



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:58 AM UTC

PDB ID : 3KVZ / pdb_00003kvz
Title : Structural basis of the activity and substrate specificity of the fluoroacetyl-CoA thioesterase FIK - wild type FIK in complex with FAcCPan
Authors : Dias, M.V.B.; Huang, F.; Chirgadze, D.Y.; Tosin, M.; Spiteller, D.; Valentine, E.F.; Leadlay, P.F.; Spencer, J.B.; Blundell, T.L.
Deposited on : 2009-11-30
Resolution : 2.10 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:

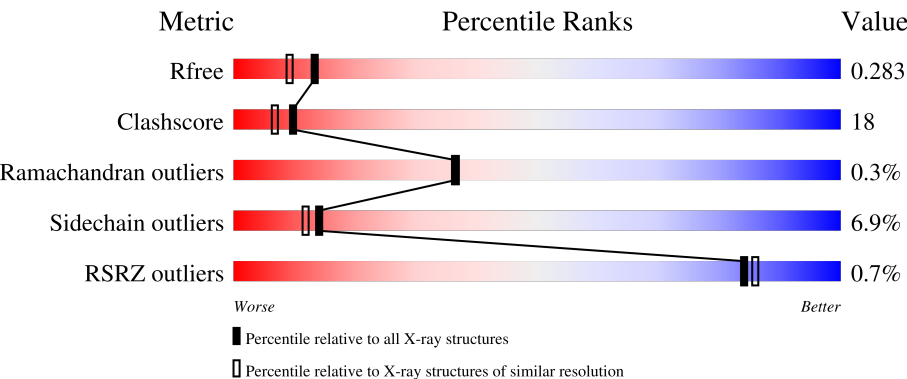
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

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

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	139	% 70% 22% ..
1	B	139	% 73% 19% ..
1	C	139	66% 27% ..
1	D	139	69% 22% 5% .

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Mol	Chain	Length	Quality of chain
1	E	139	
1	F	139	
1	G	139	
1	H	139	

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	ENV	B	201	-	-	X	-
2	ENV	E	202	-	-	X	-

2 Entry composition

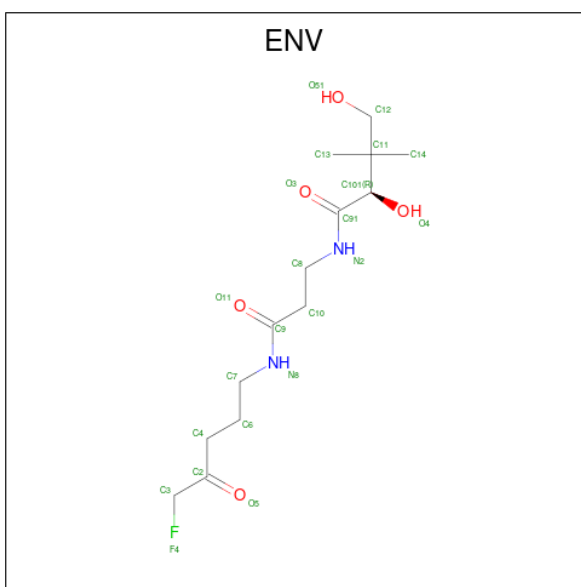
There are 3 unique types of molecules in this entry. The entry contains 8729 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Fluoroacetyl-CoA thioesterase Flk.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	133	Total	C	N	O	S	0	0	0
			1006	641	174	185	6			
1	B	133	Total	C	N	O	S	0	0	0
			1024	651	182	185	6			
1	C	133	Total	C	N	O	S	0	0	0
			1006	641	174	185	6			
1	D	133	Total	C	N	O	S	1	2	0
			1034	657	185	186	6			
1	E	133	Total	C	N	O	S	0	0	0
			1006	641	174	185	6			
1	F	133	Total	C	N	O	S	0	1	0
			1030	655	184	185	6			
1	G	133	Total	C	N	O	S	0	0	0
			1006	641	174	185	6			
1	H	133	Total	C	N	O	S	0	0	0
			1024	651	182	185	6			

- Molecule 2 is (2R)-N-{3-[(5-fluoro-4-oxopentyl)amino]-3-oxopropyl}-2,4-dihydroxy-3,3-dimethylbutanamide (CCD ID: ENV) (formula: C₁₄H₂₅FN₂O₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	F	N	O	0	0
			11	7	1	1	2		
2	E	1	Total	C	F	N	O	0	0
			11	7	1	1	2		

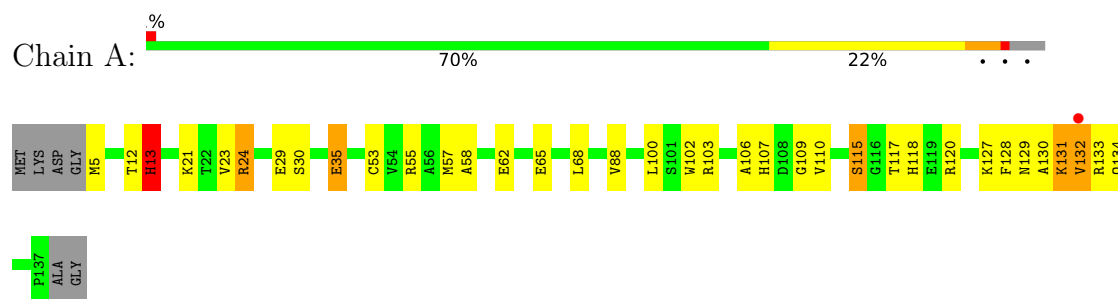
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	69	Total	O	0	0
			69	69		
3	B	56	Total	O	0	0
			56	56		
3	C	81	Total	O	0	0
			81	81		
3	D	81	Total	O	0	0
			81	81		
3	E	54	Total	O	0	0
			54	54		
3	F	67	Total	O	0	0
			67	67		
3	G	81	Total	O	0	0
			81	81		
3	H	82	Total	O	0	0
			82	82		

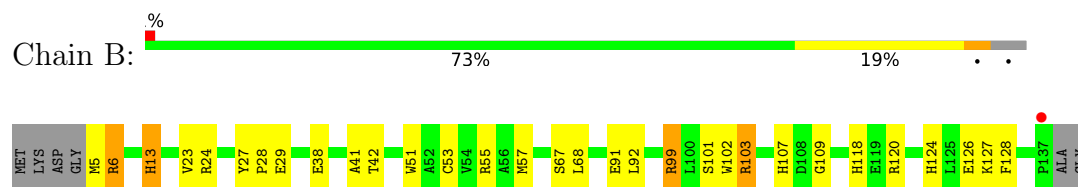
3 Residue-property plots

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.

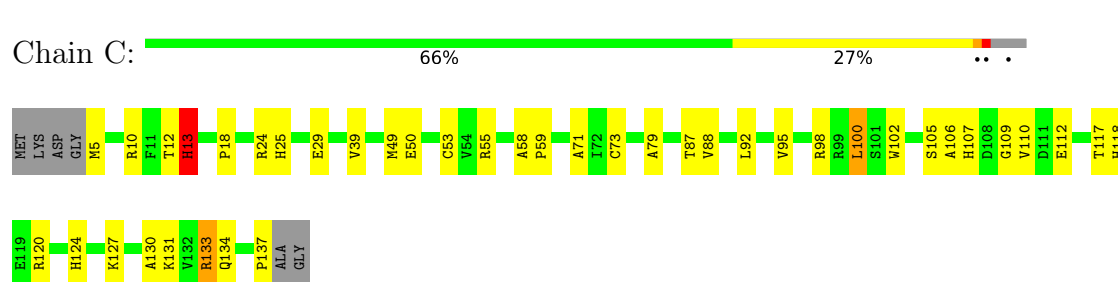
• Molecule 1: Fluoroacetyl-CoA thioesterase FlK



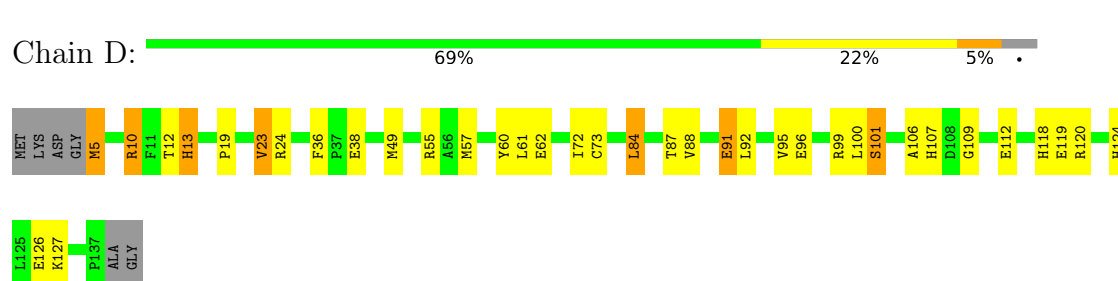
• Molecule 1: Fluoroacetyl-CoA thioesterase FlK



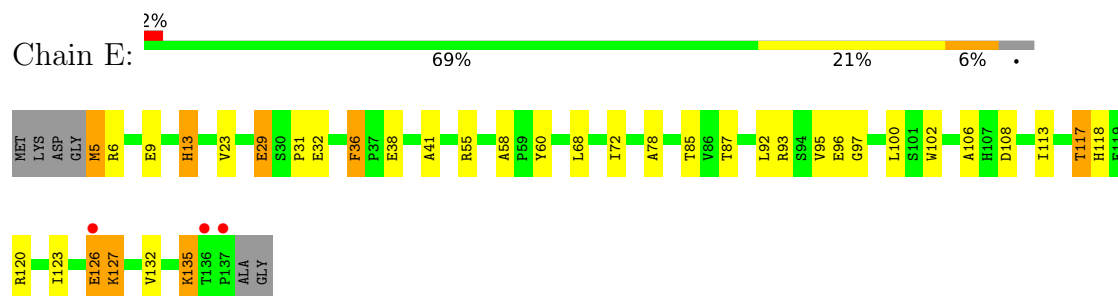
• Molecule 1: Fluoroacetyl-CoA thioesterase FlK



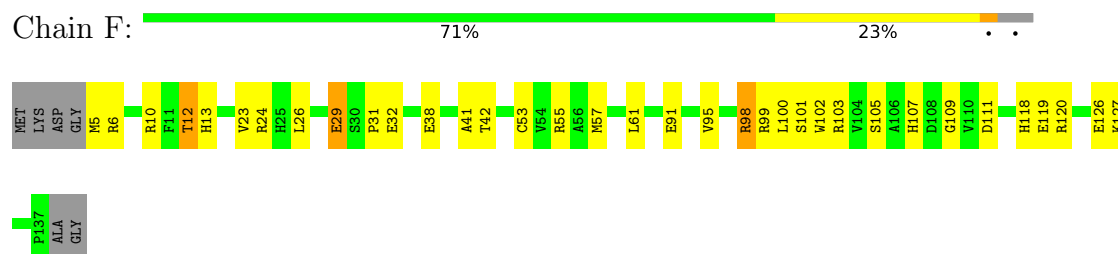
• Molecule 1: Fluoroacetyl-CoA thioesterase FlK



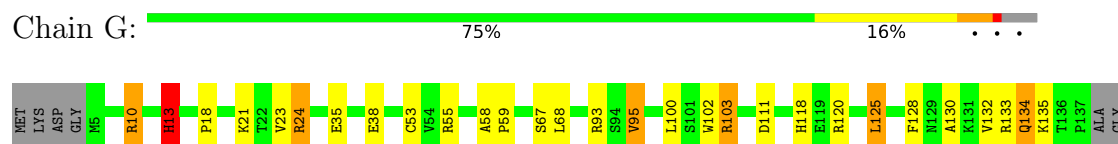
- Molecule 1: Fluoroacetyl-CoA thioesterase FLK



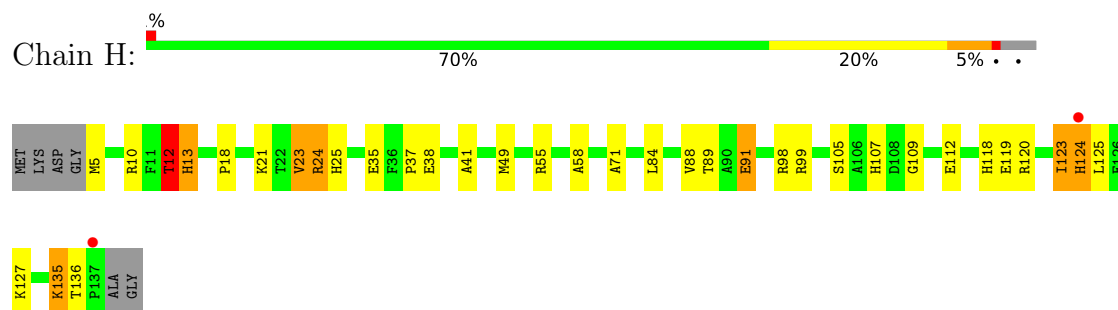
- Molecule 1: Fluoroacetyl-CoA thioesterase FLK



- Molecule 1: Fluoroacetyl-CoA thioesterase FLK



- Molecule 1: Fluoroacetyl-CoA thioesterase FLK



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.50Å 70.89Å 102.88Å 90.00° 103.06° 90.00°	Depositor
Resolution (Å)	33.70 – 2.10 33.70 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.3 (33.70-2.10) 96.2 (33.70-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.204 , 0.282 0.205 , 0.283	Depositor DCC
R_{free} test set	3193 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	23.1	Xtriage
Anisotropy	0.195	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8729	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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 45.51 % 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 1.3088e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ENV

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	0.78	0/1034	1.11	4/1410 (0.3%)
1	B	0.82	0/1053	1.00	0/1434
1	C	0.83	0/1034	1.11	6/1410 (0.4%)
1	D	0.81	0/1064	1.06	3/1449 (0.2%)
1	E	0.85	1/1034 (0.1%)	1.14	4/1410 (0.3%)
1	F	0.76	0/1064	1.05	1/1449 (0.1%)
1	G	0.81	0/1034	1.08	4/1410 (0.3%)
1	H	0.82	0/1053	1.11	6/1434 (0.4%)
All	All	0.81	1/8370 (0.0%)	1.08	28/11406 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	1
1	H	0	2
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	72	ILE	CA-CB	6.59	1.62	1.54

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	13	HIS	CB-CA-C	-8.75	93.70	109.71
1	A	58	ALA	CA-C-N	-7.82	112.85	120.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	58	ALA	C-N-CA	-7.82	112.85	120.83
1	G	13	HIS	CB-CA-C	-7.81	95.98	109.65
1	E	58	ALA	CA-C-N	-6.94	113.75	120.83
1	E	58	ALA	C-N-CA	-6.94	113.75	120.83
1	A	13	HIS	CB-CA-C	-6.89	97.23	109.70
1	C	18	PRO	CA-C-N	6.76	126.71	119.28
1	C	18	PRO	C-N-CA	6.76	126.71	119.28
1	G	18	PRO	CA-C-N	6.47	126.69	119.32
1	G	18	PRO	C-N-CA	6.47	126.69	119.32
1	H	13	HIS	N-CA-CB	-6.35	100.11	110.59
1	D	62	GLU	CA-C-N	-6.27	113.49	119.76
1	D	62	GLU	C-N-CA	-6.27	113.49	119.76
1	E	135	LYS	N-CA-C	6.22	119.03	111.82
1	F	13	HIS	N-CA-CB	-6.06	100.26	110.49
1	H	125	LEU	N-CA-C	6.04	118.36	111.11
1	D	13	HIS	N-CA-CB	-5.92	100.86	110.81
1	H	58	ALA	CA-C-N	-5.90	113.57	120.12
1	H	58	ALA	C-N-CA	-5.90	113.57	120.12
1	C	12	THR	CA-C-N	5.87	131.27	122.99
1	C	12	THR	C-N-CA	5.87	131.27	122.99
1	A	110	VAL	N-CA-C	-5.78	107.06	111.62
1	E	13	HIS	N-CA-CB	-5.37	101.78	110.81
1	C	110	VAL	CB-CA-C	-5.25	106.45	111.44
1	G	10	ARG	N-CA-C	5.25	117.66	109.52
1	H	123	ILE	CA-C-N	5.00	131.10	121.54
1	H	123	ILE	C-N-CA	5.00	131.10	121.54

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	12	THR	Peptide
1	H	12	THR	Peptide
1	H	123	ILE	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1006	0	970	32	0
1	B	1024	0	998	47	0
1	C	1006	0	970	40	0
1	D	1034	0	995	36	0
1	E	1006	0	970	35	0
1	F	1030	0	1001	53	0
1	G	1006	0	970	23	0
1	H	1024	0	998	31	0
2	B	11	0	9	9	0
2	E	11	0	9	15	0
3	A	69	0	0	5	2
3	B	56	0	0	5	0
3	C	81	0	0	7	1
3	D	81	0	0	5	1
3	E	54	0	0	1	0
3	F	67	0	0	5	1
3	G	81	0	0	3	1
3	H	82	0	0	5	2
All	All	8729	0	7890	283	7

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 18.

All (283) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:101:SER:HB3	3:F:385:HOH:O	1.51	1.11
1:A:5:MET:HE1	1:A:102:TRP:HH2	1.08	1.08
1:B:91:GLU:OE1	1:E:117:THR:HG21	1.55	1.06
1:E:127:LYS:HB2	1:E:127:LYS:NZ	1.66	1.05
1:F:98:ARG:HG2	1:F:98:ARG:HH11	1.21	1.01
1:E:127:LYS:HB2	1:E:127:LYS:HZ3	1.17	1.01
1:A:5:MET:HE1	1:A:102:TRP:CH2	1.96	1.01
1:C:124:HIS:CA	3:C:264:HOH:O	2.07	1.01
1:F:99:ARG:NH2	1:F:119:GLU:HG2	1.76	0.98
1:D:99:ARG:HH12	1:D:119:GLU:HG2	1.27	0.97
1:B:107:HIS:HD2	1:B:109:GLY:H	1.10	0.97
2:E:202:ENV:H6	1:F:42:THR:H	1.29	0.96
1:F:107[A]:HIS:HD2	1:F:109:GLY:H	1.13	0.93
1:E:118:HIS:HE1	1:E:120:ARG:HH11	1.16	0.93
1:B:6:ARG:HG3	1:B:6:ARG:HH11	1.34	0.92
1:D:10:ARG:HG3	1:D:91:GLU:HG3	1.49	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:13:HIS:HD2	1:D:55:ARG:HH11	1.19	0.91
1:A:107:HIS:HD2	1:A:109:GLY:H	1.01	0.91
1:F:119:GLU:OE2	3:F:384:HOH:O	1.90	0.89
1:B:91:GLU:OE1	1:E:117:THR:CG2	2.18	0.89
1:B:99:ARG:HH21	1:B:99:ARG:CG	1.87	0.87
2:E:202:ENV:C6	1:F:42:THR:H	1.87	0.87
1:D:13:HIS:CD2	1:D:55:ARG:HH11	1.92	0.87
1:C:118:HIS:HE1	1:C:120:ARG:HH11	1.20	0.86
2:E:202:ENV:H4A	1:F:23:VAL:HG22	1.54	0.86
1:H:107:HIS:HD2	1:H:109:GLY:H	1.23	0.86
1:D:13:HIS:HD2	1:D:55:ARG:NH1	1.74	0.85
1:C:133:ARG:HH11	1:C:133:ARG:HG2	1.42	0.85
1:D:99:ARG:NH1	1:D:119:GLU:HG2	1.91	0.84
1:H:5:MET:HA	3:H:469:HOH:O	1.75	0.84
1:B:107:HIS:CD2	1:B:109:GLY:H	1.94	0.84
1:H:24:ARG:NH1	1:H:25:HIS:NE2	2.24	0.84
1:B:13:HIS:HD2	1:B:55:ARG:HH11	1.23	0.84
1:A:107:HIS:CD2	1:A:109:GLY:H	1.93	0.83
1:G:118:HIS:HE1	1:G:120:ARG:HH11	1.25	0.83
1:B:42:THR:H	2:B:201:ENV:H4	1.44	0.83
1:F:107[A]:HIS:CD2	1:F:109:GLY:H	1.97	0.83
2:E:202:ENV:H3A	1:F:26:LEU:CD2	2.09	0.82
3:A:166:HOH:O	2:B:201:ENV:H7	1.80	0.82
1:G:103:ARG:NH2	3:G:269:HOH:O	1.97	0.79
1:B:99:ARG:HH21	1:B:99:ARG:HG3	1.47	0.79
1:A:107:HIS:HD2	1:A:109:GLY:N	1.80	0.78
1:B:24:ARG:HG2	3:B:193:HOH:O	1.82	0.78
1:A:118:HIS:HE1	1:A:120:ARG:HH11	1.30	0.78
1:F:24:ARG:NH1	1:F:38:GLU:OE2	2.18	0.76
1:H:118:HIS:HE1	1:H:120:ARG:HH11	1.34	0.75
1:H:124:HIS:HB2	1:H:127:LYS:HB3	1.68	0.74
1:D:107:HIS:HD2	1:D:109:GLY:N	1.84	0.73
1:H:5:MET:CA	3:H:469:HOH:O	2.35	0.73
1:B:101:SER:HB3	3:B:517:HOH:O	1.87	0.73
1:E:95:VAL:HG12	1:E:95:VAL:O	1.89	0.72
2:E:202:ENV:H6	1:F:42:THR:N	2.04	0.72
1:A:117:THR:HG21	1:F:91:GLU:OE1	1.89	0.72
2:E:202:ENV:H3A	1:F:26:LEU:HD23	1.70	0.72
2:E:202:ENV:H4	3:E:689:HOH:O	1.90	0.71
1:D:107:HIS:HD2	1:D:109:GLY:H	1.36	0.71
1:B:91:GLU:CB	1:B:103:ARG:NH2	2.53	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:12:THR:HG22	1:H:89:THR:HG23	1.74	0.70
1:D:5:MET:HG2	1:D:60:TYR:CG	2.26	0.70
1:C:118:HIS:CE1	1:C:120:ARG:HH11	2.07	0.69
1:C:92:LEU:HD21	1:C:95:VAL:CG2	2.23	0.69
1:D:10:ARG:HG3	1:D:91:GLU:CG	2.21	0.69
1:F:118:HIS:HE1	1:F:120:ARG:HH11	1.39	0.69
1:F:98:ARG:NH2	3:F:381:HOH:O	2.25	0.69
1:H:99:ARG:NH1	1:H:119:GLU:HB3	2.07	0.69
1:H:10:ARG:HG2	1:H:91:GLU:HG3	1.75	0.69
1:A:53:CYS:O	1:A:57:MET:HG2	1.93	0.69
1:E:126:GLU:CD	1:E:126:GLU:H	2.00	0.69
1:F:98:ARG:HG2	1:F:98:ARG:NH1	1.99	0.68
1:F:5:MET:N	3:F:376:HOH:O	2.25	0.68
1:F:103:ARG:HG2	1:F:103:ARG:HH11	1.59	0.68
1:E:118:HIS:CE1	1:E:120:ARG:HH11	2.06	0.68
1:B:6:ARG:HH11	1:B:6:ARG:CG	2.06	0.68
1:C:13:HIS:CE1	1:C:55:ARG:HH11	2.12	0.68
1:A:23:VAL:O	3:A:556:HOH:O	2.11	0.68
1:C:5:MET:HE1	1:C:102:TRP:CH2	2.30	0.67
1:B:41:ALA:HB1	2:B:201:ENV:H3	1.77	0.66
1:H:107:HIS:CD2	1:H:109:GLY:H	2.12	0.66
1:H:118:HIS:CE1	1:H:120:ARG:HH11	2.13	0.66
1:E:127:LYS:HB2	1:E:127:LYS:HZ2	1.58	0.66
1:D:24:ARG:NH1	1:D:38:GLU:OE2	2.27	0.66
1:B:91:GLU:HB2	1:B:103:ARG:NH2	2.11	0.65
1:F:24:ARG:NH1	1:F:38:GLU:CD	2.54	0.65
1:C:24:ARG:NH2	3:C:231:HOH:O	2.25	0.64
1:E:135:LYS:NZ	1:F:111:ASP:OD2	2.31	0.64
1:G:103:ARG:HH21	1:G:103:ARG:CG	2.10	0.64
1:B:99:ARG:HG3	1:B:99:ARG:NH2	2.13	0.64
1:F:24:ARG:NH1	1:F:38:GLU:OE1	2.30	0.63
1:A:13:HIS:CE1	1:A:55:ARG:HH11	2.17	0.63
1:E:92:LEU:HD21	1:E:95:VAL:HG22	1.81	0.62
1:B:13:HIS:CD2	1:B:55:ARG:HH11	2.11	0.62
1:H:18:PRO:HG2	1:H:21:LYS:HG2	1.82	0.62
1:B:124:HIS:CD2	1:B:127:LYS:HE3	2.35	0.62
1:H:24:ARG:HD3	1:H:38:GLU:OE1	2.00	0.62
1:G:118:HIS:CE1	1:G:120:ARG:HH11	2.14	0.61
1:B:91:GLU:HB2	1:B:103:ARG:HH22	1.66	0.61
1:C:53:CYS:HG	1:C:102:TRP:CG	2.18	0.61
1:D:60:TYR:HB3	3:D:319:HOH:O	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:101:SER:HB3	1:D:119:GLU:HG3	1.83	0.60
1:G:13:HIS:CE1	1:G:55:ARG:HH11	2.19	0.60
1:G:95:VAL:HG13	1:G:100:LEU:HG	1.82	0.60
1:C:58:ALA:N	1:C:59:PRO:HD2	2.17	0.60
2:E:202:ENV:H3A	1:F:26:LEU:HD22	1.81	0.60
1:A:118:HIS:CE1	1:A:120:ARG:HH11	2.15	0.60
1:A:21:LYS:HE3	1:B:27:TYR:CE1	2.36	0.60
2:E:202:ENV:H3	1:F:41:ALA:HB1	1.84	0.60
1:H:71:ALA:HB3	1:H:119:GLU:OE1	2.01	0.60
1:A:127:LYS:HD3	1:A:130:ALA:HB3	1.83	0.59
1:B:41:ALA:HB1	2:B:201:ENV:C3	2.32	0.59
1:D:92:LEU:HD21	1:D:95:VAL:CG2	2.32	0.59
1:A:118:HIS:CE1	1:A:120:ARG:HG2	2.37	0.59
1:G:58:ALA:HB3	1:G:59:PRO:HD3	1.85	0.59
1:B:91:GLU:HB3	1:B:103:ARG:NH2	2.18	0.59
1:A:68:LEU:HD22	2:B:201:ENV:H7A	1.83	0.58
1:D:118:HIS:HE1	1:D:120:ARG:HH11	1.51	0.58
1:H:5:MET:N	3:H:469:HOH:O	2.35	0.58
2:E:202:ENV:H6	1:F:41:ALA:HA	1.84	0.58
1:D:107:HIS:CD2	1:D:109:GLY:H	2.19	0.57
1:G:68:LEU:HD11	1:G:128:PHE:CZ	2.39	0.57
1:C:92:LEU:HD21	1:C:95:VAL:HG21	1.85	0.57
1:C:13:HIS:HE1	1:C:55:ARG:HH11	1.50	0.57
1:B:118:HIS:HE1	1:B:120:ARG:HH11	1.50	0.57
1:E:126:GLU:CD	1:E:126:GLU:N	2.63	0.57
1:E:29:GLU:O	1:E:31:PRO:HD3	2.05	0.57
1:A:24:ARG:HD3	3:A:155:HOH:O	2.04	0.57
1:B:126:GLU:HG2	3:B:220:HOH:O	2.04	0.57
1:E:127:LYS:NZ	1:E:127:LYS:CB	2.48	0.57
1:B:107:HIS:HD2	1:B:109:GLY:N	1.93	0.56
1:B:99:ARG:HH21	1:B:99:ARG:HG2	1.68	0.56
1:G:103:ARG:NH1	3:G:269:HOH:O	2.39	0.56
1:H:13:HIS:CD2	1:H:55:ARG:HH11	2.24	0.56
1:B:57:MET:HE1	1:B:67:SER:HB3	1.88	0.56
1:C:5:MET:HE1	1:C:102:TRP:HH2	1.69	0.56
1:E:5:MET:HE2	1:E:92:LEU:HD22	1.86	0.55
1:E:13:HIS:CE1	1:E:55:ARG:HH11	2.25	0.55
1:A:53:CYS:HG	1:A:102:TRP:CG	2.25	0.55
1:A:115:SER:HB2	3:A:674:HOH:O	2.05	0.55
1:A:117:THR:HG22	1:F:10:ARG:HH21	1.72	0.55
1:F:53:CYS:O	1:F:57:MET:HG3	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:GLU:HB3	1:B:103:ARG:HH21	1.71	0.55
1:C:55:ARG:HB3	3:C:246:HOH:O	2.06	0.55
1:E:100:LEU:N	1:E:100:LEU:HD12	2.21	0.54
1:E:23:VAL:HA	1:E:41:ALA:HB2	1.88	0.54
1:D:5:MET:HE3	1:D:60:TYR:CE2	2.43	0.54
1:F:99:ARG:NH2	1:F:119:GLU:CG	2.62	0.54
1:F:118:HIS:CE1	1:F:120:ARG:HH11	2.23	0.54
1:E:92:LEU:HD21	1:E:95:VAL:CG2	2.37	0.54
1:G:13:HIS:HE1	1:G:55:ARG:HH11	1.54	0.54
1:F:5:MET:HE1	1:F:102:TRP:HH2	1.73	0.53
1:A:131:LYS:O	1:A:134:GLN:HG2	2.08	0.53
1:C:130:ALA:HA	1:C:133:ARG:HD2	1.89	0.53
1:C:133:ARG:HD3	3:C:265:HOH:O	2.08	0.53
1:D:5:MET:HG2	1:D:60:TYR:CD2	2.43	0.53
1:F:98:ARG:HH11	1:F:98:ARG:CG	2.07	0.53
1:B:42:THR:H	2:B:201:ENV:C4	2.18	0.53
1:C:71:ALA:O	1:C:118:HIS:HD2	1.92	0.53
1:E:6:ARG:O	1:E:9:GLU:HB2	2.09	0.53
1:A:13:HIS:CE1	1:A:55:ARG:HD3	2.44	0.52
1:A:35:GLU:N	3:A:154:HOH:O	2.09	0.52
1:C:13:HIS:HE1	1:C:55:ARG:HD3	1.74	0.52
1:G:134:GLN:HG3	1:G:135:LYS:N	2.24	0.51
1:A:30:SER:HB2	1:B:51:TRP:CZ2	2.46	0.51
1:D:24:ARG:HD3	3:D:285:HOH:O	2.11	0.51
1:B:91:GLU:OE1	1:B:103:ARG:NH2	2.44	0.51
1:H:23:VAL:HA	1:H:41:ALA:HB2	1.93	0.51
1:B:6:ARG:HG3	1:B:6:ARG:NH1	2.14	0.50
1:C:49:MET:HA	1:C:88:VAL:HG11	1.92	0.50
1:C:137:PRO:HD3	1:D:84:LEU:HD13	1.91	0.50
1:E:118:HIS:CE1	1:E:120:ARG:HG2	2.45	0.50
1:D:10:ARG:CG	1:D:91:GLU:HG3	2.34	0.49
1:D:118:HIS:CE1	1:D:120:ARG:HH11	2.30	0.49
1:G:24:ARG:HD3	1:G:38:GLU:OE2	2.12	0.49
1:H:49:MET:HA	1:H:88:VAL:HG11	1.94	0.49
1:E:68:LEU:HG	1:E:123:ILE:HD13	1.95	0.49
1:D:57:MET:HE2	1:D:61:LEU:HD21	1.94	0.49
1:G:53:CYS:HG	1:G:102:TRP:CG	2.31	0.49
1:A:13:HIS:HE1	1:A:55:ARG:HD3	1.77	0.49
1:C:133:ARG:HG2	1:C:133:ARG:NH1	2.16	0.49
1:F:107[A]:HIS:HD2	1:F:109:GLY:N	1.96	0.49
1:A:5:MET:CE	1:A:102:TRP:CH2	2.84	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:103:ARG:NH2	1:G:103:ARG:CG	2.71	0.49
1:B:99:ARG:CG	1:B:99:ARG:NH2	2.58	0.48
1:E:5:MET:HG2	1:E:60:TYR:CD2	2.48	0.48
1:G:130:ALA:HA	1:G:133:ARG:NH1	2.28	0.48
2:E:202:ENV:C3	1:F:26:LEU:HD22	2.42	0.48
1:H:136:THR:HB	3:H:683:HOH:O	2.13	0.48
1:C:50:GLU:HG2	1:C:118:HIS:CE1	2.49	0.48
1:E:38:GLU:HA	1:E:38:GLU:OE2	2.14	0.48
1:H:13:HIS:HD2	1:H:55:ARG:NH1	2.11	0.48
1:A:117:THR:CG2	1:F:91:GLU:OE1	2.60	0.47
1:H:24:ARG:HH11	1:H:25:HIS:CD2	2.32	0.47
1:B:5:MET:HE2	1:B:92:LEU:HD22	1.96	0.47
1:C:10:ARG:NH2	3:C:664:HOH:O	2.28	0.47
1:C:107:HIS:HD2	1:C:109:GLY:H	1.61	0.47
1:E:127:LYS:HZ3	1:E:127:LYS:CB	2.05	0.47
2:E:202:ENV:H6A	1:F:42:THR:H	1.76	0.47
1:F:107[A]:HIS:CD2	1:F:109:GLY:N	2.77	0.47
1:G:103:ARG:HH21	1:G:103:ARG:HG3	1.80	0.47
1:D:19:PRO:HB3	3:D:311:HOH:O	2.15	0.47
1:G:103:ARG:NH2	1:G:103:ARG:HG2	2.30	0.47
2:E:202:ENV:C4	1:F:23:VAL:HG22	2.36	0.47
1:F:126:GLU:HA	1:F:126:GLU:OE1	2.15	0.46
1:F:29:GLU:O	1:F:31:PRO:HD3	2.16	0.46
1:F:107[B]:HIS:HD2	1:F:109:GLY:H	1.62	0.46
1:G:125:LEU:HD21	1:H:37:PRO:HG3	1.97	0.46
1:H:99:ARG:HH11	1:H:119:GLU:HB3	1.79	0.46
1:B:24:ARG:NH1	1:B:38:GLU:OE2	2.48	0.46
1:C:95:VAL:HG22	1:C:100:LEU:HD23	1.98	0.46
1:A:88:VAL:HG22	1:A:106:ALA:HB2	1.98	0.46
1:F:103:ARG:HG2	1:F:103:ARG:NH1	2.28	0.46
1:D:92:LEU:HD21	1:D:95:VAL:HG22	1.98	0.46
1:E:87:THR:O	1:E:106:ALA:HA	2.15	0.46
1:C:73:CYS:HA	1:D:73:CYS:HA	1.98	0.46
1:B:53:CYS:HG	1:B:102:TRP:CG	2.34	0.45
1:C:118:HIS:CE1	1:C:120:ARG:CG	2.99	0.45
1:C:39:VAL:HG11	1:C:79:ALA:HB1	1.98	0.45
1:C:98:ARG:CB	3:C:263:HOH:O	2.65	0.45
1:H:99:ARG:HH12	1:H:119:GLU:HB3	1.81	0.45
1:C:13:HIS:CE1	1:C:55:ARG:HD3	2.50	0.45
1:H:71:ALA:O	1:H:118:HIS:HD2	1.98	0.45
1:B:124:HIS:HD1	1:B:124:HIS:C	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:95:VAL:HG13	1:D:100:LEU:HG	1.98	0.45
1:A:128:PHE:O	1:A:132:VAL:HG12	2.16	0.45
1:F:95:VAL:HG13	1:F:100:LEU:HG	1.98	0.45
1:B:126:GLU:CD	3:B:220:HOH:O	2.60	0.44
1:E:23:VAL:HG11	1:E:36:PHE:CD2	2.51	0.44
1:H:24:ARG:NH1	1:H:25:HIS:CD2	2.84	0.44
1:C:131:LYS:O	1:C:134:GLN:HG2	2.17	0.44
1:D:49:MET:HA	1:D:88:VAL:HG11	2.00	0.44
1:B:28:PRO:HD2	1:B:29:GLU:OE2	2.17	0.44
1:G:35:GLU:HG3	3:G:430:HOH:O	2.16	0.44
1:B:23:VAL:HG22	2:B:201:ENV:H6	1.99	0.44
1:C:71:ALA:O	1:C:118:HIS:CD2	2.70	0.44
1:E:85:THR:O	1:E:108:ASP:HA	2.17	0.44
1:B:68:LEU:HD11	1:B:128:PHE:CZ	2.52	0.43
1:A:117:THR:CG2	1:F:10:ARG:HH21	2.31	0.43
1:G:93:ARG:HD3	1:G:93:ARG:HA	1.80	0.43
1:G:67:SER:O	1:G:68:LEU:HD23	2.18	0.43
1:D:13:HIS:CD2	1:D:55:ARG:NH1	2.62	0.43
1:E:5:MET:HG2	1:E:60:TYR:CG	2.53	0.43
1:F:61:LEU:HD23	1:F:61:LEU:HA	1.75	0.43
1:H:84:LEU:HD23	1:H:84:LEU:HA	1.82	0.43
1:E:78:ALA:HB3	1:E:113:ILE:HG22	2.01	0.43
1:F:98:ARG:NH1	1:F:98:ARG:CG	2.72	0.43
1:E:5:MET:HE2	1:E:5:MET:HB3	1.91	0.43
1:C:5:MET:HE1	1:C:102:TRP:CZ2	2.54	0.42
1:D:10:ARG:NH2	3:D:276:HOH:O	2.51	0.42
1:F:23:VAL:HA	1:F:41:ALA:HB2	2.00	0.42
1:B:6:ARG:CG	1:B:6:ARG:NH1	2.75	0.42
1:F:32:GLU:H	1:F:32:GLU:CD	2.27	0.42
1:B:118:HIS:CE1	1:B:120:ARG:HH11	2.32	0.42
1:G:23:VAL:HG13	3:H:699:HOH:O	2.19	0.42
1:B:126:GLU:CG	3:B:220:HOH:O	2.65	0.42
1:C:5:MET:CE	1:C:102:TRP:CH2	3.00	0.42
1:C:87:THR:O	1:C:106:ALA:HA	2.20	0.42
1:C:112:GLU:HB3	3:C:544:HOH:O	2.19	0.42
1:F:119:GLU:CD	3:F:384:HOH:O	2.52	0.42
1:A:100:LEU:HD12	1:A:100:LEU:N	2.35	0.42
1:E:5:MET:HE1	1:E:102:TRP:CH2	2.54	0.41
1:E:32:GLU:HG2	1:F:55:ARG:HG2	2.02	0.41
1:H:10:ARG:HG2	1:H:91:GLU:CG	2.47	0.41
1:B:42:THR:N	2:B:201:ENV:H3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:HIS:CD2	1:B:109:GLY:N	2.75	0.41
1:D:124[B]:HIS:CG	1:D:127:LYS:HD3	2.56	0.41
2:E:202:ENV:H7	1:F:42:THR:OG1	2.20	0.41
1:F:103:ARG:NH1	1:F:105:SER:HB2	2.35	0.41
1:C:118:HIS:CE1	1:C:120:ARG:HG2	2.56	0.41
1:C:24:ARG:HG3	1:C:25:HIS:CD2	2.55	0.41
1:E:95:VAL:O	1:E:97:GLY:N	2.54	0.41
1:G:111:ASP:OD2	1:H:135:LYS:NZ	2.48	0.41
1:C:117:THR:CG2	1:H:91:GLU:OE2	2.69	0.41
1:C:117:THR:HG23	1:H:91:GLU:OE2	2.21	0.41
1:E:93:ARG:HA	1:E:93:ARG:HD3	1.87	0.41
1:F:118:HIS:CE1	1:F:120:ARG:CG	3.04	0.41
1:A:62:GLU:O	1:A:65:GLU:HB2	2.21	0.41
1:D:87:THR:O	1:D:106:ALA:HA	2.21	0.40
1:D:96:GLU:HG3	3:D:317:HOH:O	2.20	0.40
1:D:23:VAL:HG21	1:D:36:PHE:CD1	2.56	0.40
1:A:129:ASN:HA	1:A:132:VAL:HG13	2.03	0.40
2:E:202:ENV:H6	1:F:41:ALA:CA	2.49	0.40
1:B:41:ALA:HA	2:B:201:ENV:H6A	2.04	0.40

All (7) 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)
3:F:365:HOH:O	3:F:371:HOH:O[2_545]	1.76	0.44
3:G:405:HOH:O	3:H:473:HOH:O[2_556]	2.01	0.19
3:A:141:HOH:O	3:A:156:HOH:O[2_645]	2.07	0.13
3:H:484:HOH:O	3:H:493:HOH:O[2_556]	2.09	0.11
3:A:153:HOH:O	3:A:159:HOH:O[2_655]	2.12	0.08
3:C:234:HOH:O	3:C:246:HOH:O[2_656]	2.14	0.06
3:D:295:HOH:O	3:D:718:HOH:O[2_656]	2.14	0.06

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	131/139 (94%)	130 (99%)	1 (1%)	0	100	100
1	B	131/139 (94%)	129 (98%)	2 (2%)	0	100	100
1	C	131/139 (94%)	128 (98%)	3 (2%)	0	100	100
1	D	132/139 (95%)	129 (98%)	3 (2%)	0	100	100
1	E	131/139 (94%)	123 (94%)	6 (5%)	2 (2%)	8	4
1	F	132/139 (95%)	129 (98%)	3 (2%)	0	100	100
1	G	131/139 (94%)	127 (97%)	4 (3%)	0	100	100
1	H	131/139 (94%)	129 (98%)	1 (1%)	1 (1%)	16	12
All	All	1050/1112 (94%)	1024 (98%)	23 (2%)	3 (0%)	36	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	96	GLU
1	H	124	HIS
1	E	36	PHE

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	105/113 (93%)	95 (90%)	10 (10%)	8	5
1	B	108/113 (96%)	104 (96%)	4 (4%)	30	33
1	C	105/113 (93%)	99 (94%)	6 (6%)	18	17
1	D	109/113 (96%)	99 (91%)	10 (9%)	8	6
1	E	105/113 (93%)	99 (94%)	6 (6%)	18	17
1	F	109/113 (96%)	104 (95%)	5 (5%)	24	25
1	G	105/113 (93%)	96 (91%)	9 (9%)	10	7
1	H	108/113 (96%)	99 (92%)	9 (8%)	10	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	854/904 (94%)	795 (93%)	59 (7%)	14	12

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	THR
1	A	13	HIS
1	A	24	ARG
1	A	29	GLU
1	A	35	GLU
1	A	103	ARG
1	A	115	SER
1	A	131	LYS
1	A	132	VAL
1	A	133	ARG
1	B	6	ARG
1	B	13	HIS
1	B	99	ARG
1	B	103	ARG
1	C	13	HIS
1	C	29	GLU
1	C	100	LEU
1	C	105	SER
1	C	127	LYS
1	C	133	ARG
1	D	5	MET
1	D	10	ARG
1	D	12	THR
1	D	23	VAL
1	D	72	ILE
1	D	84	LEU
1	D	91	GLU
1	D	101	SER
1	D	112	GLU
1	D	126	GLU
1	E	5	MET
1	E	29	GLU
1	E	117	THR
1	E	126	GLU
1	E	127	LYS
1	E	132	VAL
1	F	6	ARG

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Mol	Chain	Res	Type
1	F	12	THR
1	F	29	GLU
1	F	98	ARG
1	F	127	LYS
1	G	10	ARG
1	G	13	HIS
1	G	21	LYS
1	G	24	ARG
1	G	95	VAL
1	G	103	ARG
1	G	125	LEU
1	G	132	VAL
1	G	134	GLN
1	H	12	THR
1	H	23	VAL
1	H	24	ARG
1	H	35	GLU
1	H	91	GLU
1	H	98	ARG
1	H	105	SER
1	H	112	GLU
1	H	135	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	HIS
1	A	20	HIS
1	A	25	HIS
1	A	107	HIS
1	A	118	HIS
1	B	13	HIS
1	B	25	HIS
1	B	107	HIS
1	B	118	HIS
1	B	124	HIS
1	C	13	HIS
1	C	20	HIS
1	C	25	HIS
1	C	107	HIS
1	C	118	HIS
1	D	13	HIS

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Mol	Chain	Res	Type
1	D	107	HIS
1	D	118	HIS
1	E	20	HIS
1	E	25	HIS
1	E	118	HIS
1	E	134	GLN
1	F	13	HIS
1	F	118	HIS
1	F	134	GLN
1	G	13	HIS
1	G	20	HIS
1	G	118	HIS
1	H	13	HIS
1	H	107	HIS
1	H	118	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 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	ENV	E	202	-	9,10,21	0.43	0	10,11,27	1.39	2 (20%)
2	ENV	B	201	-	9,10,21	0.56	0	10,11,27	1.62	4 (40%)

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	ENV	E	202	-	-	2/7/9/28	-
2	ENV	B	201	-	-	5/7/9/28	-

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	202	ENV	C7-N8-C9	-3.16	117.89	122.56
2	B	201	ENV	O5-C2-C3	-2.56	117.78	121.76
2	B	201	ENV	C6-C7-N8	2.55	119.35	112.20
2	E	202	ENV	C6-C4-C2	-2.42	108.45	114.59
2	B	201	ENV	C4-C2-C3	2.25	122.31	117.30
2	B	201	ENV	O11-C9-C10	-2.16	118.21	122.05

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	202	ENV	C2-C4-C6-C7
2	B	201	ENV	C10-C9-N8-C7
2	B	201	ENV	O11-C9-N8-C7
2	B	201	ENV	C2-C4-C6-C7
2	E	202	ENV	C4-C6-C7-N8
2	B	201	ENV	O5-C2-C4-C6
2	B	201	ENV	C3-C2-C4-C6

There are no ring outliers.

2 monomers are involved in 24 short contacts:

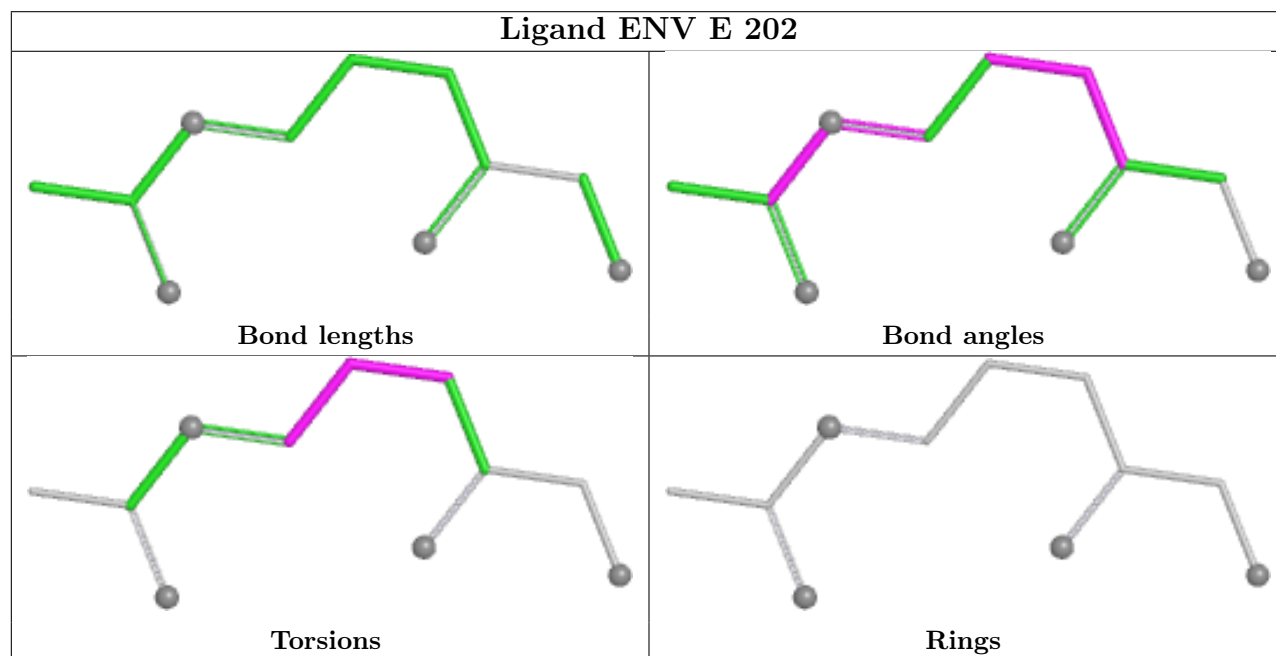
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	202	ENV	15	0

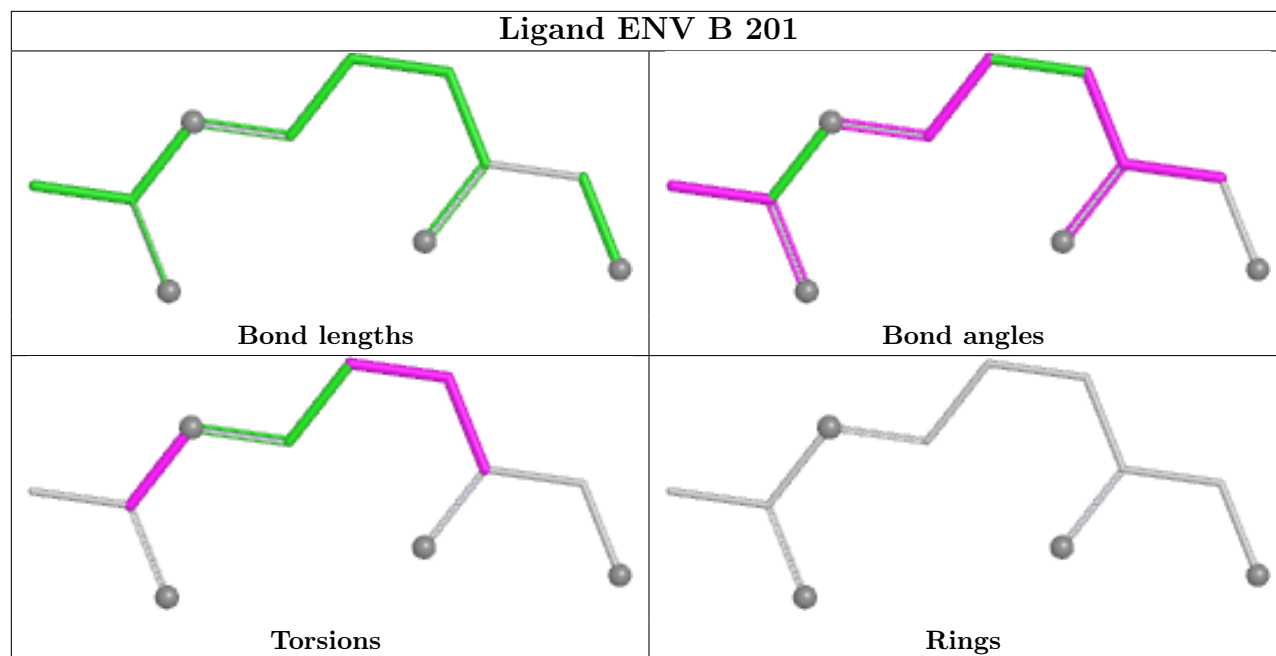
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	201	ENV	9	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	133/139 (95%)	0.03	1 (0%) 82 84	13, 24, 45, 50	1 (0%)
1	B	133/139 (95%)	-0.07	1 (0%) 82 84	12, 24, 40, 52	1 (0%)
1	C	133/139 (95%)	-0.25	0 100 100	11, 20, 39, 50	0
1	D	133/139 (95%)	-0.20	0 100 100	10, 20, 37, 45	2 (1%)
1	E	133/139 (95%)	-0.04	3 (2%) 61 64	13, 23, 38, 48	0
1	F	133/139 (95%)	-0.06	0 100 100	5, 23, 44, 51	2 (1%)
1	G	133/139 (95%)	-0.23	0 100 100	11, 20, 38, 44	1 (0%)
1	H	133/139 (95%)	-0.22	2 (1%) 72 74	11, 20, 35, 45	1 (0%)
All	All	1064/1112 (95%)	-0.13	7 (0%) 84 86	5, 22, 40, 52	8 (0%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	136	THR	4.2
1	E	126	GLU	2.5
1	H	124	HIS	2.4
1	A	132	VAL	2.3
1	B	137	PRO	2.3
1	H	137	PRO	2.2
1	E	137	PRO	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](#)

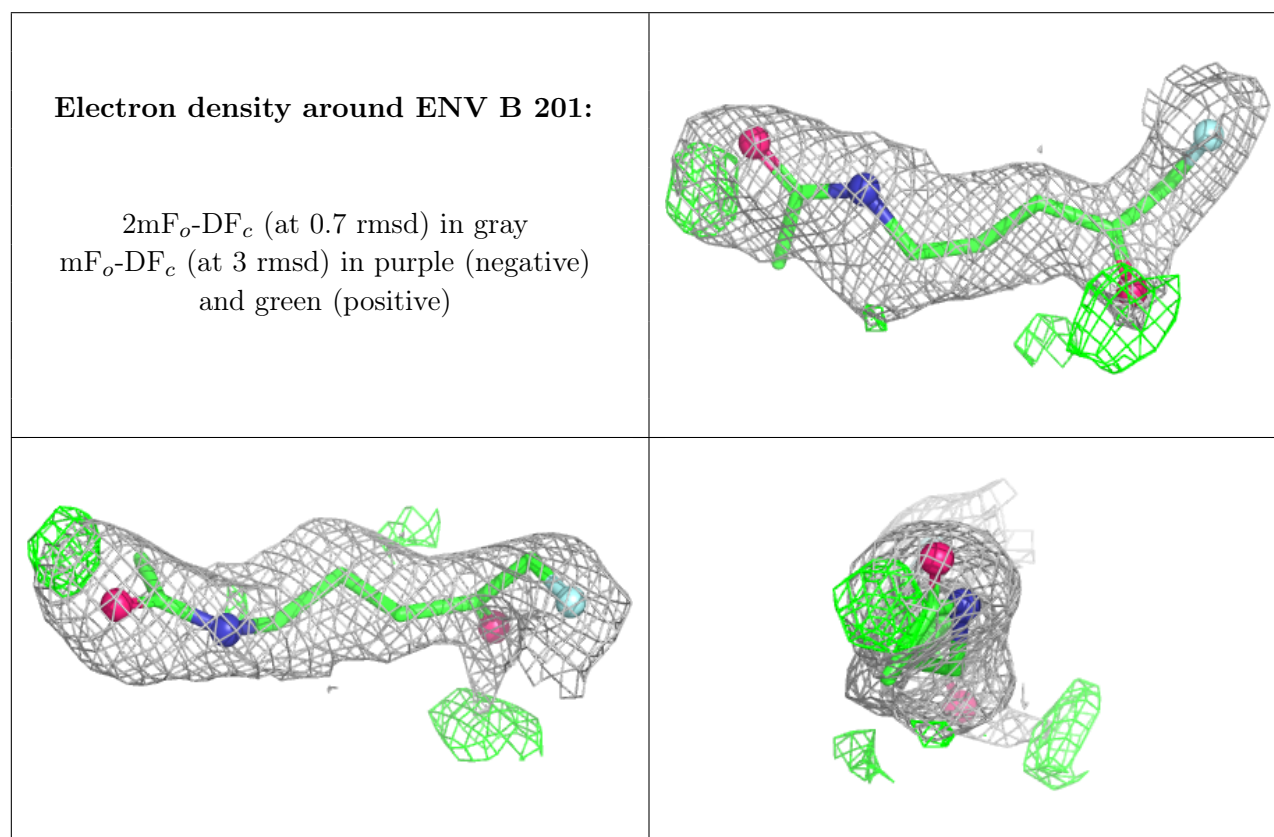
There are no oligosaccharides in this entry.

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.

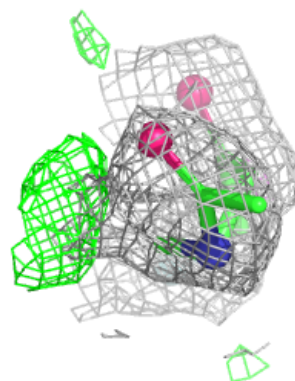
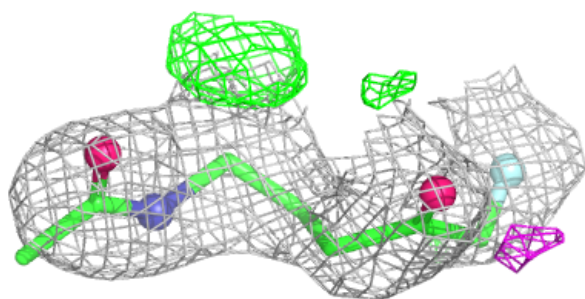
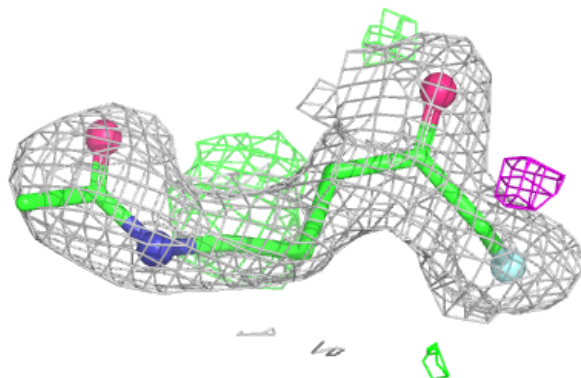
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ENV	B	201	11/22	0.79	0.17	39,41,46,47	0
2	ENV	E	202	11/22	0.84	0.13	39,42,46,46	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around ENV E 202:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.