



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 03:36 AM EDT

PDB ID : 1XVE / pdb_00001xve
Title : soluble methane monooxygenase hydroxylase: 3-bromo-3-butenol soaked structure
Authors : Sazinsky, M.H.; Lippard, S.J.
Deposited on : 2004-10-27
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

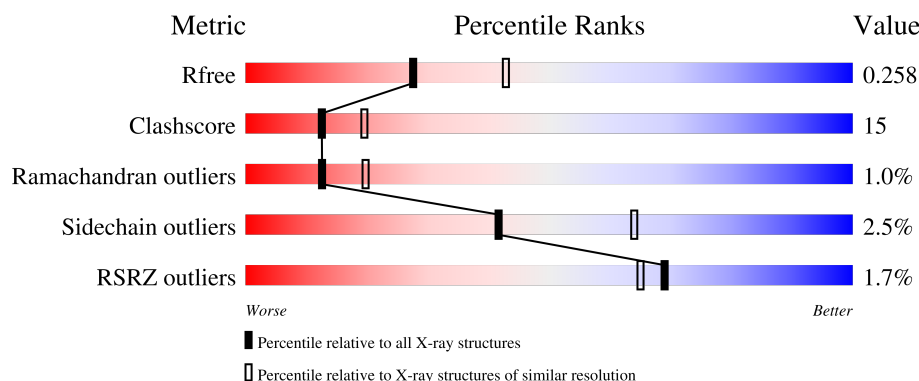
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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

Mol	Chain	Length	Quality of chain
1	A	527	0% 66% 28% • •
1	B	527	2% 63% 31% • •
2	C	389	72% 26% •
2	D	389	2% 63% 34% •
3	E	170	0% 78% 18% • •

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Mol	Chain	Length	Quality of chain
3	F	170	8% 52% 42%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 17840 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 Methane monooxygenase component A alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	510	Total	C	N	O	S	0	0	0
			4138	2649	709	762	18			
1	B	510	Total	C	N	O	S	0	0	0
			4137	2646	711	762	18			

- Molecule 2 is a protein called Methane monooxygenase component A beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	388	Total	C	N	O	S	0	0	0
			3163	2036	545	574	8			
2	D	388	Total	C	N	O	S	0	0	0
			3151	2028	543	572	8			

- Molecule 3 is a protein called Methane monooxygenase component A gamma chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	166	Total	C	N	O	S	0	0	0
			1364	864	245	250	5			
3	F	166	Total	C	N	O	S	0	0	0
			1358	860	243	250	5			

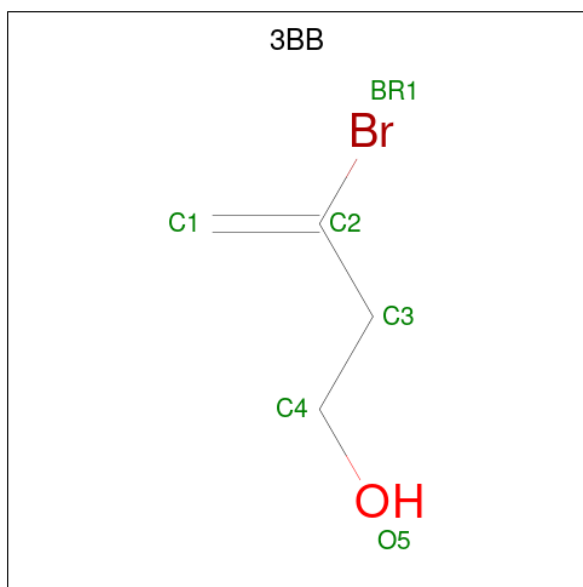
- Molecule 4 is FE (III) ION (CCD ID: FE) (formula: Fe).

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

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Ca 1 1	0	0
5	C	1	Total Ca 1 1	0	0

- Molecule 6 is 3-BROMOBUT-3-EN-1-OL (CCD ID: 3BB) (formula: C₄H₇BrO).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Br C O 6 1 4 1	0	0
6	A	1	Total Br C O 6 1 4 1	0	0
6	A	1	Total Br C O 6 1 4 1	0	0
6	A	1	Total Br C O 6 1 4 1	0	0
6	B	1	Total Br C O 6 1 4 1	0	0
6	B	1	Total Br C O 6 1 4 1	0	0
6	B	1	Total Br C O 6 1 4 1	0	0
6	C	1	Total Br C O 6 1 4 1	0	0
6	C	1	Total Br C O 6 1 4 1	0	0
6	D	1	Total Br C O 6 1 4 1	0	0

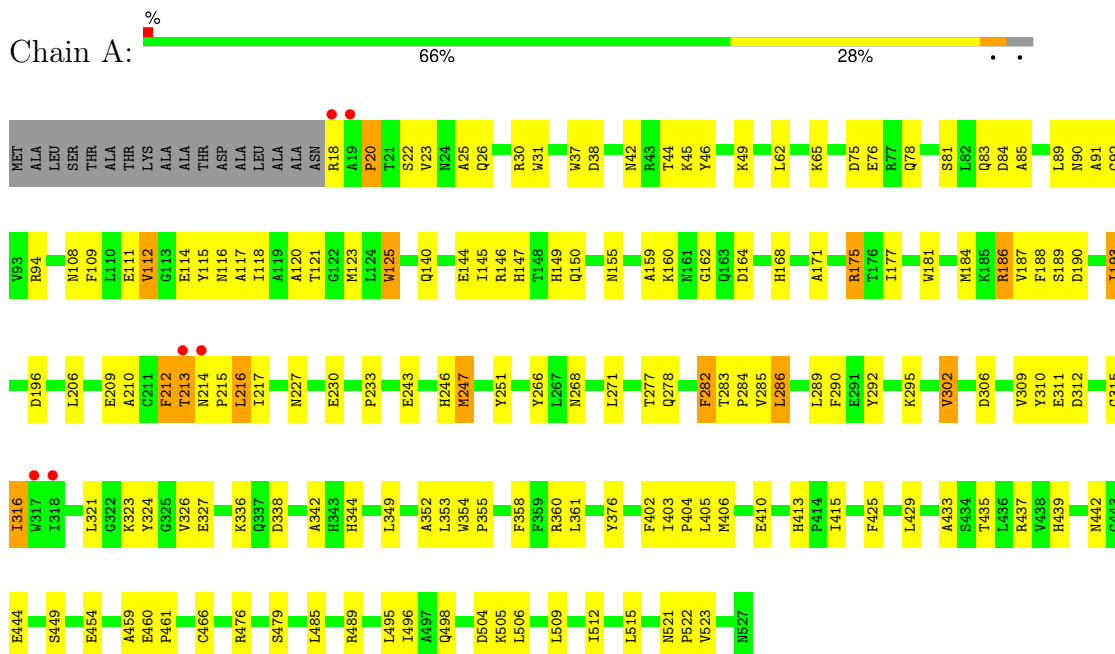
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	112	Total 112	O 112	0	0
7	B	100	Total 100	O 100	0	0
7	C	123	Total 123	O 123	0	0
7	D	46	Total 46	O 46	0	0
7	E	65	Total 65	O 65	0	0
7	F	17	Total 17	O 17	0	0

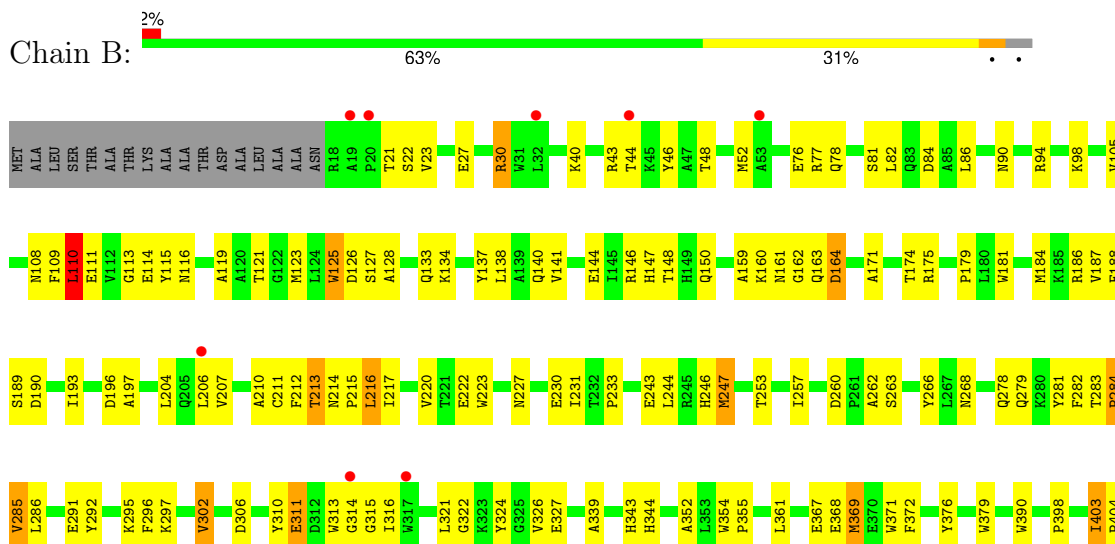
3 Residue-property plots

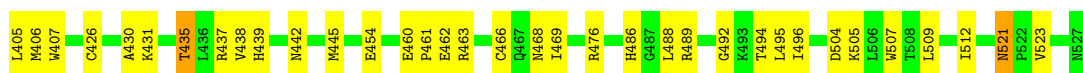
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: Methane monooxygenase component A alpha chain



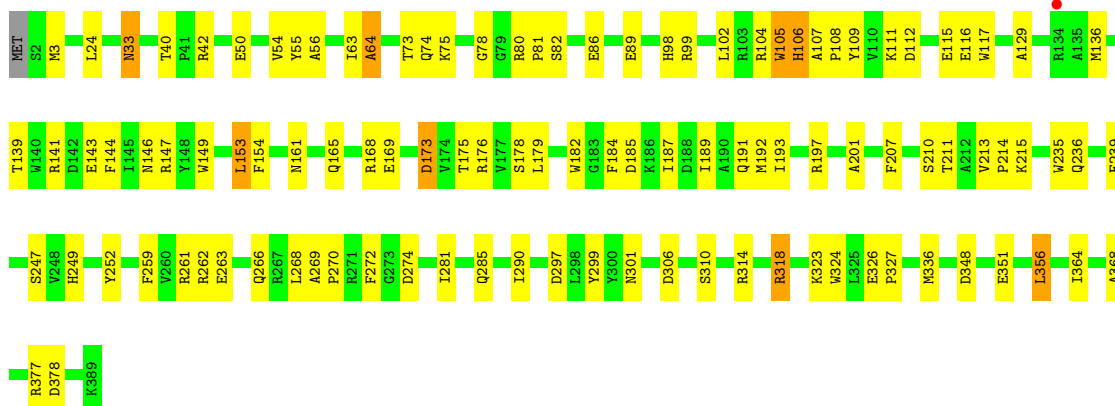
- Molecule 1: Methane monooxygenase component A alpha chain





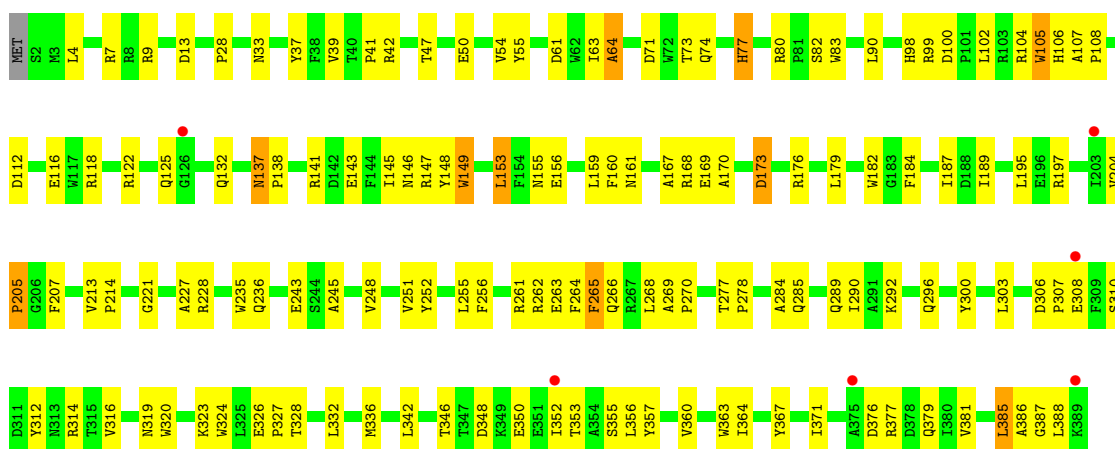
• Molecule 2: Methane monooxygenase component A beta chain

Chain C: 72% 26%



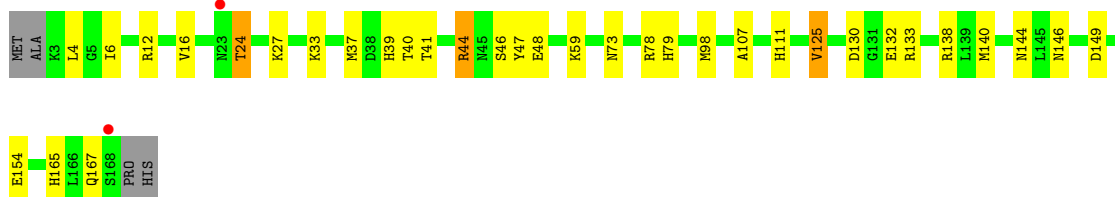
• Molecule 2: Methane monooxygenase component A beta chain

Chain D: 2% 63% 34%

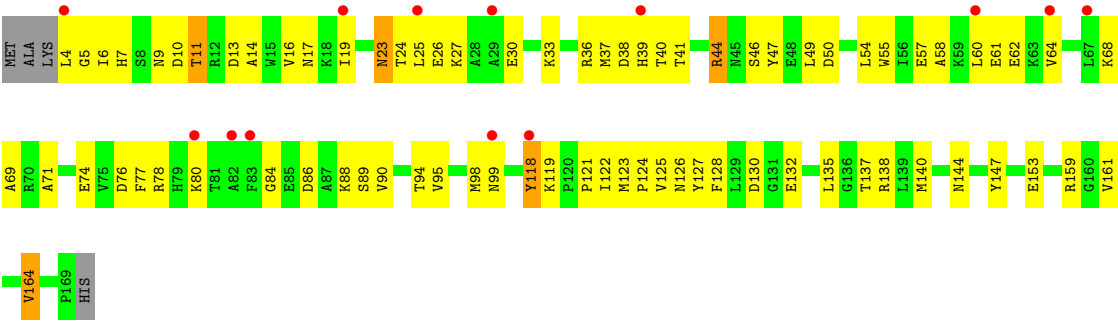


• Molecule 3: Methane monooxygenase component A gamma chain

Chain E: 78% 18%



• Molecule 3: Methane monooxygenase component A gamma chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.47Å 171.94Å 220.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.80 – 2.40 29.80 – 2.40	Depositor EDS
% Data completeness (in resolution range)	89.9 (29.80-2.40) 90.0 (29.80-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.68 (at 2.39Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.202 , 0.260 0.200 , 0.258	Depositor DCC
R_{free} test set	9570 reflections (9.37%)	wwPDB-VP
Wilson B-factor (Å ²)	34.8	Xtriage
Anisotropy	0.113	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17840	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE, CA, 3BB

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.40	0/4263	0.95	17/5797 (0.3%)
1	B	0.40	0/4262	0.94	19/5796 (0.3%)
2	C	0.45	0/3259	0.91	15/4430 (0.3%)
2	D	0.37	0/3247	0.91	17/4417 (0.4%)
3	E	0.46	0/1392	0.90	3/1876 (0.2%)
3	F	0.36	0/1387	0.89	4/1873 (0.2%)
All	All	0.41	0/17810	0.93	75/24189 (0.3%)

There are no bond length outliers.

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	6	ILE	N-CA-C	11.05	121.72	110.23
1	B	339	ALA	N-CA-C	8.73	120.48	110.97
1	B	164	ASP	CA-C-N	7.95	127.87	119.05
1	B	164	ASP	C-N-CA	7.95	127.87	119.05
1	A	213	THR	N-CA-C	7.79	119.41	111.07
3	F	118	TYR	N-CA-C	7.75	122.73	113.28
1	A	266	TYR	N-CA-C	7.24	122.67	113.55
1	A	164	ASP	CA-C-N	7.16	126.78	119.19
1	A	164	ASP	C-N-CA	7.16	126.78	119.19
2	C	318	ARG	N-CA-C	-6.99	103.75	111.36
2	D	204	VAL	CA-C-N	6.87	128.43	119.84
2	D	204	VAL	C-N-CA	6.87	128.43	119.84
2	C	236	GLN	N-CA-C	6.66	121.58	113.38
1	A	285	VAL	N-CA-C	6.62	117.41	110.72
2	D	105	TRP	N-CA-C	-6.57	100.49	109.95
1	A	145	ILE	N-CA-C	-6.56	104.10	110.72
2	D	149	TRP	N-CA-C	-6.49	103.71	111.69
2	D	106	HIS	N-CA-C	6.47	118.88	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	295	LYS	N-CA-C	-6.35	104.24	112.68
2	D	42	ARG	N-CA-C	-6.28	105.75	113.41
1	A	309	VAL	N-CA-C	6.18	116.34	110.53
2	D	155	ASN	N-CA-C	-6.15	104.48	111.07
1	A	247	MET	N-CA-C	-6.11	104.53	111.07
1	B	426	CYS	CA-C-N	6.06	126.23	119.32
1	B	426	CYS	C-N-CA	6.06	126.23	119.32
1	A	212	PHE	N-CA-C	6.01	120.43	111.96
1	A	193	ILE	N-CA-C	5.96	119.37	113.53
2	C	144	PHE	N-CA-C	5.92	117.82	111.36
1	B	243	GLU	N-CA-C	5.92	117.73	111.28
2	C	105	TRP	N-CA-C	-5.91	101.45	109.95
3	E	39	HIS	N-CA-C	5.85	123.14	113.89
2	D	13	ASP	CA-C-N	5.83	125.30	119.24
2	D	13	ASP	C-N-CA	5.83	125.30	119.24
1	B	430	ALA	N-CA-C	5.81	118.48	110.35
2	C	169	GLU	N-CA-C	5.80	120.64	113.50
3	F	147	TYR	N-CA-C	5.72	118.25	111.33
3	E	79	HIS	N-CA-C	5.66	122.59	114.39
2	D	77	HIS	N-CA-C	-5.62	101.58	109.96
2	C	78	GLY	N-CA-C	-5.59	107.25	113.79
1	A	25	ALA	N-CA-C	5.57	117.03	111.07
2	C	104	ARG	N-CA-C	5.55	117.74	109.25
2	C	24	LEU	N-CA-C	5.54	116.67	109.64
1	B	212	PHE	N-CA-C	5.46	119.61	112.13
3	E	73	ASN	N-CA-C	-5.45	103.50	110.53
1	B	204	LEU	N-CA-C	5.44	117.07	111.03
1	B	110	LEU	N-CA-C	-5.38	105.49	111.36
1	A	358	PHE	N-CA-C	-5.37	104.99	112.30
2	C	252	TYR	N-CA-C	5.34	116.79	110.97
2	D	252	TYR	N-CA-C	5.32	116.76	111.07
2	C	249	HIS	N-CA-C	5.31	118.22	111.69
2	D	371	ILE	N-CA-C	-5.30	107.81	112.90
1	A	496	ILE	N-CA-C	-5.29	105.56	110.53
1	B	82	LEU	N-CA-C	5.27	116.71	111.07
1	B	162	GLY	N-CA-C	5.26	120.66	112.60
2	D	227	ALA	N-CA-C	-5.25	105.20	111.03
1	A	282	PHE	N-CA-C	5.24	116.99	111.28
1	B	431	LYS	N-CA-C	-5.23	107.07	113.50
1	A	460	GLU	CA-C-N	5.23	124.68	119.24
1	A	460	GLU	C-N-CA	5.23	124.68	119.24
2	C	106	HIS	N-CA-C	5.21	117.36	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	86	GLU	N-CA-C	5.21	119.26	113.01
1	B	148	THR	N-CA-C	-5.20	105.51	111.07
3	F	130	ASP	N-CA-C	-5.18	105.71	111.36
2	D	137	ASN	CA-C-N	5.17	125.22	119.32
2	D	137	ASN	C-N-CA	5.17	125.22	119.32
2	D	265	PHE	N-CA-C	5.16	116.91	111.28
1	A	62	LEU	N-CA-C	5.16	118.41	110.42
2	C	299	TYR	N-CA-C	5.15	118.72	112.23
2	C	149	TRP	N-CA-C	-5.13	105.87	111.82
1	B	213	THR	N-CA-C	5.11	116.54	110.97
2	C	56	ALA	N-CA-C	-5.07	105.93	111.82
1	B	285	VAL	N-CA-C	5.06	115.67	110.36
2	D	236	GLN	N-CA-C	5.05	119.53	113.17
1	B	521	ASN	CA-C-N	5.05	126.15	119.84
1	B	521	ASN	C-N-CA	5.05	126.15	119.84

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4138	0	3897	135	0
1	B	4137	0	3888	150	0
2	C	3163	0	2986	91	0
2	D	3151	0	2960	117	0
3	E	1364	0	1352	29	0
3	F	1358	0	1335	68	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	24	0	19	4	0
6	B	18	0	14	2	0
6	C	12	0	10	2	0
6	D	6	0	5	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	112	0	0	2	0
7	B	100	0	0	4	0
7	C	123	0	0	1	0
7	D	46	0	0	0	0
7	E	65	0	0	1	0
7	F	17	0	0	0	0
All	All	17840	0	16466	518	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 15.

All (518) 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)
3:F:80:LYS:HE2	3:F:84:GLY:HA2	1.23	1.10
1:B:210:ALA:HA	1:B:247:MET:HE1	1.38	1.02
2:D:352:ILE:HD13	2:D:388:LEU:HD21	1.51	0.92
1:A:44:THR:HG22	1:A:46:TYR:H	1.34	0.92
1:B:352:ALA:HA	1:B:404:PRO:HB2	1.53	0.90
1:B:44:THR:HG22	1:B:46:TYR:H	1.38	0.88
1:A:227:ASN:HD21	1:A:295:LYS:H	1.21	0.87
3:F:36:ARG:NH1	3:F:119:LYS:HB3	1.93	0.83
1:A:78:GLN:HE22	1:A:150:GLN:HE21	1.25	0.83
1:A:155:ASN:HD22	1:A:168:HIS:HD2	1.23	0.82
1:A:435:THR:HG21	1:A:437:ARG:HE	1.46	0.81
2:D:100:ASP:OD1	2:D:104:ARG:HD3	1.81	0.81
1:B:283:THR:HB	1:B:284:PRO:HD3	1.64	0.80
2:C:270:PRO:HB3	2:D:270:PRO:HB3	1.62	0.79
2:D:319:ASN:OD1	3:F:78:ARG:HD3	1.81	0.79
2:D:102:LEU:HD12	2:D:290:ILE:HG23	1.66	0.78
1:B:78:GLN:HE22	1:B:150:GLN:HE21	1.30	0.77
1:B:227:ASN:HD21	1:B:296:PHE:H	1.31	0.77
1:A:352:ALA:HA	1:A:404:PRO:HB2	1.67	0.77
2:D:261:ARG:HE	2:D:285:GLN:HE22	1.33	0.76
3:F:57:GLU:O	3:F:61:GLU:HG3	1.85	0.76
3:E:41:THR:O	3:E:44:ARG:HD2	1.87	0.75
1:A:227:ASN:ND2	1:A:295:LYS:H	1.85	0.74
3:E:24:THR:HG22	3:E:27:LYS:H	1.52	0.74
3:F:9:ASN:OD1	3:F:11:THR:HG23	1.87	0.74
1:A:338:ASP:OD2	1:A:433:ALA:HB2	1.88	0.74
1:B:495:LEU:HD11	1:B:512:ILE:HG13	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:TYR:OH	1:B:344:HIS:HD2	1.69	0.74
3:F:41:THR:O	3:F:44:ARG:HD2	1.88	0.73
2:C:261:ARG:HE	2:C:285:GLN:HE22	1.34	0.73
3:E:12:ARG:O	3:E:16:VAL:HG23	1.89	0.73
2:C:102:LEU:HD12	2:C:290:ILE:HG23	1.71	0.73
2:C:146:ASN:HD21	2:C:197:ARG:HH21	1.38	0.72
3:F:13:ASP:O	3:F:16:VAL:HG22	1.89	0.72
1:A:216:LEU:HD13	1:A:286:LEU:HD11	1.71	0.72
1:B:206:LEU:HD11	1:B:321:LEU:HD11	1.73	0.71
1:B:268:ASN:HD21	1:B:327:GLU:H	1.39	0.71
1:A:292:TYR:OH	1:A:344:HIS:HD2	1.74	0.70
1:B:144:GLU:OE2	1:B:144:GLU:HA	1.90	0.70
2:D:167:ALA:O	2:D:176:ARG:NH1	2.25	0.70
3:F:33:LYS:O	3:F:37:MET:HG2	1.91	0.70
2:C:326:GLU:HB3	2:C:327:PRO:HD3	1.72	0.69
1:B:175:ARG:HD2	1:B:181:TRP:CE2	2.26	0.69
3:F:58:ALA:O	3:F:62:GLU:HG3	1.92	0.69
1:B:214:ASN:HB3	1:B:215:PRO:HD3	1.74	0.69
3:E:98:MET:HE1	3:E:107:ALA:CB	2.22	0.68
1:A:20:PRO:HG3	2:C:129:ALA:HB2	1.75	0.68
2:D:352:ILE:CD1	2:D:388:LEU:HD21	2.24	0.68
2:C:111:LYS:O	2:C:115:GLU:HG3	1.94	0.68
2:D:102:LEU:CD1	2:D:290:ILE:HG23	2.24	0.67
1:B:128:ALA:O	1:B:134:LYS:HE2	1.94	0.67
1:B:281:TYR:O	1:B:284:PRO:HD2	1.95	0.67
1:A:214:ASN:HB3	1:A:215:PRO:HD3	1.76	0.67
3:F:80:LYS:CE	3:F:84:GLY:HA2	2.15	0.66
1:A:140:GLN:O	1:A:144:GLU:HG2	1.96	0.66
3:E:146:ASN:HB3	3:E:149:ASP:OD2	1.96	0.66
1:A:125:TRP:HE1	2:C:161:ASN:ND2	1.94	0.66
1:B:179:PRO:HB3	1:B:469:ILE:HD13	1.78	0.65
2:C:261:ARG:HE	2:C:285:GLN:NE2	1.94	0.65
2:D:107:ALA:HB3	2:D:108:PRO:HD3	1.77	0.65
2:C:3:MET:HE3	2:D:28:PRO:HG3	1.77	0.65
2:C:259:PHE:CE1	2:C:356:LEU:HD13	2.31	0.65
3:F:95:VAL:HG12	3:F:99:ASN:HD21	1.62	0.65
1:A:284:PRO:HB3	1:A:342:ALA:HB1	1.78	0.64
1:B:230:GLU:OE2	2:D:9:ARG:HD3	1.97	0.64
2:C:146:ASN:ND2	2:C:197:ARG:HH21	1.95	0.64
1:A:435:THR:CG2	1:A:437:ARG:HE	2.11	0.64
1:A:83:GLN:HB3	1:B:77:ARG:HH12	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:439:HIS:HB3	3:F:161:VAL:HG21	1.79	0.64
1:B:171:ALA:O	1:B:175:ARG:HG2	1.99	0.63
2:D:261:ARG:HE	2:D:285:GLN:NE2	1.95	0.63
1:B:227:ASN:ND2	1:B:296:PHE:H	1.97	0.63
2:C:176:ARG:HB2	2:C:176:ARG:NH1	2.12	0.63
1:B:216:LEU:O	1:B:220:VAL:HG23	1.99	0.63
2:D:71:ASP:HB2	3:F:54:LEU:HD11	1.81	0.63
2:D:255:LEU:HD12	2:D:328:THR:HG21	1.81	0.63
2:D:189:ILE:HD12	2:D:284:ALA:HB2	1.81	0.62
1:B:230:GLU:C	1:B:233:PRO:HD2	2.25	0.62
1:A:402:PHE:O	1:A:403:ILE:HD12	1.99	0.62
2:C:364:ILE:HA	2:C:368:ALA:HB3	1.82	0.62
1:B:438:VAL:HB	3:F:164:VAL:HG22	1.82	0.62
1:B:78:GLN:NE2	1:B:150:GLN:HE21	1.98	0.61
2:C:201:ALA:HA	2:C:207:PHE:HB3	1.81	0.61
2:C:3:MET:HE3	2:D:28:PRO:CD	2.30	0.61
1:B:445:MET:HB3	1:B:523:VAL:HG21	1.82	0.61
1:A:78:GLN:NE2	1:A:150:GLN:HE21	1.98	0.61
2:C:213:VAL:HB	2:C:214:PRO:HD3	1.83	0.61
1:B:140:GLN:O	1:B:144:GLU:HG2	2.01	0.60
1:A:84:ASP:HB3	1:B:81:SER:OG	2.02	0.60
2:D:47:THR:OG1	2:D:50:GLU:HG3	2.01	0.60
2:D:385:LEU:C	2:D:387:GLY:H	2.09	0.60
1:B:123:MET:HE3	1:B:197:ALA:HA	1.83	0.60
2:C:247:SER:HG	2:C:324:TRP:CD1	2.20	0.60
1:B:116:ASN:CG	1:B:189:SER:HA	2.26	0.60
3:F:119:LYS:HA	3:F:128:PHE:CE1	2.37	0.60
1:B:495:LEU:HD11	1:B:512:ILE:CG1	2.32	0.59
2:D:125:GLN:NE2	6:D:509:3BB:H41	2.17	0.59
2:C:269:ALA:HB3	2:C:270:PRO:HD3	1.84	0.59
2:D:61:ASP:OD1	3:F:7:HIS:HD2	1.85	0.59
1:A:49:LYS:HD3	3:E:144:ASN:HD22	1.67	0.59
2:C:3:MET:HE3	2:D:28:PRO:CG	2.32	0.59
1:A:439:HIS:HE1	1:A:454:GLU:OE1	1.86	0.59
3:F:61:GLU:O	3:F:121:PRO:HG2	2.02	0.59
1:B:291:GLU:OE1	1:B:343:HIS:HE1	1.85	0.59
2:C:348:ASP:OD2	2:C:351:GLU:HG3	2.03	0.58
1:B:115:TYR:OH	2:D:173:ASP:HA	2.03	0.58
1:B:435:THR:HG22	7:B:1218:HOH:O	2.02	0.58
2:D:352:ILE:HG13	2:D:353:THR:N	2.18	0.58
1:A:108:ASN:HD21	1:A:175:ARG:HE	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:360:ARG:HG2	1:A:498:GLN:HB2	1.85	0.58
1:B:119:ALA:HB1	2:D:168:ARG:HD2	1.84	0.58
1:B:108:ASN:HD21	1:B:175:ARG:HE	1.51	0.57
1:A:146:ARG:HB2	2:C:106:HIS:CE1	2.39	0.57
1:A:175:ARG:HG3	1:A:181:TRP:CD2	2.39	0.57
1:B:211:CYS:HB2	1:B:313:TRP:CD1	2.39	0.57
2:C:40:THR:H	6:C:510:3BB:C1	2.17	0.57
1:A:302:VAL:HG22	1:A:376:TYR:CZ	2.39	0.57
3:F:95:VAL:HG12	3:F:99:ASN:ND2	2.19	0.57
1:B:216:LEU:C	1:B:216:LEU:HD12	2.30	0.57
1:B:48:THR:O	3:F:137:THR:HG23	2.05	0.57
1:A:403:ILE:HG22	1:A:405:LEU:H	1.70	0.57
2:C:107:ALA:HB3	2:C:108:PRO:HD3	1.86	0.57
1:B:186:ARG:HD3	1:B:186:ARG:C	2.30	0.57
3:F:23:ASN:N	3:F:23:ASN:HD22	2.02	0.57
1:A:310:TYR:CZ	1:A:336:LYS:HD2	2.40	0.57
1:B:282:PHE:O	1:B:286:LEU:HB2	2.04	0.56
2:D:262:ARG:HA	2:D:266:GLN:HB3	1.87	0.56
1:A:187:VAL:HG12	1:A:277:THR:HG22	1.88	0.56
3:F:23:ASN:HD22	3:F:23:ASN:H	1.52	0.56
1:B:184:MET:HE2	1:B:188:PHE:HB2	1.86	0.56
2:D:296:GLN:O	2:D:300:TYR:HB2	2.05	0.56
1:A:302:VAL:HG22	1:A:376:TYR:CE2	2.41	0.56
1:A:81:SER:OG	1:B:84:ASP:HB3	2.05	0.56
1:A:213:THR:O	1:A:217:ILE:HG12	2.06	0.56
3:F:11:THR:O	3:F:14:ALA:HB3	2.06	0.56
1:A:184:MET:HE2	1:A:188:PHE:HB2	1.88	0.56
1:B:354:TRP:CG	1:B:355:PRO:HD3	2.41	0.56
1:B:504:ASP:OD2	1:B:505:LYS:HG3	2.05	0.56
1:A:360:ARG:HD2	1:A:489:ARG:NH2	2.21	0.56
1:B:213:THR:O	1:B:217:ILE:HG12	2.05	0.56
1:B:278:GLN:NE2	1:B:282:PHE:HE2	2.03	0.56
1:A:89:LEU:HD21	1:B:230:GLU:HG3	1.88	0.55
1:A:144:GLU:HA	1:A:144:GLU:OE2	2.06	0.55
2:D:39:VAL:O	2:D:41:PRO:HD3	2.06	0.55
1:A:116:ASN:CG	1:A:189:SER:HA	2.32	0.55
1:B:184:MET:HE3	1:B:184:MET:HA	1.87	0.55
2:D:153:LEU:C	2:D:153:LEU:HD12	2.32	0.55
2:D:263:GLU:OE2	2:D:263:GLU:HA	2.07	0.55
1:B:460:GLU:OE1	1:B:463:ARG:HD3	2.07	0.55
2:C:176:ARG:HB2	2:C:176:ARG:HH11	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:4:LEU:HD11	3:F:10:ASP:OD2	2.06	0.55
1:B:184:MET:HE2	1:B:188:PHE:CG	2.42	0.55
2:D:235:TRP:CD1	2:D:235:TRP:C	2.85	0.55
1:A:209:GLU:HA	1:A:213:THR:HB	1.89	0.55
1:A:212:PHE:O	1:A:216:LEU:HB3	2.07	0.54
3:F:90:VAL:HG11	3:F:118:TYR:CZ	2.42	0.54
2:D:376:ASP:OD2	2:D:379:GLN:HG2	2.07	0.54
2:D:348:ASP:OD2	2:D:350:GLU:HB2	2.07	0.54
3:E:4:LEU:O	3:E:4:LEU:HG	2.08	0.54
1:B:211:CYS:HB2	1:B:313:TRP:CG	2.42	0.54
1:A:184:MET:HE2	1:A:188:PHE:CG	2.43	0.54
2:D:189:ILE:HD11	2:D:284:ALA:HA	1.90	0.54
2:D:213:VAL:HB	2:D:214:PRO:CD	2.38	0.54
1:A:227:ASN:HD21	1:A:295:LYS:N	1.98	0.54
3:F:30:GLU:OE2	3:F:30:GLU:HA	2.08	0.54
1:A:196:ASP:HB2	3:E:140:MET:SD	2.48	0.54
1:B:163:GLN:HA	2:C:3:MET:CE	2.38	0.54
1:B:403:ILE:HG22	1:B:406:MET:HE3	1.88	0.54
2:C:269:ALA:HB1	2:C:274:ASP:HB3	1.90	0.53
2:C:112:ASP:O	2:C:116:GLU:HG3	2.09	0.53
2:C:153:LEU:C	2:C:153:LEU:HD12	2.33	0.53
1:A:406:MET:O	1:A:410:GLU:HG3	2.09	0.53
2:D:112:ASP:O	2:D:116:GLU:HG3	2.07	0.53
2:D:179:LEU:HD23	2:D:182:TRP:CE3	2.43	0.53
3:F:80:LYS:HE2	3:F:84:GLY:CA	2.17	0.53
1:B:398:PRO:HG3	1:B:507:TRP:CD1	2.43	0.53
2:C:89:GLU:CD	3:E:125:VAL:HG13	2.34	0.53
1:A:312:ASP:O	1:A:316:ILE:HB	2.09	0.53
2:D:54:VAL:O	2:D:55:TYR:HB2	2.09	0.53
2:D:102:LEU:HB2	2:D:104:ARG:HD2	1.91	0.53
3:F:44:ARG:HD3	3:F:47:TYR:CZ	2.43	0.53
2:C:314:ARG:O	2:C:318:ARG:HB2	2.09	0.53
1:B:369:MET:HE2	1:B:379:TRP:CH2	2.44	0.53
1:B:193:ILE:HD11	2:D:82:SER:HB3	1.91	0.52
1:B:281:TYR:CZ	1:B:285:VAL:HG21	2.44	0.52
2:C:266:GLN:HE22	2:D:132:GLN:CD	2.17	0.52
1:A:206:LEU:O	1:A:210:ALA:HB3	2.09	0.52
2:C:40:THR:OG1	6:C:510:3BB:H41	2.08	0.52
2:D:277:THR:HB	2:D:278:PRO:HD3	1.90	0.52
1:A:498:GLN:HG3	1:A:506:LEU:HD22	1.92	0.52
1:B:521:ASN:OD1	1:B:523:VAL:HG12	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:90:VAL:HG11	3:F:118:TYR:CE2	2.45	0.52
1:B:175:ARG:HD2	1:B:181:TRP:CD2	2.44	0.52
2:D:356:LEU:CD1	2:D:385:LEU:HD13	2.40	0.52
1:A:160:LYS:HA	2:C:33:ASN:HB2	1.91	0.52
2:C:102:LEU:CD1	2:C:290:ILE:HG23	2.38	0.52
2:C:211:THR:C	2:C:214:PRO:HD2	2.35	0.52
3:E:154:GLU:HG3	7:E:225:HOH:O	2.10	0.52
3:E:165:HIS:HE1	3:E:167:GLN:HE21	1.58	0.52
1:A:184:MET:HE3	1:A:184:MET:HA	1.90	0.51
1:A:344:HIS:HE1	1:A:376:TYR:CD2	2.28	0.51
1:B:361:LEU:HD23	6:B:1178:3BB:H41	1.91	0.51
2:D:147:ARG:HD2	2:D:148:TYR:CE1	2.45	0.51
1:A:121:THR:HG21	1:A:140:GLN:CG	2.40	0.51
3:F:23:ASN:N	3:F:23:ASN:ND2	2.59	0.51
1:B:44:THR:OG1	1:B:127:SER:HA	2.10	0.51
1:B:223:TRP:CZ3	1:B:297:LYS:HA	2.46	0.51
1:B:476:ARG:NH1	3:F:5:GLY:HA3	2.25	0.51
1:B:175:ARG:NH1	1:B:181:TRP:CZ2	2.79	0.51
1:B:188:PHE:CE1	1:B:282:PHE:HZ	2.29	0.51
2:C:98:HIS:HE1	2:C:178:SER:OG	1.94	0.51
2:D:336:MET:CE	2:D:352:ILE:HD12	2.41	0.51
3:F:77:PHE:O	3:F:77:PHE:CD1	2.64	0.51
1:B:23:VAL:HG13	1:B:27:GLU:OE2	2.11	0.51
2:D:285:GLN:O	2:D:289:GLN:HG2	2.11	0.51
3:F:39:HIS:CD2	3:F:49:LEU:HD12	2.46	0.51
1:A:188:PHE:CE1	1:A:282:PHE:HZ	2.29	0.51
1:A:361:LEU:HD23	6:A:1175:3BB:H41	1.92	0.51
1:A:251:TYR:CD2	1:A:321:LEU:HD21	2.46	0.50
1:A:206:LEU:HD11	1:A:321:LEU:CD1	2.40	0.50
1:B:186:ARG:HD3	1:B:186:ARG:O	2.12	0.50
2:D:256:PHE:HA	2:D:332:LEU:HD21	1.93	0.50
2:D:90:LEU:HD13	2:D:303:LEU:HD13	1.92	0.50
2:D:324:TRP:C	2:D:327:PRO:HD2	2.37	0.50
2:C:306:ASP:O	2:C:310:SER:HB2	2.10	0.50
1:B:439:HIS:HB3	3:F:161:VAL:CG2	2.40	0.50
2:D:357:TYR:CD1	2:D:381:VAL:HG21	2.47	0.50
1:A:206:LEU:HD11	1:A:321:LEU:HD11	1.93	0.50
1:B:210:ALA:HA	1:B:247:MET:CE	2.27	0.50
1:B:257:ILE:O	1:B:263:SER:HB2	2.12	0.50
3:E:98:MET:HE1	3:E:107:ALA:HB2	1.92	0.50
1:A:193:ILE:HD11	2:C:82:SER:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:TYR:OH	1:A:344:HIS:CD2	2.62	0.50
1:B:163:GLN:HA	2:C:3:MET:HE1	1.94	0.50
1:B:164:ASP:OD1	1:B:489:ARG:NH2	2.45	0.50
2:D:228:ARG:HG2	2:D:228:ARG:HH11	1.77	0.49
1:A:403:ILE:HD13	1:A:515:LEU:CD1	2.41	0.49
1:B:160:LYS:HA	2:D:33:ASN:HB2	1.93	0.49
2:C:136:MET:SD	2:C:141:ARG:HB2	2.52	0.49
2:C:235:TRP:CD1	2:C:235:TRP:C	2.90	0.49
3:F:61:GLU:HB3	3:F:121:PRO:HD3	1.93	0.49
2:D:310:SER:O	2:D:314:ARG:HG3	2.12	0.49
3:F:125:VAL:HG23	3:F:126:ASN:N	2.28	0.49
2:D:105:TRP:O	2:D:108:PRO:HD2	2.12	0.49
3:F:19:ILE:HG21	3:F:60:LEU:HD12	1.95	0.49
2:C:175:THR:O	2:C:179:LEU:HB2	2.13	0.49
2:D:63:ILE:HD11	2:D:83:TRP:O	2.13	0.49
2:D:184:PHE:O	2:D:187:ILE:HG22	2.13	0.49
2:C:33:ASN:HD22	2:C:33:ASN:H	1.60	0.49
2:D:77:HIS:CD2	3:F:140:MET:HG2	2.47	0.49
1:B:159:ALA:O	2:D:33:ASN:HB2	2.13	0.49
1:B:322:GLY:C	1:B:324:TYR:H	2.21	0.49
1:A:243:GLU:O	1:A:247:MET:HG2	2.13	0.48
3:F:36:ARG:HA	3:F:40:THR:HG23	1.94	0.48
1:A:108:ASN:HD21	1:A:175:ARG:NE	2.11	0.48
1:B:23:VAL:HB	2:D:195:LEU:CD1	2.43	0.48
3:F:38:ASP:HB2	3:F:39:HIS:CE1	2.48	0.48
2:C:161:ASN:HB3	2:C:235:TRP:CE2	2.48	0.48
1:A:85:ALA:HB2	1:B:81:SER:HB3	1.95	0.48
1:A:159:ALA:O	2:C:33:ASN:HB2	2.13	0.48
1:B:206:LEU:HD11	1:B:321:LEU:CD1	2.43	0.48
2:C:268:LEU:O	2:C:272:PHE:HD1	1.96	0.48
2:D:213:VAL:HB	2:D:214:PRO:HD3	1.95	0.48
1:A:65:LYS:HZ3	2:C:192:MET:HE2	1.79	0.48
2:C:297:ASP:O	2:C:301:ASN:HB3	2.14	0.48
2:C:105:TRP:O	2:C:108:PRO:HD2	2.13	0.48
1:A:22:SER:OG	1:A:23:VAL:N	2.47	0.48
1:A:289:LEU:HD23	6:A:1175:3BB:BR1	2.69	0.47
1:A:459:ALA:C	1:A:461:PRO:HD3	2.39	0.47
1:A:149:HIS:CE1	2:C:105:TRP:HB2	2.49	0.47
1:A:283:THR:HB	1:A:284:PRO:HD3	1.95	0.47
1:B:175:ARG:HD2	1:B:181:TRP:CZ2	2.49	0.47
2:C:154:PHE:CZ	2:C:215:LYS:HB2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:118:TYR:HB3	3:F:123:MET:HB2	1.97	0.47
2:D:277:THR:N	2:D:278:PRO:CD	2.76	0.47
2:D:385:LEU:C	2:D:387:GLY:N	2.73	0.47
1:B:137:TYR:O	1:B:141:VAL:HG23	2.14	0.47
2:D:63:ILE:O	2:D:64:ALA:C	2.57	0.47
2:D:77:HIS:CG	3:F:140:MET:HG2	2.49	0.47
3:F:64:VAL:HG12	3:F:64:VAL:O	2.13	0.47
3:F:69:ALA:C	3:F:71:ALA:H	2.23	0.47
1:B:121:THR:HG21	1:B:140:GLN:CG	2.44	0.47
1:B:437:ARG:NH1	1:B:454:GLU:OE2	2.48	0.47
2:D:146:ASN:HB2	2:D:207:PHE:CE1	2.50	0.47
2:D:269:ALA:HB3	2:D:270:PRO:HD3	1.97	0.47
1:A:31:TRP:CH2	2:C:210:SER:HA	2.49	0.47
1:A:65:LYS:HE2	2:C:192:MET:HE2	1.96	0.47
1:A:521:ASN:OD1	1:A:523:VAL:HG12	2.14	0.47
3:F:24:THR:HB	3:F:27:LYS:CB	2.45	0.47
1:A:206:LEU:HD23	1:A:271:LEU:HD13	1.97	0.47
1:B:278:GLN:HE21	1:B:282:PHE:HE2	1.62	0.47
3:F:98:MET:HG3	3:F:138:ARG:HG2	1.97	0.47
1:B:138:LEU:HD22	2:D:160:PHE:CZ	2.50	0.46
2:D:159:LEU:HD22	2:D:248:VAL:HG13	1.98	0.46
2:D:377:ARG:O	2:D:381:VAL:HG23	2.15	0.46
1:A:186:ARG:O	1:A:186:ARG:HD3	2.15	0.46
2:D:80:ARG:HG3	3:F:132:GLU:HG2	1.97	0.46
2:D:292:LYS:HD2	2:D:367:TYR:OH	2.15	0.46
1:A:83:GLN:HB3	1:B:77:ARG:NH1	2.28	0.46
1:A:121:THR:HG21	1:A:140:GLN:HG2	1.98	0.46
1:B:121:THR:HG21	1:B:140:GLN:HB3	1.98	0.46
2:C:263:GLU:OE2	2:C:263:GLU:HA	2.15	0.46
2:C:281:ILE:O	2:C:285:GLN:HG2	2.15	0.46
1:A:26:GLN:HG2	7:A:1273:HOH:O	2.15	0.46
1:A:186:ARG:HA	2:C:73:THR:OG1	2.16	0.46
2:C:179:LEU:HD12	2:C:182:TRP:CE3	2.50	0.46
1:B:21:THR:HG22	1:B:22:SER:N	2.31	0.46
2:D:360:VAL:O	2:D:364:ILE:HG13	2.15	0.46
1:B:186:ARG:HA	2:D:73:THR:OG1	2.16	0.46
2:C:109:TYR:OH	2:C:184:PHE:HB3	2.16	0.46
1:B:302:VAL:HG13	1:B:376:TYR:HE2	1.81	0.45
1:A:114:GLU:CD	1:A:147:HIS:HB3	2.41	0.45
2:D:169:GLU:O	2:D:170:ALA:C	2.59	0.45
3:E:46:SER:OG	3:E:48:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:266:TYR:CD2	3:F:144:ASN:HB2	2.51	0.45
1:B:488:LEU:HD13	1:B:492:GLY:O	2.16	0.45
2:D:316:VAL:O	2:D:319:ASN:HB3	2.16	0.45
1:A:344:HIS:HE1	1:A:376:TYR:CE2	2.34	0.45
3:E:165:HIS:CE1	3:E:167:GLN:HE21	2.34	0.45
1:A:186:ARG:HD3	1:A:186:ARG:C	2.42	0.45
1:A:495:LEU:HD11	1:A:512:ILE:HG13	1.99	0.45
3:F:44:ARG:HG3	3:F:46:SER:O	2.17	0.45
2:D:243:GLU:HB2	2:D:320:TRP:CZ2	2.52	0.45
3:F:153:GLU:H	3:F:153:GLU:CD	2.25	0.45
1:B:98:LYS:NZ	1:B:368:GLU:OE2	2.50	0.45
1:B:105:VAL:O	1:B:109:PHE:HB2	2.17	0.45
1:B:125:TRP:CD1	1:B:125:TRP:C	2.95	0.45
1:B:210:ALA:CA	1:B:247:MET:HE1	2.27	0.45
1:B:297:LYS:HG2	1:B:371:TRP:CE2	2.51	0.45
1:B:442:ASN:ND2	3:F:44:ARG:O	2.46	0.45
2:D:324:TRP:O	2:D:327:PRO:HD2	2.16	0.45
1:B:160:LYS:HE3	1:B:161:ASN:HD21	1.82	0.45
2:C:165:GLN:OE1	2:C:239:PHE:HA	2.17	0.45
2:C:270:PRO:C	2:C:272:PHE:H	2.25	0.45
3:E:111:HIS:HE1	3:E:132:GLU:OE2	2.00	0.45
3:F:118:TYR:O	3:F:119:LYS:C	2.58	0.45
2:C:102:LEU:HD21	6:D:509:3BB:H31	1.98	0.45
1:A:92:GLY:O	1:A:162:GLY:HA2	2.17	0.44
1:A:466:CYS:HB2	2:C:73:THR:HA	1.99	0.44
3:F:16:VAL:HG23	3:F:17:ASN:N	2.32	0.44
1:A:115:TYR:OH	2:C:173:ASP:HA	2.18	0.44
1:A:125:TRP:CD1	1:A:125:TRP:O	2.71	0.44
1:B:190:ASP:HB3	2:D:74:GLN:O	2.17	0.44
1:A:360:ARG:HD2	1:A:489:ARG:HH22	1.82	0.44
1:A:476:ARG:HH12	3:E:6:ILE:HG13	1.81	0.44
2:C:153:LEU:HB3	2:C:193:ILE:HG21	2.00	0.44
2:C:197:ARG:CZ	2:C:214:PRO:HG2	2.47	0.44
3:F:94:THR:HG22	3:F:135:LEU:HD21	2.00	0.44
1:B:468:ASN:HA	7:B:1220:HOH:O	2.18	0.44
3:E:44:ARG:HD3	3:E:47:TYR:CZ	2.53	0.44
3:E:98:MET:HE1	3:E:107:ALA:HB1	1.99	0.44
2:D:179:LEU:HD21	2:D:245:ALA:HB2	2.00	0.44
1:A:186:ARG:HD2	1:A:277:THR:HG23	2.00	0.44
1:B:146:ARG:HG2	1:B:150:GLN:OE1	2.17	0.44
1:B:461:PRO:HG2	3:F:159:ARG:CZ	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:42:ARG:HB2	2:C:99:ARG:HG3	2.00	0.44
2:D:145:ILE:HG22	2:D:146:ASN:N	2.33	0.44
3:F:124:PRO:O	3:F:125:VAL:C	2.60	0.44
1:A:403:ILE:HD13	1:A:515:LEU:HD13	1.98	0.44
1:A:177:ILE:HG12	1:A:485:LEU:HB2	2.00	0.44
1:B:188:PHE:CZ	1:B:282:PHE:HZ	2.36	0.44
1:B:196:ASP:HB2	3:F:140:MET:SD	2.58	0.44
1:B:306:ASP:O	1:B:310:TYR:HB2	2.17	0.44
1:B:466:CYS:HB2	2:D:73:THR:HA	2.00	0.44
2:D:161:ASN:HB3	2:D:235:TRP:CE2	2.53	0.44
2:D:263:GLU:CD	2:D:355:SER:HB2	2.43	0.44
2:D:264:PHE:O	2:D:268:LEU:HG	2.17	0.44
3:F:125:VAL:HG23	3:F:126:ASN:H	1.83	0.44
2:D:356:LEU:HD12	2:D:385:LEU:HD13	2.00	0.43
3:E:165:HIS:HE1	3:E:167:GLN:HG3	1.82	0.43
3:F:76:ASP:C	3:F:78:ARG:H	2.26	0.43
1:A:190:ASP:HB3	2:C:74:GLN:O	2.18	0.43
1:B:110:LEU:HD11	1:B:217:ILE:CD1	2.48	0.43
2:D:143:GLU:O	2:D:147:ARG:HB3	2.18	0.43
3:F:76:ASP:C	3:F:78:ARG:N	2.75	0.43
2:C:146:ASN:HD21	2:C:197:ARG:NH2	2.10	0.43
1:A:75:ASP:OD2	1:A:146:ARG:NH1	2.52	0.43
1:B:43:ARG:HD2	1:B:43:ARG:C	2.43	0.43
1:B:44:THR:HG23	1:B:126:ASP:OD1	2.18	0.43
1:B:108:ASN:O	1:B:111:GLU:HB3	2.18	0.43
1:B:113:GLY:HA2	1:B:188:PHE:HB3	1.99	0.43
2:C:187:ILE:O	2:C:191:GLN:HG3	2.18	0.43
2:C:310:SER:O	2:C:314:ARG:HG3	2.19	0.43
2:D:149:TRP:HB2	2:D:265:PHE:CE2	2.54	0.43
2:D:262:ARG:O	2:D:266:GLN:HB3	2.18	0.43
2:D:357:TYR:CE1	2:D:381:VAL:HG21	2.53	0.43
3:F:55:TRP:O	3:F:58:ALA:HB3	2.19	0.43
1:B:52:MET:HE3	1:B:253:THR:HG23	2.00	0.43
3:E:98:MET:HE2	3:E:138:ARG:HG2	2.01	0.43
2:C:63:ILE:O	2:C:64:ALA:C	2.62	0.43
3:F:86:ASP:O	3:F:89:SER:HB2	2.19	0.43
1:A:121:THR:HG21	1:A:140:GLN:CD	2.44	0.43
1:B:344:HIS:HE1	1:B:376:TYR:CE2	2.36	0.43
2:D:37:TYR:CD1	2:D:37:TYR:C	2.97	0.43
2:C:143:GLU:O	2:C:147:ARG:HB3	2.19	0.42
1:A:91:ALA:HB1	7:A:1178:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:LEU:HD13	1:B:231:ILE:HD13	2.01	0.42
1:B:213:THR:OG1	6:B:1176:3BB:BR1	2.70	0.42
1:B:445:MET:HE3	1:B:523:VAL:HG22	1.99	0.42
2:C:185:ASP:O	2:C:189:ILE:HG13	2.19	0.42
1:A:109:PHE:HB3	1:A:184:MET:SD	2.59	0.42
1:A:302:VAL:HG22	1:A:376:TYR:OH	2.19	0.42
1:B:437:ARG:HD2	1:B:437:ARG:N	2.34	0.42
2:C:112:ASP:OD1	2:D:118:ARG:NH2	2.49	0.42
2:D:342:LEU:HD22	2:D:346:THR:HG21	2.00	0.42
1:A:323:LYS:HE2	1:A:324:TYR:CZ	2.54	0.42
2:C:323:LYS:HD2	3:E:78:ARG:HD2	2.01	0.42
3:F:86:ASP:HB3	3:F:89:SER:OG	2.19	0.42
1:A:306:ASP:O	1:A:310:TYR:HB2	2.18	0.42
1:B:196:ASP:O	1:B:197:ALA:C	2.63	0.42
1:B:260:ASP:OD2	1:B:262:ALA:HB3	2.19	0.42
1:B:460:GLU:HG2	2:D:77:HIS:CE1	2.54	0.42
1:B:489:ARG:HG3	1:B:494:THR:O	2.20	0.42
1:A:246:HIS:N	1:A:246:HIS:CD2	2.87	0.42
1:A:403:ILE:HG22	1:A:405:LEU:HB2	2.01	0.42
1:B:246:HIS:CD2	1:B:246:HIS:N	2.88	0.42
1:B:390:TRP:HE1	1:B:407:TRP:CG	2.38	0.42
1:B:486:HIS:C	1:B:488:LEU:H	2.28	0.42
1:A:108:ASN:O	1:A:111:GLU:HB3	2.20	0.42
2:C:81:PRO:HB3	7:C:748:HOH:O	2.19	0.42
2:C:336:MET:CE	2:C:356:LEU:HD21	2.49	0.42
2:D:385:LEU:O	2:D:387:GLY:N	2.52	0.42
3:F:88:LYS:HB2	3:F:127:TYR:CE2	2.54	0.42
1:A:125:TRP:HE1	2:C:161:ASN:HD22	1.64	0.42
1:A:171:ALA:O	1:A:175:ARG:HB3	2.20	0.42
1:A:283:THR:HB	1:A:284:PRO:CD	2.50	0.42
1:A:403:ILE:CG2	1:A:405:LEU:HB2	2.50	0.42
2:C:336:MET:HE2	2:C:356:LEU:HD21	2.00	0.42
2:D:145:ILE:O	2:D:149:TRP:HB3	2.19	0.42
2:D:153:LEU:HD12	2:D:153:LEU:O	2.19	0.42
2:D:263:GLU:HB3	2:D:355:SER:HB2	2.01	0.42
2:D:385:LEU:HD12	2:D:385:LEU:HA	1.87	0.42
1:A:18:ARG:O	1:A:18:ARG:HG2	2.19	0.42
1:A:521:ASN:HA	1:A:522:PRO:HD2	1.93	0.42
1:B:125:TRP:HE1	2:D:161:ASN:ND2	2.17	0.42
2:C:75:LYS:HB3	2:C:80:ARG:O	2.19	0.42
1:B:23:VAL:HB	2:D:195:LEU:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:ARG:HD3	1:B:30:ARG:C	2.45	0.41
2:C:50:GLU:OE1	2:C:99:ARG:NH1	2.53	0.41
3:E:40:THR:C	3:E:41:THR:HG23	2.45	0.41
3:F:25:LEU:HD22	3:F:68:LYS:HA	2.01	0.41
1:B:227:ASN:HD21	1:B:296:PHE:N	2.08	0.41
1:B:367:GLU:HG3	7:B:1241:HOH:O	2.20	0.41
1:B:405:LEU:HD12	1:B:405:LEU:HA	1.85	0.41
1:B:460:GLU:HB3	1:B:463:ARG:HG3	2.01	0.41
2:D:54:VAL:HG12	2:D:55:TYR:CD2	2.55	0.41
2:D:376:ASP:HB3	2:D:379:GLN:HB2	2.01	0.41
1:A:268:ASN:HD21	1:A:327:GLU:H	1.67	0.41
2:D:308:GLU:O	2:D:308:GLU:HG3	2.20	0.41
2:D:312:TYR:O	2:D:316:VAL:HG23	2.20	0.41
3:E:98:MET:HE3	3:E:98:MET:O	2.20	0.41
1:A:476:ARG:HG3	1:A:476:ARG:HH11	1.85	0.41
1:B:114:GLU:CD	1:B:147:HIS:HB3	2.45	0.41
1:B:266:TYR:HD2	3:F:144:ASN:CB	2.33	0.41
2:C:3:MET:HE3	2:D:28:PRO:N	2.36	0.41
2:D:363:TRP:O	2:D:363:TRP:CG	2.73	0.41
3:E:165:HIS:CE1	3:E:167:GLN:HG3	2.55	0.41
1:A:49:LYS:CD	3:E:144:ASN:HD22	2.33	0.41
1:B:184:MET:HE2	1:B:188:PHE:CB	2.50	0.41
2:D:357:TYR:CE1	2:D:381:VAL:HG11	2.55	0.41
1:A:109:PHE:O	1:A:112:VAL:HG12	2.20	0.41
1:A:230:GLU:C	1:A:233:PRO:HD2	2.45	0.41
1:B:372:PHE:HB3	1:B:379:TRP:CD2	2.56	0.41
1:B:460:GLU:N	1:B:461:PRO:HD3	2.36	0.41
1:B:495:LEU:HD21	1:B:509:LEU:HA	2.03	0.41
1:A:171:ALA:O	1:A:175:ARG:HD2	2.21	0.41
1:B:52:MET:HE2	1:B:133:GLN:NE2	2.35	0.41
2:C:266:GLN:NE2	2:D:132:GLN:CD	2.78	0.41
1:A:76:GLU:HG2	1:B:76:GLU:OE2	2.20	0.41
2:D:306:ASP:HA	2:D:307:PRO:HD3	1.90	0.41
3:E:33:LYS:O	3:E:37:MET:HG2	2.21	0.41
3:F:95:VAL:O	3:F:99:ASN:ND2	2.54	0.41
1:A:118:ILE:HG12	1:A:144:GLU:HB2	2.03	0.41
1:A:184:MET:HE2	1:A:188:PHE:CB	2.51	0.41
1:A:321:LEU:O	1:A:326:VAL:HB	2.20	0.41
1:A:425:PHE:CE2	1:A:449:SER:HB3	2.55	0.41
1:A:479:SER:O	1:A:509:LEU:HD11	2.21	0.41
1:B:174:THR:HG21	1:B:496:ILE:CD1	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:LEU:HD23	1:B:286:LEU:HA	1.91	0.41
1:B:313:TRP:O	1:B:315:GLY:N	2.54	0.41
1:B:376:TYR:O	1:B:379:TRP:HB2	2.21	0.41
2:D:82:SER:O	2:D:168:ARG:NH2	2.42	0.41
2:D:156:GLU:HA	2:D:156:GLU:OE2	2.21	0.41
1:A:117:ALA:HA	1:A:120:ALA:HB3	2.02	0.41
1:A:361:LEU:CD2	6:A:1175:3BB:H41	2.51	0.41
1:A:415:ILE:HB	6:A:1174:3BB:H31	2.03	0.41
1:B:321:LEU:HB3	1:B:326:VAL:HG21	2.03	0.41
2:C:54:VAL:O	2:C:55:TYR:HB2	2.20	0.41
3:E:59:LYS:HD3	3:E:59:LYS:HA	1.77	0.41
1:A:44:THR:HG22	1:A:45:LYS:N	2.36	0.40
1:A:65:LYS:NZ	2:C:192:MET:HE2	2.36	0.40
1:A:123:MET:HB2	2:C:168:ARG:HD3	2.03	0.40
1:A:354:TRP:CG	1:A:355:PRO:HD3	2.56	0.40
2:D:137:ASN:HA	2:D:138:PRO:HD3	1.89	0.40
3:E:130:ASP:O	3:E:133:ARG:HB3	2.21	0.40
1:A:37:TRP:O	1:A:42:ASN:ND2	2.54	0.40
1:A:278:GLN:NE2	1:A:282:PHE:HE2	2.19	0.40
1:A:444:GLU:HA	1:A:444:GLU:OE1	2.21	0.40
1:A:504:ASP:O	1:A:505:LYS:HB2	2.21	0.40
1:B:184:MET:CE	1:B:187:VAL:HG23	2.52	0.40
7:B:1226:HOH:O	2:D:7:ARG:HD2	2.20	0.40
2:D:197:ARG:NH1	2:D:197:ARG:HB3	2.36	0.40
3:E:27:LYS:HE3	3:E:27:LYS:HB2	1.97	0.40
3:F:24:THR:HG22	3:F:26:GLU:HB3	2.03	0.40
1:A:286:LEU:HD22	1:A:290:PHE:CE1	2.56	0.40
1:A:413:HIS:CD2	1:A:429:LEU:HB2	2.57	0.40
1:B:462:GLU:OE1	1:B:462:GLU:N	2.47	0.40
2:C:211:THR:O	2:C:214:PRO:HD2	2.21	0.40
2:C:262:ARG:HA	2:C:266:GLN:HB3	2.02	0.40
2:D:323:LYS:HB2	3:F:78:ARG:NH1	2.35	0.40
2:D:326:GLU:CB	2:D:327:PRO:HD3	2.52	0.40
1:A:188:PHE:CE1	1:A:282:PHE:CZ	3.08	0.40
1:B:244:LEU:HA	1:B:247:MET:HG3	2.03	0.40
2:C:33:ASN:HD22	2:C:33:ASN:N	2.19	0.40
1:A:349:LEU:O	1:A:353:LEU:HD12	2.21	0.40
1:B:163:GLN:HA	2:C:3:MET:HE2	2.03	0.40
1:B:207:VAL:O	1:B:211:CYS:HB3	2.20	0.40
2:D:98:HIS:CD2	2:D:99:ARG:H	2.40	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	508/527 (96%)	481 (95%)	22 (4%)	5 (1%)	12	20
1	B	508/527 (96%)	463 (91%)	39 (8%)	6 (1%)	10	16
2	C	386/389 (99%)	373 (97%)	12 (3%)	1 (0%)	36	50
2	D	386/389 (99%)	357 (92%)	23 (6%)	6 (2%)	7	11
3	E	164/170 (96%)	158 (96%)	6 (4%)	0	100	100
3	F	164/170 (96%)	142 (87%)	18 (11%)	4 (2%)	4	5
All	All	2116/2172 (97%)	1974 (93%)	120 (6%)	22 (1%)	12	20

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	40	LYS
1	A	315	GLY
1	B	311	GLU
1	B	316	ILE
2	D	64	ALA
2	D	221	GLY
2	D	386	ALA
2	D	141	ARG
2	D	205	PRO
3	F	122	ILE
1	A	94	ARG
1	B	284	PRO
2	C	64	ALA
3	F	44	ARG
3	F	74	GLU
1	A	311	GLU
1	B	94	ARG
1	B	314	GLY
2	D	251	VAL
1	A	316	ILE

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Mol	Chain	Res	Type
3	F	50	ASP
1	A	20	PRO

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	423/442 (96%)	412 (97%)	11 (3%)	40	63
1	B	422/442 (96%)	409 (97%)	13 (3%)	35	57
2	C	315/323 (98%)	307 (98%)	8 (2%)	42	64
2	D	312/323 (97%)	306 (98%)	6 (2%)	50	71
3	E	143/147 (97%)	140 (98%)	3 (2%)	47	69
3	F	142/147 (97%)	139 (98%)	3 (2%)	47	69
All	All	1757/1824 (96%)	1713 (98%)	44 (2%)	42	64

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ARG
1	A	38	ASP
1	A	90	ASN
1	A	112	VAL
1	A	125	TRP
1	A	175	ARG
1	A	186	ARG
1	A	216	LEU
1	A	286	LEU
1	A	302	VAL
1	A	442	ASN
1	B	30	ARG
1	B	90	ASN
1	B	110	LEU
1	B	125	TRP
1	B	216	LEU

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Mol	Chain	Res	Type
1	B	222	GLU
1	B	247	MET
1	B	279	GLN
1	B	302	VAL
1	B	311	GLU
1	B	369	MET
1	B	403	ILE
1	B	435	THR
2	C	33	ASN
2	C	117	TRP
2	C	139	THR
2	C	153	LEU
2	C	173	ASP
2	C	356	LEU
2	C	377	ARG
2	C	378	ASP
2	D	4	LEU
2	D	122	ARG
2	D	153	LEU
2	D	173	ASP
2	D	205	PRO
2	D	385	LEU
3	E	24	THR
3	E	44	ARG
3	E	125	VAL
3	F	11	THR
3	F	23	ASN
3	F	164	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (80) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	42	ASN
1	A	54	ASN
1	A	78	GLN
1	A	90	ASN
1	A	100	ASN
1	A	108	ASN
1	A	133	GLN
1	A	168	HIS
1	A	227	ASN

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Mol	Chain	Res	Type
1	A	249	ASN
1	A	268	ASN
1	A	272	ASN
1	A	273	ASN
1	A	278	GLN
1	A	279	GLN
1	A	343	HIS
1	A	344	HIS
1	A	366	GLN
1	A	382	HIS
1	A	411	ASN
1	A	413	HIS
1	A	439	HIS
1	A	442	ASN
1	A	472	GLN
1	A	516	ASN
1	B	59	GLN
1	B	78	GLN
1	B	90	ASN
1	B	108	ASN
1	B	133	GLN
1	B	161	ASN
1	B	205	GLN
1	B	227	ASN
1	B	249	ASN
1	B	252	GLN
1	B	268	ASN
1	B	273	ASN
1	B	278	GLN
1	B	279	GLN
1	B	337	GLN
1	B	343	HIS
1	B	344	HIS
1	B	411	ASN
1	B	413	HIS
1	B	439	HIS
1	B	451	GLN
1	B	472	GLN
1	B	527	ASN
2	C	33	ASN
2	C	98	HIS
2	C	125	GLN

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Mol	Chain	Res	Type
2	C	146	ASN
2	C	155	ASN
2	C	161	ASN
2	C	236	GLN
2	C	266	GLN
2	C	285	GLN
2	C	293	GLN
2	C	296	GLN
2	C	301	ASN
2	D	98	HIS
2	D	125	GLN
2	D	161	ASN
2	D	266	GLN
2	D	282	ASN
2	D	301	ASN
3	E	45	ASN
3	E	111	HIS
3	E	144	ASN
3	E	158	GLN
3	E	165	HIS
3	E	167	GLN
3	F	7	HIS
3	F	23	ASN
3	F	45	ASN
3	F	99	ASN
3	F	134	GLN
3	F	144	ASN
3	F	167	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 for Mogul analysis.

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
6	3BB	B	1176	4	4,5,5	0.36	0	2,5,5	0.68	0
6	3BB	A	1172	4	4,5,5	0.30	0	2,5,5	0.75	0
6	3BB	D	509	-	4,5,5	0.42	0	2,5,5	0.27	0
6	3BB	A	1174	-	4,5,5	0.31	0	2,5,5	0.63	0
6	3BB	C	508	-	4,5,5	0.34	0	2,5,5	0.27	0
6	3BB	A	1175	-	4,5,5	0.43	0	2,5,5	0.41	0
6	3BB	B	1178	-	4,5,5	0.48	0	2,5,5	0.48	0
6	3BB	C	510	-	4,5,5	0.42	0	2,5,5	0.28	0
6	3BB	A	1173	-	4,5,5	0.23	0	2,5,5	0.28	0
6	3BB	B	1177	-	4,5,5	0.21	0	2,5,5	0.33	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
6	3BB	B	1176	4	-	0/2/3/3	-
6	3BB	A	1172	4	-	0/2/3/3	-
6	3BB	D	509	-	-	0/2/3/3	-
6	3BB	A	1174	-	-	0/2/3/3	-
6	3BB	C	508	-	-	0/2/3/3	-
6	3BB	A	1175	-	-	0/2/3/3	-
6	3BB	B	1178	-	-	0/2/3/3	-
6	3BB	C	510	-	-	0/2/3/3	-
6	3BB	A	1173	-	-	0/2/3/3	-
6	3BB	B	1177	-	-	0/2/3/3	-

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
6	B	1176	3BB	1	0
6	D	509	3BB	2	0
6	A	1174	3BB	1	0
6	A	1175	3BB	3	0
6	B	1178	3BB	1	0
6	C	510	3BB	2	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

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	510/527 (96%)	-0.15	6 (1%) 76 73	20, 36, 64, 94	0
1	B	510/527 (96%)	-0.02	8 (1%) 70 66	22, 38, 74, 92	0
2	C	388/389 (99%)	-0.45	1 (0%) 90 88	15, 28, 53, 78	0
2	D	388/389 (99%)	0.31	6 (1%) 72 68	25, 47, 79, 104	0
3	E	166/170 (97%)	-0.28	2 (1%) 76 73	18, 32, 55, 86	0
3	F	166/170 (97%)	0.99	13 (7%) 19 15	40, 61, 85, 107	0
All	All	2128/2172 (97%)	-0.01	36 (1%) 69 65	15, 38, 73, 107	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	168	SER	3.5
3	F	4	LEU	3.5
2	D	389	LYS	3.4
1	A	213	THR	3.3
1	A	19	ALA	3.2
1	A	318	ILE	3.1
1	B	317	TRP	3.0
2	D	352	ILE	2.9
1	A	317	TRP	2.8
1	B	20	PRO	2.8
1	B	19	ALA	2.8
1	B	314	GLY	2.6
3	F	99	ASN	2.6
1	B	206	LEU	2.5
1	A	214	ASN	2.4
3	F	60	LEU	2.4
3	F	39	HIS	2.3
2	D	375	ALA	2.3
1	B	44	THR	2.3

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Mol	Chain	Res	Type	RSRZ
3	F	25	LEU	2.3
3	F	80	LYS	2.3
1	A	18	ARG	2.3
3	F	64	VAL	2.3
3	F	29	ALA	2.3
3	F	118	TYR	2.2
3	F	82	ALA	2.2
3	E	23	ASN	2.1
1	B	32	LEU	2.1
3	F	83	PHE	2.1
2	D	308	GLU	2.1
2	D	203	ILE	2.1
1	B	53	ALA	2.0
3	F	19	ILE	2.0
2	C	134	ARG	2.0
3	F	67	LEU	2.0
2	D	126	GLY	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	3BB	C	510	6/6	0.84	0.22	95,97,99,102	0
6	3BB	D	509	6/6	0.84	0.25	91,93,94,95	0
6	3BB	A	1174	6/6	0.85	0.25	84,90,92,98	0
6	3BB	B	1178	6/6	0.88	0.20	62,65,66,71	0
6	3BB	A	1175	6/6	0.88	0.20	69,72,75,81	0
6	3BB	B	1177	6/6	0.88	0.33	105,107,109,112	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	3BB	A	1173	6/6	0.89	0.25	101,102,102,107	0
6	3BB	B	1176	6/6	0.89	0.21	104,112,114,121	0
5	CA	A	673	1/1	0.89	0.11	56,56,56,56	0
6	3BB	A	1172	6/6	0.90	0.19	78,82,84,90	0
6	3BB	C	508	6/6	0.92	0.19	91,96,97,102	0
5	CA	C	674	1/1	0.94	0.10	48,48,48,48	0
4	FE	B	1174	1/1	0.98	0.03	44,44,44,44	0
4	FE	A	1171	1/1	0.99	0.02	37,37,37,37	0
4	FE	A	1170	1/1	0.99	0.02	39,39,39,39	0
4	FE	B	1175	1/1	0.99	0.02	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.