



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 10:02 PM UTC

PDB ID : 1TG6 / pdb_00001tg6
Title : Crystallography and mutagenesis point to an essential role for the N-terminus of human mitochondrial ClpP
Authors : Kang, S.G.; Maurizi, M.R.; Thompson, M.; Mueser, T.; Ahvazi, B.
Deposited on : 2004-05-28
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

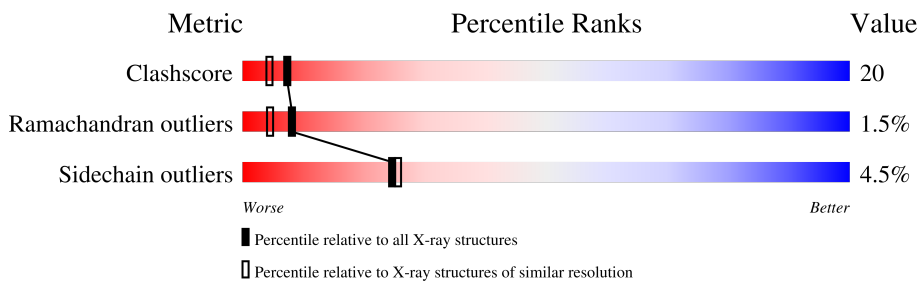
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	277	
1	B	277	
1	C	277	
1	D	277	
1	E	277	
1	F	277	
1	G	277	

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
4	GOL	B	1000	-	X	-	-
4	GOL	B	1001	-	X	-	-
4	GOL	C	1002	-	X	-	-
4	GOL	D	1003	-	X	-	-
4	GOL	E	1004	-	X	-	-
4	GOL	F	1005	-	X	-	-
5	FME	D	1101	-	-	X	-
5	FME	D	1102	-	-	X	-
5	FME	D	1103	-	-	X	-
5	FME	D	1104	-	-	X	-
5	FME	D	1106	-	-	X	-

2 Entry composition [i](#)

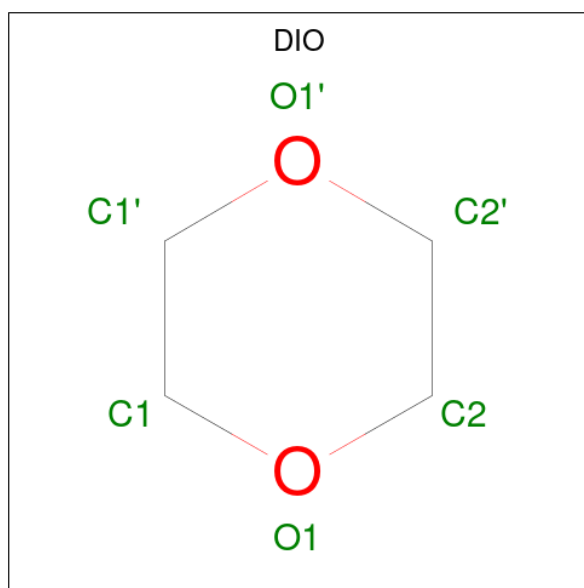
There are 6 unique types of molecules in this entry. The entry contains 11064 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Putative ATP-dependent Clp protease proteolytic subunit.

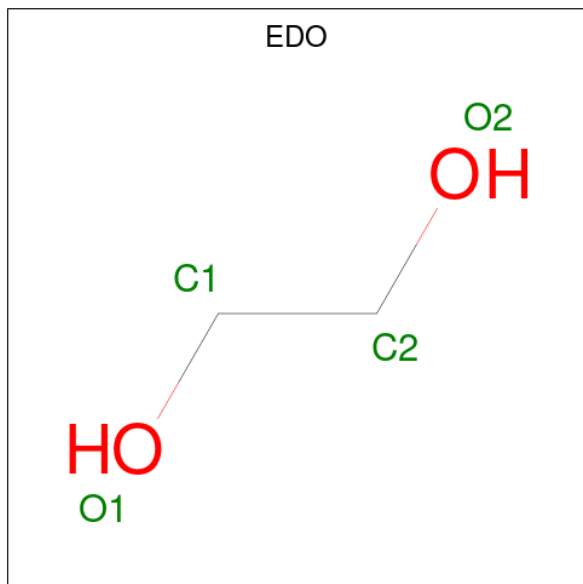
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	184	Total	C	N	O	S	0	0	0
			1420	906	243	258	13			
1	B	183	Total	C	N	O	S	0	0	0
			1413	901	242	257	13			
1	C	183	Total	C	N	O	S	0	0	0
			1413	901	242	257	13			
1	D	184	Total	C	N	O	S	0	0	0
			1420	906	243	258	13			
1	E	196	Total	C	N	O	S	0	0	0
			1514	962	258	281	13			
1	F	187	Total	C	N	O	S	0	0	0
			1441	917	247	264	13			
1	G	194	Total	C	N	O	S	0	0	0
			1496	951	254	278	13			

- Molecule 2 is 1,4-DIETHYLENE DIOXIDE (CCD ID: DIO) (formula: C₄H₈O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 4 2	0	0
2	B	1	Total C O 6 4 2	0	0
2	D	1	Total C O 6 4 2	0	0
2	E	1	Total C O 6 4 2	0	0
2	F	1	Total C O 6 4 2	0	0
2	G	1	Total C O 6 4 2	0	0

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



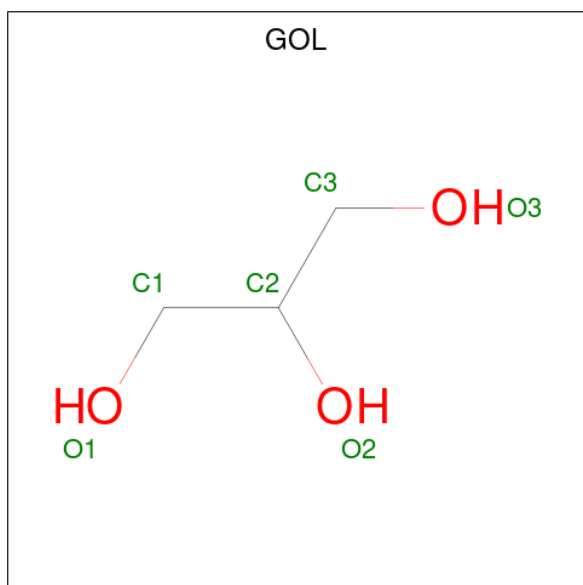
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0

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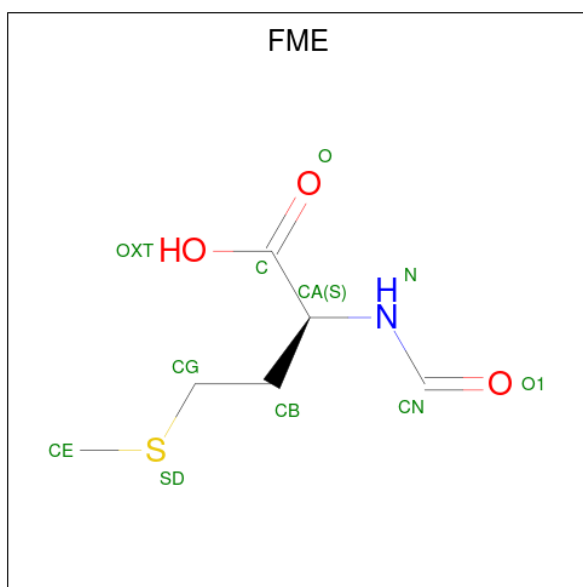
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	F	1	Total	C	O	0	0
			4	2	2		
3	G	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	D	1	Total	C	N	O	S	0	0
			10	6	1	2	1		
5	D	1	Total	C	N	O	S	0	0
			10	6	1	2	1		
5	D	1	Total	C	N	O	S	0	0
			10	6	1	2	1		
5	D	1	Total	C	N	O	S	0	0
			10	6	1	2	1		
5	D	1	Total	C	N	O	S	0	0
			10	6	1	2	1		
5	D	1	Total	C	N	O	S	0	0
			10	6	1	2	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	77	Total	O	0	0
			77	77		
6	B	90	Total	O	0	0
			90	90		
6	C	109	Total	O	0	0
			109	109		
6	D	128	Total	O	0	0
			128	128		
6	E	132	Total	O	0	0
			132	132		

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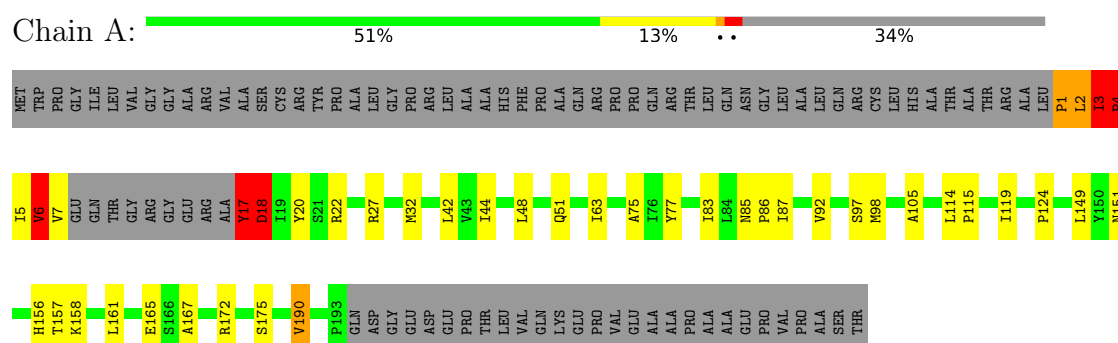
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	126	Total 126	O 126	0	0
6	G	111	Total 111	O 111	0	0

3 Residue-property plots [i](#)

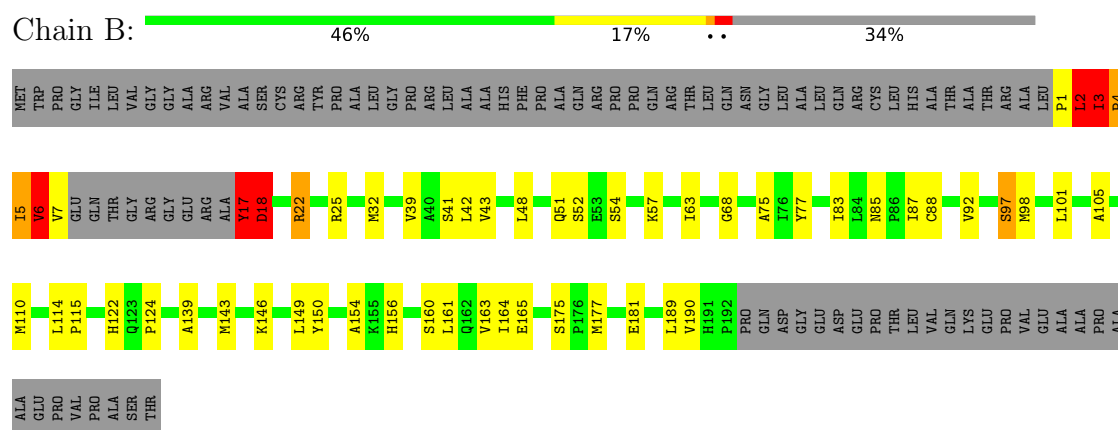
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

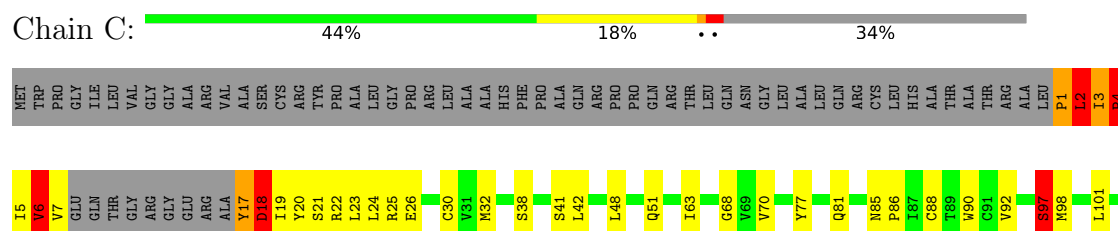
- Molecule 1: Putative ATP-dependent Clp protease proteolytic subunit

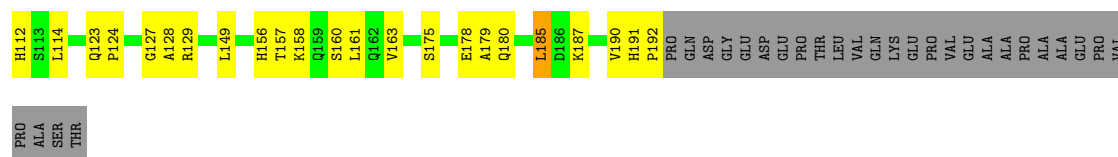


- Molecule 1: Putative ATP-dependent Clp protease proteolytic subunit



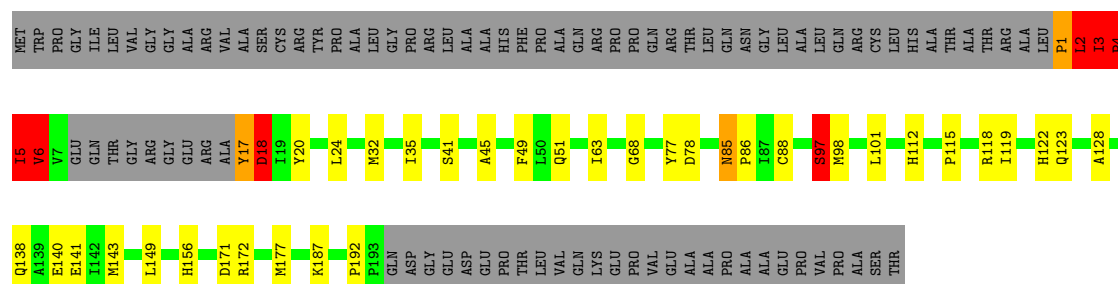
- Molecule 1: Putative ATP-dependent Clp protease proteolytic subunit





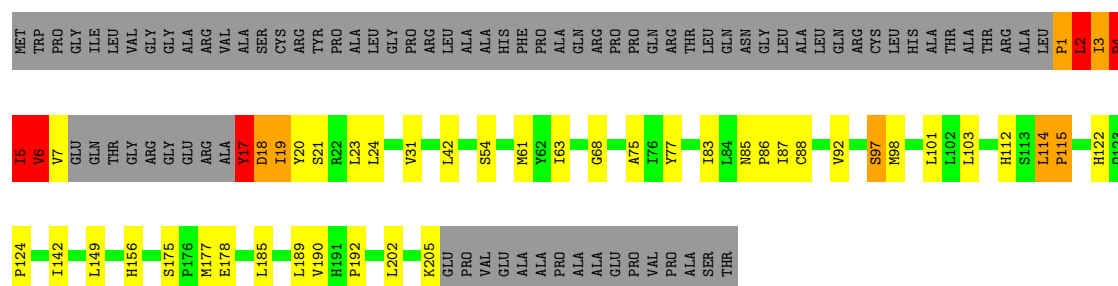
- Molecule 1: Putative ATP-dependent Clp protease proteolytic subunit

Chain D: 51% 12% 34%



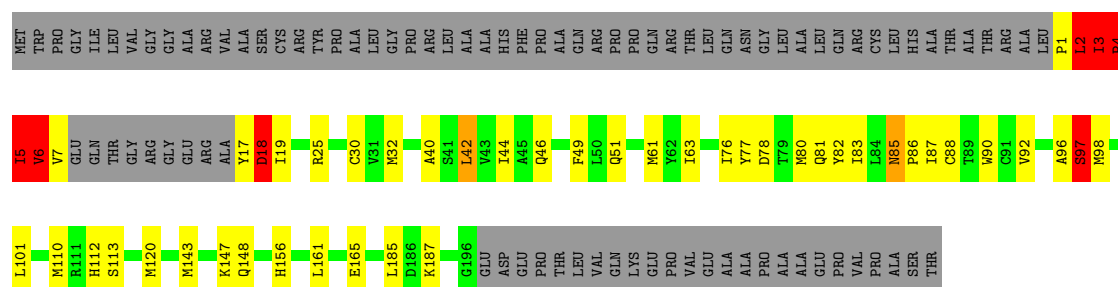
- Molecule 1: Putative ATP-dependent Clp protease proteolytic subunit

Chain E: 53% 13% 29%



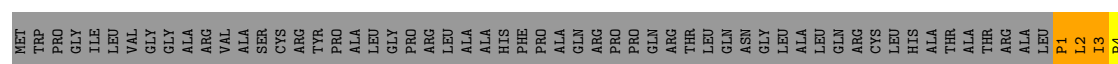
- Molecule 1: Putative ATP-dependent Clp protease proteolytic subunit

Chain F: 49% 15% 32%



- Molecule 1: Putative ATP-dependent Clp protease proteolytic subunit

Chain G: 49% 18% 30%



I5	V6	V7	GLU	GLN	THR	GLY	GLY	ARG	GLY	GLU	ARG	ALA	Y17	D18	I19	Y20	S21	R22	L23	L24	I28	M32	L42	Q46	L47	L48	Q51	S54	N55	K56	K57	Y62	I63	G68	V69	V70	A75	I76	Y77	I83	L84	N85	P86	I87	C88	A95	A96	S97	M98
G99	S100	L101	H112	S113	L114	R118	I119	M120	I121	H122	M143	L149	Y150	N151	H156	L161	D171	R172	S175	E178	K187	V188	L189	V190	H191	P192	L202	V203	GLN	LYS	GLU	PRO	VAL	GLU	ALA	ALA	PRO	ALA	ALA	GLU	PRO	VAL	PRO	ALA	SER	THR			

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.57Å 119.00Å 118.65Å 90.00° 130.16° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.224 , 0.262	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11064	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FME, EDO, GOL, DIO

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	0.74	3/1447 (0.2%)	1.30	18/1959 (0.9%)
1	B	0.77	4/1439 (0.3%)	1.26	18/1947 (0.9%)
1	C	0.54	2/1439 (0.1%)	1.17	19/1947 (1.0%)
1	D	0.76	6/1447 (0.4%)	1.40	26/1959 (1.3%)
1	E	0.92	9/1542 (0.6%)	1.36	24/2088 (1.1%)
1	F	1.62	10/1468 (0.7%)	1.61	26/1987 (1.3%)
1	G	0.77	2/1524 (0.1%)	1.10	12/2065 (0.6%)
All	All	0.93	36/10306 (0.3%)	1.32	143/13952 (1.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	E	0	2
1	F	0	3
1	G	0	3
All	All	0	10

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	6	VAL	C-N	-50.66	0.62	1.33
1	F	7	VAL	N-CA	-24.70	0.99	1.46
1	G	6	VAL	C-N	-21.47	1.03	1.33
1	B	17	TYR	C-N	18.38	1.60	1.33
1	E	17	TYR	C-N	16.47	1.56	1.33

The worst 5 of 143 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	6	VAL	O-C-N	-36.90	76.45	122.57
1	E	6	VAL	O-C-N	-19.73	97.90	122.57
1	D	6	VAL	O-C-N	18.79	146.06	122.57
1	A	6	VAL	CA-C-N	-18.37	88.64	121.70
1	A	6	VAL	C-N-CA	-18.37	88.64	121.70

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	6	VAL	Mainchain
1	B	6	VAL	Mainchain
1	E	17	TYR	Peptide
1	E	6	VAL	Mainchain
1	F	2	LEU	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	1420	0	1465	52	0
1	B	1413	0	1458	61	0
1	C	1413	0	1458	67	0
1	D	1420	0	1464	72	0
1	E	1514	0	1551	53	0
1	F	1441	0	1479	73	0
1	G	1496	0	1529	109	0
2	A	6	0	8	1	0
2	B	6	0	8	2	0
2	D	6	0	8	1	0
2	E	6	0	8	2	0
2	F	6	0	8	1	0
2	G	6	0	8	0	0
3	A	4	0	5	1	0
3	B	8	0	10	2	0
3	C	8	0	10	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	4	0	5	0	0
3	F	4	0	5	0	0
3	G	4	0	5	0	0
4	B	12	0	8	3	0
4	C	6	0	4	0	0
4	D	6	0	4	2	0
4	E	6	0	4	0	0
4	F	6	0	4	1	0
5	D	70	0	70	56	0
6	A	77	0	0	3	0
6	B	90	0	0	4	0
6	C	109	0	0	2	0
6	D	128	0	0	7	0
6	E	132	0	0	1	0
6	F	126	0	0	3	0
6	G	111	0	0	6	0
All	All	11064	0	10586	427	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 20.

The worst 5 of 427 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:17:TYR:CG	1:G:5:ILE:HD11	1.27	1.66
1:G:5:ILE:HG22	1:G:17:TYR:CE2	1.37	1.58
1:F:17:TYR:CD2	1:G:5:ILE:HD11	1.04	1.55
1:F:17:TYR:CE2	1:G:5:ILE:CD1	1.91	1.51
1:F:17:TYR:CD2	1:G:5:ILE:CD1	1.90	1.49

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	180/277 (65%)	172 (96%)	4 (2%)	4 (2%)	5	2
1	B	179/277 (65%)	170 (95%)	5 (3%)	4 (2%)	5	2
1	C	179/277 (65%)	172 (96%)	5 (3%)	2 (1%)	11	8
1	D	180/277 (65%)	174 (97%)	2 (1%)	4 (2%)	5	2
1	E	192/277 (69%)	186 (97%)	5 (3%)	1 (0%)	24	22
1	F	183/277 (66%)	174 (95%)	6 (3%)	3 (2%)	7	4
1	G	190/277 (69%)	181 (95%)	8 (4%)	1 (0%)	24	22
All	All	1283/1939 (66%)	1229 (96%)	35 (3%)	19 (2%)	8	4

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	LEU
1	A	4	PRO
1	B	2	LEU
1	B	3	ILE
1	C	18	ASP

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	150/226 (66%)	148 (99%)	2 (1%)	61	69
1	B	156/226 (69%)	149 (96%)	7 (4%)	24	25
1	C	156/226 (69%)	146 (94%)	10 (6%)	16	14
1	D	157/226 (70%)	150 (96%)	7 (4%)	24	25
1	E	168/226 (74%)	161 (96%)	7 (4%)	26	28
1	F	159/226 (70%)	151 (95%)	8 (5%)	22	22
1	G	131/226 (58%)	124 (95%)	7 (5%)	20	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1077/1582 (68%)	1029 (96%)	48 (4%)	24	25

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	4	PRO
1	F	4	PRO
1	E	5	ILE
1	E	142	ILE
1	F	6	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	81	GLN
1	G	51	GLN
1	F	112	HIS
1	F	180	GLN
1	G	151	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

27 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
5	FME	D	1104	-	8,9,10	0.83	0	8,9,11	1.94	2 (25%)
5	FME	D	1106	-	8,9,10	1.09	2 (25%)	8,9,11	1.91	3 (37%)
2	DIO	A	800	-	6,6,6	1.76	1 (16%)	6,6,6	0.46	0
5	FME	D	1105	-	8,9,10	0.89	0	8,9,11	1.81	2 (25%)
5	FME	D	1103	-	8,9,10	0.94	0	8,9,11	1.84	2 (25%)
2	DIO	D	802	-	6,6,6	1.72	1 (16%)	6,6,6	0.46	0
4	GOL	B	1001	-	5,5,5	4.19	3 (60%)	5,5,5	5.90	2 (40%)
3	EDO	F	906	-	3,3,3	1.05	0	2,2,2	0.29	0
3	EDO	D	905	-	3,3,3	1.03	0	2,2,2	0.31	0
4	GOL	F	1005	-	5,5,5	3.95	3 (60%)	5,5,5	5.91	2 (40%)
3	EDO	A	900	-	3,3,3	1.04	0	2,2,2	0.34	0
3	EDO	C	904	-	3,3,3	0.98	0	2,2,2	0.28	0
3	EDO	G	907	-	3,3,3	1.01	0	2,2,2	0.29	0
2	DIO	B	801	-	6,6,6	1.73	1 (16%)	6,6,6	0.45	0
5	FME	D	1101	-	8,9,10	0.79	0	8,9,11	2.03	2 (25%)
3	EDO	B	901	-	3,3,3	1.00	0	2,2,2	0.33	0
4	GOL	E	1004	-	5,5,5	4.22	3 (60%)	5,5,5	5.94	2 (40%)
2	DIO	G	805	-	6,6,6	1.73	1 (16%)	6,6,6	0.43	0
4	GOL	C	1002	-	5,5,5	4.03	3 (60%)	5,5,5	5.90	2 (40%)
2	DIO	E	803	-	6,6,6	1.80	1 (16%)	6,6,6	0.44	0
3	EDO	B	902	-	3,3,3	1.03	0	2,2,2	0.34	0
3	EDO	C	903	-	3,3,3	1.04	0	2,2,2	0.34	0
4	GOL	B	1000	-	5,5,5	4.08	3 (60%)	5,5,5	5.89	2 (40%)
5	FME	D	1100	-	8,9,10	0.99	0	8,9,11	1.89	2 (25%)
4	GOL	D	1003	-	5,5,5	4.12	3 (60%)	5,5,5	5.90	2 (40%)
2	DIO	F	804	-	6,6,6	1.73	1 (16%)	6,6,6	0.45	0
5	FME	D	1102	-	8,9,10	1.06	1 (12%)	8,9,11	2.22	3 (37%)

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
5	FME	D	1104	-	-	1/7/9/11	-
5	FME	D	1106	-	-	2/7/9/11	-
2	DIO	A	800	-	-	-	0/1/1/1
5	FME	D	1105	-	-	2/7/9/11	-
5	FME	D	1103	-	-	2/7/9/11	-
2	DIO	D	802	-	-	-	0/1/1/1
4	GOL	B	1001	-	-	2/4/4/4	-
3	EDO	F	906	-	-	1/1/1/1	-
3	EDO	D	905	-	-	0/1/1/1	-
4	GOL	F	1005	-	-	2/4/4/4	-
3	EDO	A	900	-	-	0/1/1/1	-
3	EDO	C	904	-	-	0/1/1/1	-
3	EDO	G	907	-	-	0/1/1/1	-
5	FME	D	1101	-	-	2/7/9/11	-
2	DIO	B	801	-	-	-	0/1/1/1
3	EDO	B	901	-	-	0/1/1/1	-
4	GOL	E	1004	-	-	2/4/4/4	-
2	DIO	G	805	-	-	-	0/1/1/1
4	GOL	C	1002	-	-	2/4/4/4	-
2	DIO	E	803	-	-	-	0/1/1/1
3	EDO	B	902	-	-	0/1/1/1	-
3	EDO	C	903	-	-	0/1/1/1	-
4	GOL	B	1000	-	-	2/4/4/4	-
5	FME	D	1100	-	-	1/7/9/11	-
4	GOL	D	1003	-	-	2/4/4/4	-
2	DIO	F	804	-	-	-	0/1/1/1
5	FME	D	1102	-	-	2/7/9/11	-

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1004	GOL	C3-C2	-8.29	1.20	1.51
4	D	1003	GOL	C3-C2	-8.25	1.20	1.51
4	B	1001	GOL	C3-C2	-8.23	1.20	1.51
4	B	1000	GOL	C3-C2	-8.01	1.21	1.51
4	C	1002	GOL	C3-C2	-7.95	1.21	1.51

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1004	GOL	O3-C3-C2	11.20	160.82	110.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1003	GOL	O3-C3-C2	11.14	160.53	110.38
4	B	1001	GOL	O3-C3-C2	11.13	160.48	110.38
4	C	1002	GOL	O3-C3-C2	11.13	160.47	110.38
4	B	1000	GOL	O3-C3-C2	11.08	160.27	110.38

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1000	GOL	O1-C1-C2-O2
4	B	1000	GOL	C1-C2-C3-O3
4	B	1001	GOL	O1-C1-C2-O2
4	B	1001	GOL	C1-C2-C3-O3
4	C	1002	GOL	C1-C2-C3-O3

There are no ring outliers.

20 monomers are involved in 74 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	1104	FME	11	0
5	D	1106	FME	7	0
2	A	800	DIO	1	0
5	D	1105	FME	5	0
5	D	1103	FME	10	0
2	D	802	DIO	1	0
4	B	1001	GOL	2	0
4	F	1005	GOL	1	0
3	A	900	EDO	1	0
2	B	801	DIO	2	0
5	D	1101	FME	10	0
3	B	901	EDO	1	0
2	E	803	DIO	2	0
3	B	902	EDO	1	0
3	C	903	EDO	2	0
4	B	1000	GOL	1	0
5	D	1100	FME	5	0
4	D	1003	GOL	2	0
2	F	804	DIO	1	0
5	D	1102	FME	8	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	E	1
1	G	1
1	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	6:VAL	C	7:VAL	N	1.15
1	G	6:VAL	C	7:VAL	N	1.03
1	F	6:VAL	C	7:VAL	N	0.62

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.