	61	GLN
1	B	63	PHE
1	B	64	LEU
1	B	65	ASP
1	B	78	VAL
1	B	87	ILE
1	B	88	GLU
1	B	89	THR
1	C	4	LYS
1	C	5	VAL
1	C	6	THR
1	C	7	LEU
1	C	9	THR
1	C	11	ASP
1	C	16	ILE
1	C	18	VAL

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Mol	Chain	Res	Type
1	C	25	LEU
1	C	26	ASP
1	C	33	LEU
1	C	40	ARG
1	C	44	CYS
1	C	50	LYS
1	C	51	LEU
1	C	63	PHE
1	C	64	LEU
1	C	68	GLN
1	C	69	ILE
1	C	73	TYR
1	C	86	VAL
1	C	87	ILE
1	C	91	LYS
1	C	92	GLU
1	C	93	GLU
1	C	95	LEU
1	D	2	SER
1	D	4	LYS
1	D	5	VAL
1	D	6	THR
1	D	7	LEU
1	D	8	LYS
1	D	11	ASP
1	D	16	ILE
1	D	18	VAL
1	D	25	LEU
1	D	26	ASP
1	D	33	LEU
1	D	34	ASP
1	D	35	LEU
1	D	37	TYR
1	D	38	SER
1	D	40	ARG
1	D	44	CYS
1	D	50	LYS
1	D	51	LEU
1	D	53	SER
1	D	60	ASP
1	D	61	GLN
1	D	63	PHE

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Mol	Chain	Res	Type
1	D	66	ASP
1	D	69	ILE
1	D	76	THR
1	D	86	VAL
1	D	89	THR
1	D	90	HIS
1	D	91	LYS
1	D	93	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	GLN
1	A	70	GLN
1	C	61	GLN
1	C	70	GLN
1	D	14	ASN
1	D	61	GLN
1	D	68	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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	FES	C	97	1	0,4,4	0.00	-	-		
2	FES	A	97	1	0,4,4	0.00	-	-		
2	FES	D	97	1	0,4,4	0.00	-	-		
2	FES	B	97	1	0,4,4	0.00	-	-		

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	FES	C	97	1	-	-	0/1/1/1
2	FES	A	97	1	-	-	0/1/1/1
2	FES	D	97	1	-	-	0/1/1/1
2	FES	B	97	1	-	-	0/1/1/1

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.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	97	FES	4	0
2	A	97	FES	3	0
2	D	97	FES	3	0
2	B	97	FES	2	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 [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	96/96 (100%)	0.02	2 (2%) 63 61	8, 13, 16, 23	0
1	B	96/96 (100%)	0.06	2 (2%) 63 61	6, 13, 15, 17	0
1	C	96/96 (100%)	0.01	0 100 100	4, 13, 17, 18	0
1	D	96/96 (100%)	-0.05	0 100 100	6, 13, 16, 19	0
All	All	384/384 (100%)	0.01	4 (1%) 82 81	4, 13, 16, 23	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	64	LEU	3.4
1	A	66	ASP	2.6
1	A	64	LEU	2.3
1	B	66	ASP	2.1

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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	FES	C	97	4/4	0.98	0.05	3,10,12,18	0
2	FES	A	97	4/4	0.98	0.05	5,7,12,13	0
2	FES	B	97	4/4	0.98	0.04	5,8,10,12	0
2	FES	D	97	4/4	0.99	0.05	10,11,13,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.