



wwPDB X-ray Structure Validation Summary Report

Mar 6, 2026 – 10:45 PM UTC


PDB ID : 1A2V / pdb_00001a2v
Title : COPPER AMINE OXIDASE FROM HANSENULA POLYMORPHA
Authors : Li, R.; Mathews, F.S.
Deposited on : 1998-01-12
Resolution : 2.40 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)
Xtrriage (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

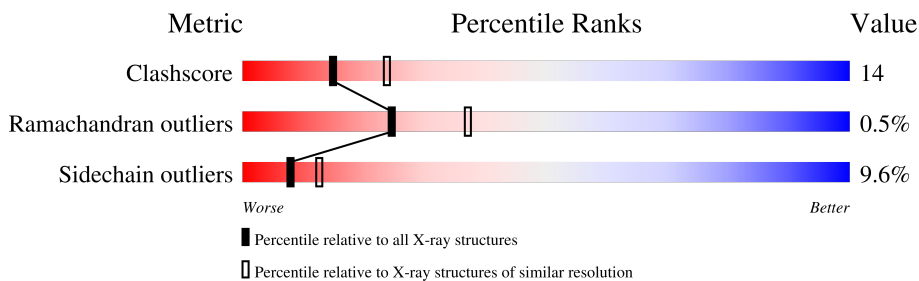
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	655	
1	B	655	
1	C	655	
1	D	655	
1	E	655	
1	F	655	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 33726 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 METHYLAMINE OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	655	5194	3305	892	974	23	0	0	0
1	B	655	5194	3305	892	974	23	0	0	0
1	C	655	5194	3305	892	974	23	0	0	0
1	D	655	5194	3305	892	974	23	0	0	0
1	E	655	5194	3305	892	974	23	0	0	0
1	F	655	5194	3305	892	974	23	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	405	TPQ	TYR	modified residue	UNP P12807
B	405	TPQ	TYR	modified residue	UNP P12807
C	405	TPQ	TYR	modified residue	UNP P12807
D	405	TPQ	TYR	modified residue	UNP P12807
E	405	TPQ	TYR	modified residue	UNP P12807
F	405	TPQ	TYR	modified residue	UNP P12807

- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Cu 1	0	0
2	B	1	Total 1	Cu 1	0	0
2	C	1	Total 1	Cu 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Cu 1 1	0	0
2	E	1	Total Cu 1 1	0	0
2	F	1	Total Cu 1 1	0	0

- Molecule 3 is water.

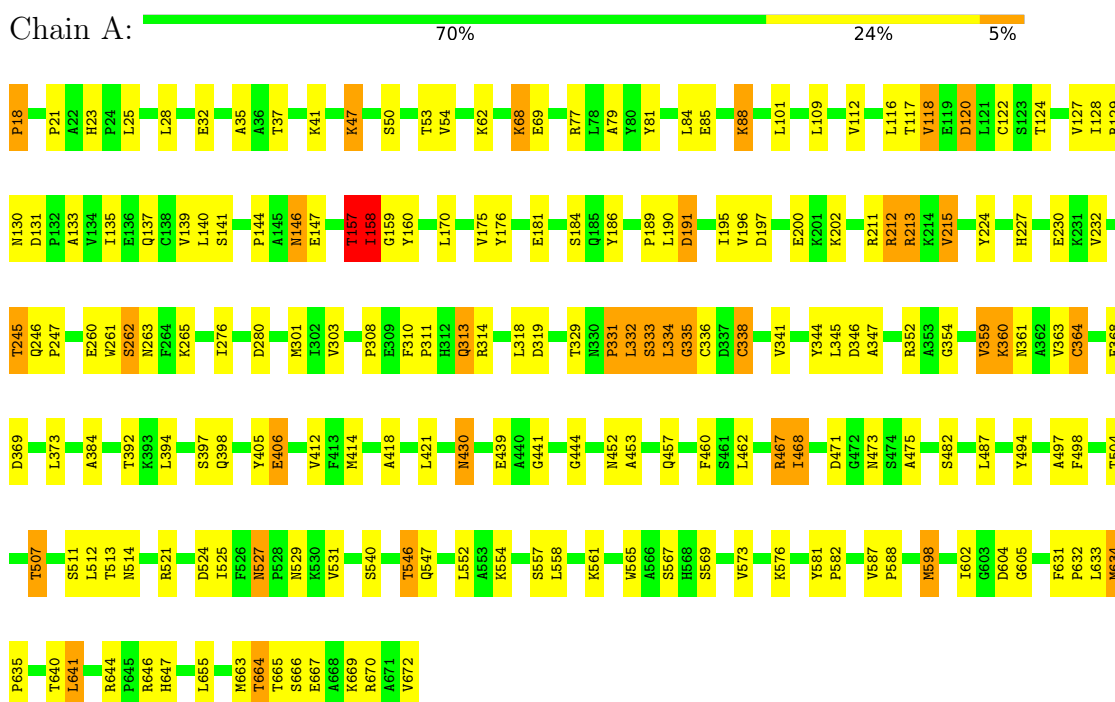
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	499	Total O 499 499	0	0
3	B	453	Total O 453 453	0	0
3	C	474	Total O 474 474	0	0
3	D	415	Total O 415 415	0	0
3	E	335	Total O 335 335	0	0
3	F	380	Total O 380 380	0	0

3 Residue-property plots

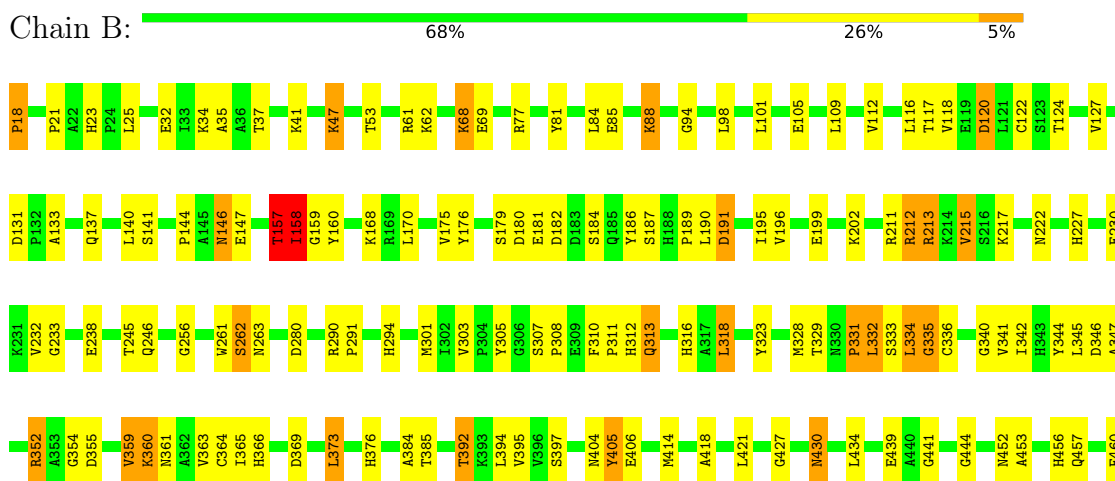
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

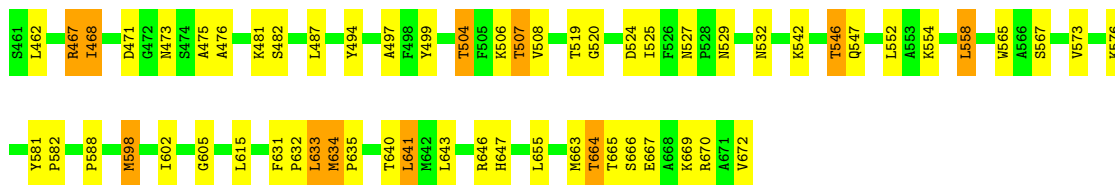
Note EDS was not executed.

- Molecule 1: METHYLAMINE OXIDASE

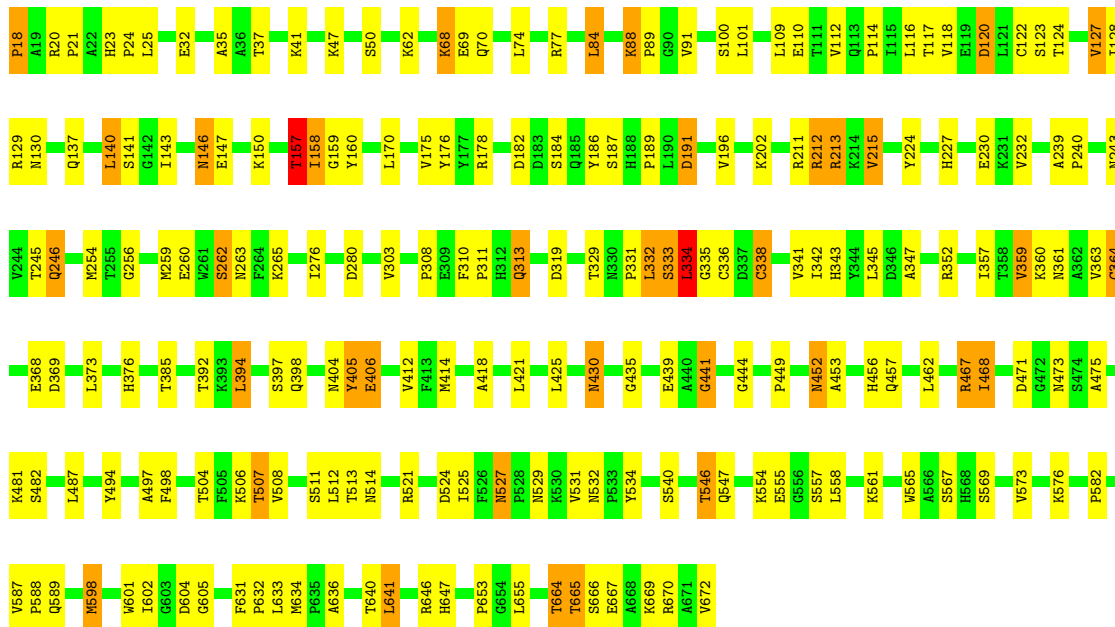


- Molecule 1: METHYLAMINE OXIDASE

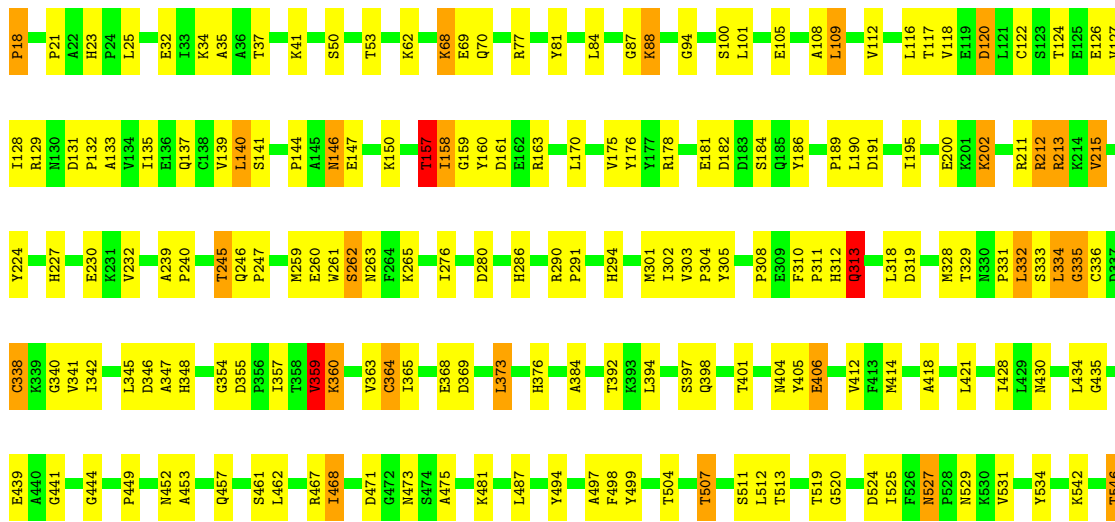


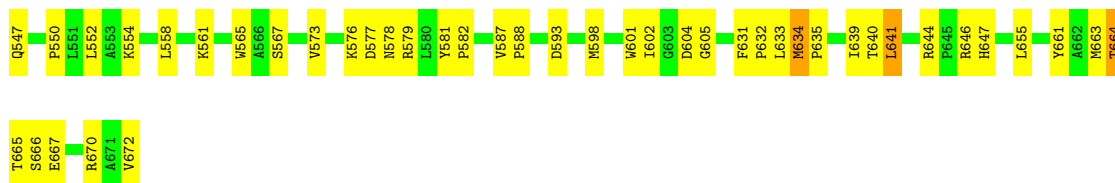


• Molecule 1: METHYLAMINE OXIDASE



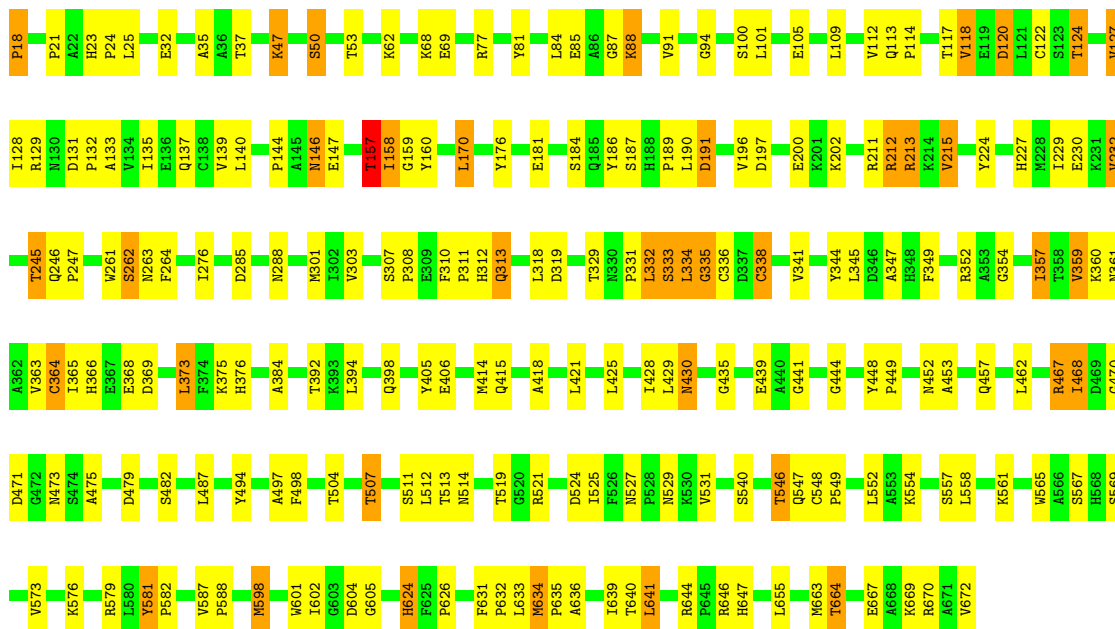
• Molecule 1: METHYLAMINE OXIDASE





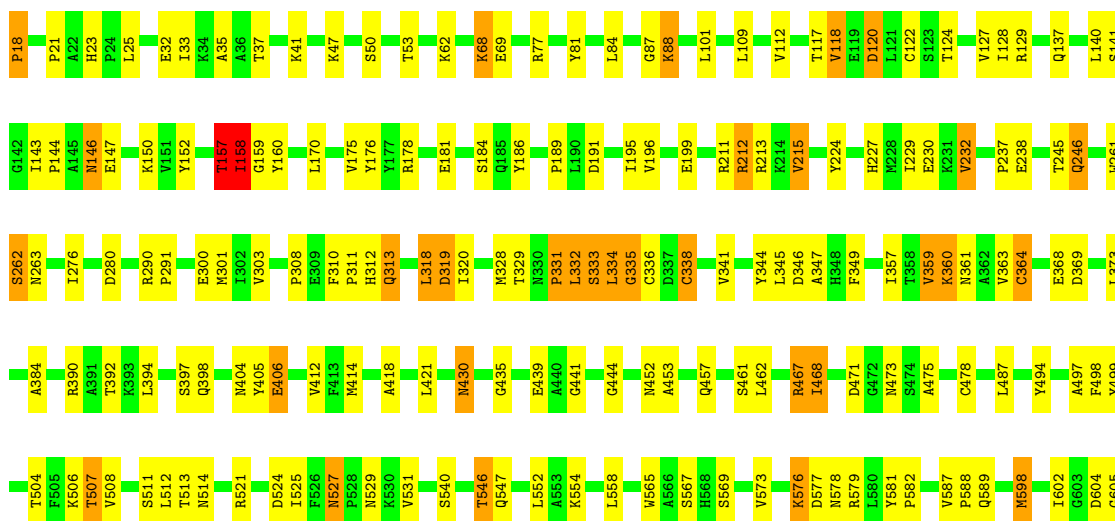
• Molecule 1: METHYLAMINE OXIDASE

Chain E: 67% 27% 6%



• Molecule 1: METHYLAMINE OXIDASE

Chain F: 69% 25% 5%



F631	T640	R644	L655	S660	T664	K669
P632	L641	P645	L656	S661	T665	R670
L633	L642	R646	L657	S662	S666	A671
M634	L643	R647	L658	S663	E667	V672
P635	L644	R648	L659	S664	A668	

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	138.77Å 148.22Å 234.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.40	Depositor
% Data completeness (in resolution range)	83.6 (100.00-2.40)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.184 , 0.224	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	33726	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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: CU, TPQ

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	0.61	1/5329 (0.0%)	1.06	29/7251 (0.4%)
1	B	0.66	2/5329 (0.0%)	1.10	32/7251 (0.4%)
1	C	0.67	3/5329 (0.1%)	1.10	32/7251 (0.4%)
1	D	0.64	1/5329 (0.0%)	1.09	29/7251 (0.4%)
1	E	0.63	2/5329 (0.0%)	1.08	32/7251 (0.4%)
1	F	0.64	2/5329 (0.0%)	1.10	28/7251 (0.4%)
All	All	0.64	11/31974 (0.0%)	1.09	182/43506 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	598	MET	SD-CE	-8.45	1.58	1.79
1	C	598	MET	SD-CE	-7.04	1.61	1.79
1	E	634	MET	SD-CE	7.04	1.97	1.79
1	A	598	MET	SD-CE	-6.46	1.63	1.79
1	F	598	MET	SD-CE	-6.18	1.64	1.79

The worst 5 of 182 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	332	LEU	N-CA-C	10.20	123.65	111.82
1	A	332	LEU	N-CA-C	9.73	123.10	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	332	LEU	N-CA-C	9.63	122.99	111.82
1	D	332	LEU	N-CA-C	9.58	122.93	111.82
1	E	332	LEU	N-CA-C	9.30	122.61	111.82

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	305	TYR	Sidechain

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	5194	0	5033	136	0
1	B	5194	0	5034	148	0
1	C	5194	0	5034	139	0
1	D	5194	0	5033	165	0
1	E	5194	0	5033	155	0
1	F	5194	0	5033	144	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	499	0	0	7	0
3	B	453	0	0	6	0
3	C	474	0	0	5	0
3	D	415	0	0	9	0
3	E	335	0	0	5	0
3	F	380	0	0	7	0
All	All	33726	0	30200	838	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 14.

The worst 5 of 838 close contacts within the same asymmetric unit are listed below, sorted by

their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:546:THR:CG2	1:D:546:THR:HG21	1.57	1.32
1:A:546:THR:HG21	1:B:546:THR:CG2	1.64	1.27
1:E:546:THR:CG2	1:F:546:THR:HG21	1.64	1.26
1:A:546:THR:CG2	1:B:546:THR:HG21	1.67	1.24
1:C:546:THR:HG21	1:D:546:THR:CG2	1.69	1.22

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	652/655 (100%)	616 (94%)	33 (5%)	3 (0%)	24	37
1	B	652/655 (100%)	616 (94%)	34 (5%)	2 (0%)	36	50
1	C	652/655 (100%)	616 (94%)	32 (5%)	4 (1%)	21	32
1	D	652/655 (100%)	617 (95%)	32 (5%)	3 (0%)	24	37
1	E	652/655 (100%)	619 (95%)	30 (5%)	3 (0%)	24	37
1	F	652/655 (100%)	613 (94%)	36 (6%)	3 (0%)	24	37
All	All	3912/3930 (100%)	3697 (94%)	197 (5%)	18 (0%)	24	37

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	512	LEU
1	E	468	ILE
1	E	512	LEU
1	A	512	LEU
1	D	333	SER

5.3.2 Protein sidechains [i](#)

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	565/565 (100%)	511 (90%)	54 (10%)	8	12
1	B	565/565 (100%)	510 (90%)	55 (10%)	8	12
1	C	565/565 (100%)	509 (90%)	56 (10%)	7	11
1	D	565/565 (100%)	512 (91%)	53 (9%)	8	13
1	E	565/565 (100%)	509 (90%)	56 (10%)	7	11
1	F	565/565 (100%)	512 (91%)	53 (9%)	8	13
All	All	3390/3390 (100%)	3063 (90%)	327 (10%)	8	12

5 of 327 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	146	ASN
1	F	146	ASN
1	E	215	VAL
1	E	467	ARG
1	F	334	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 125 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	578	ASN
1	F	243	ASN
1	D	330	ASN
1	F	149	HIS
1	F	450	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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
1	TPQ	D	405	1	13,14,15	2.71	7 (53%)	13,19,21	1.03	1 (7%)
1	TPQ	E	405	1	13,14,15	2.41	6 (46%)	13,19,21	0.90	0
1	TPQ	F	405	1	13,14,15	2.65	4 (30%)	13,19,21	1.01	0
1	TPQ	B	405	1	13,14,15	2.59	5 (38%)	13,19,21	0.94	0
1	TPQ	C	405	1	13,14,15	2.59	7 (53%)	13,19,21	1.00	0
1	TPQ	A	405	1	13,14,15	2.53	6 (46%)	13,19,21	0.92	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
1	TPQ	D	405	1	-	4/5/22/24	0/1/1/1
1	TPQ	E	405	1	-	4/5/22/24	0/1/1/1
1	TPQ	F	405	1	-	4/5/22/24	0/1/1/1
1	TPQ	B	405	1	-	3/5/22/24	0/1/1/1
1	TPQ	C	405	1	-	4/5/22/24	0/1/1/1
1	TPQ	A	405	1	-	4/5/22/24	0/1/1/1

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	405	TPQ	C1-C2	-7.27	1.39	1.49
1	D	405	TPQ	C1-C2	-7.01	1.39	1.49
1	C	405	TPQ	C1-C2	-6.91	1.39	1.49
1	F	405	TPQ	C1-C2	-6.85	1.39	1.49
1	A	405	TPQ	C1-C2	-6.81	1.39	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	405	TPQ	C6-C1-C2	2.17	120.20	118.66

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	405	TPQ	N-CA-CB-C1
1	A	405	TPQ	C-CA-CB-C1
1	B	405	TPQ	N-CA-CB-C1
1	B	405	TPQ	C-CA-CB-C1
1	C	405	TPQ	N-CA-CB-C1

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	405	TPQ	1	0
1	C	405	TPQ	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

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.