



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 05:58 am GMT

PDB ID : 2O7D
Title : Tyrosine ammonia-lyase from Rhodobacter sphaeroides, complexed with caffeine
Authors : Louie, G.V.; Bowman, M.E.; Moffitt, M.C.; Baiga, T.J.; Moore, B.S.; Noel, J.P.
Deposited on : 2006-12-10
Resolution : 1.90 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

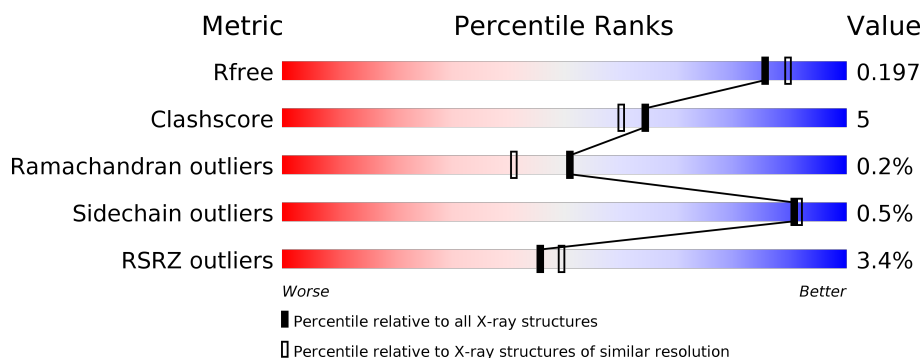
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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.



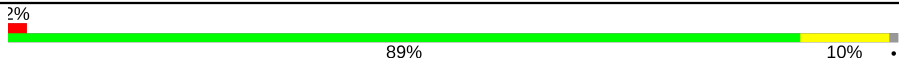

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	521	<div> <div>4%</div> <div>89%</div> <div>10%</div> </div>
1	B	521	<div> <div>2%</div> <div>85%</div> <div>14%</div> </div>
1	C	521	<div> <div>2%</div> <div>88%</div> <div>10%</div> </div>
1	D	521	<div> <div>5%</div> <div>86%</div> <div>12%</div> </div>
1	E	521	<div> <div>3%</div> <div>90%</div> <div>9%</div> </div>
1	F	521	<div> <div>2%</div> <div>89%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	521	
1	H	521	

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	DHC	A	701	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 33789 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 histidine ammonia-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	515	Total	C	N	O	S	0	0	0
			3813	2363	731	705	14			
1	B	515	Total	C	N	O	S	0	0	0
			3813	2363	731	705	14			
1	C	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			
1	D	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			
1	E	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			
1	F	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			
1	G	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			
1	H	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			

There are 24 discrepancies between the modelled and reference sequences:

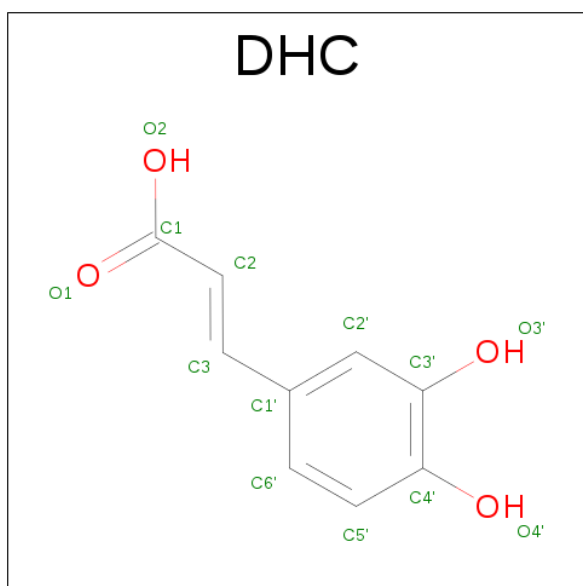
Chain	Residue	Modelled	Actual	Comment	Reference
A	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
A	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
A	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
B	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
B	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
B	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
C	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
C	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
C	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
D	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
D	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
D	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
E	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
E	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
F	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
F	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
F	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
G	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
G	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
G	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
H	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
H	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
H	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0

- Molecule 2 is CAFFEIC ACID (three-letter code: DHC) (formula: $C_9H_8O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	9	4		
2	B	1	Total	C	O	0	0
			13	9	4		
2	C	1	Total	C	O	0	0
			13	9	4		
2	D	1	Total	C	O	0	0
			13	9	4		
2	E	1	Total	C	O	0	0
			13	9	4		
2	F	1	Total	C	O	0	0
			13	9	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	G	1	Total	C	O	0	0
			13	9	4		
2	H	1	Total	C	O	0	0
			13	9	4		

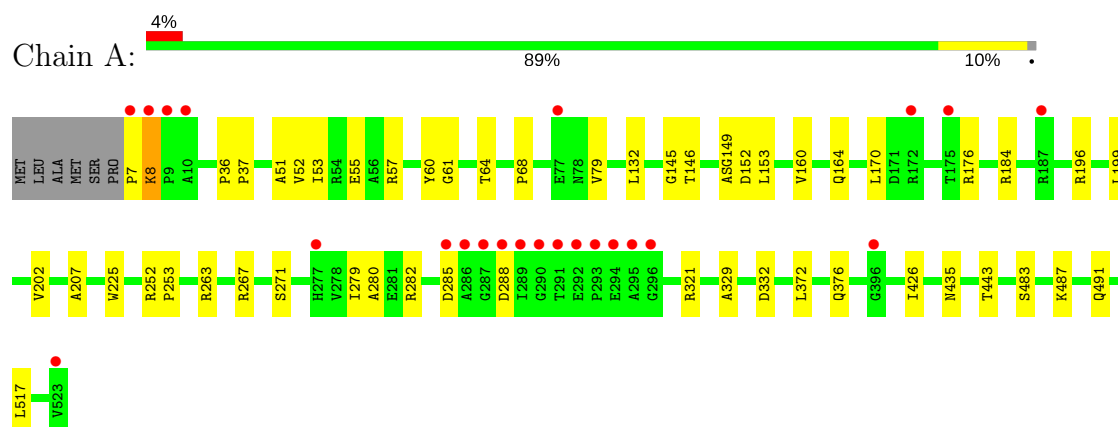
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	360	Total	O	0	0
			360	360		
3	B	369	Total	O	0	0
			369	369		
3	C	407	Total	O	0	0
			407	407		
3	D	404	Total	O	0	0
			404	404		
3	E	382	Total	O	0	0
			382	382		
3	F	491	Total	O	0	0
			491	491		
3	G	431	Total	O	0	0
			431	431		
3	H	379	Total	O	0	0
			379	379		

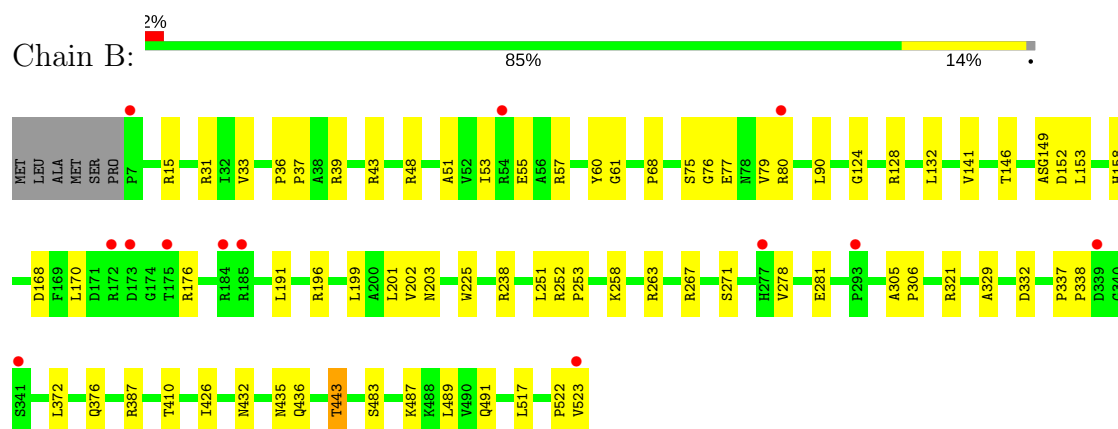
3 Residue-property plots [i](#)

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

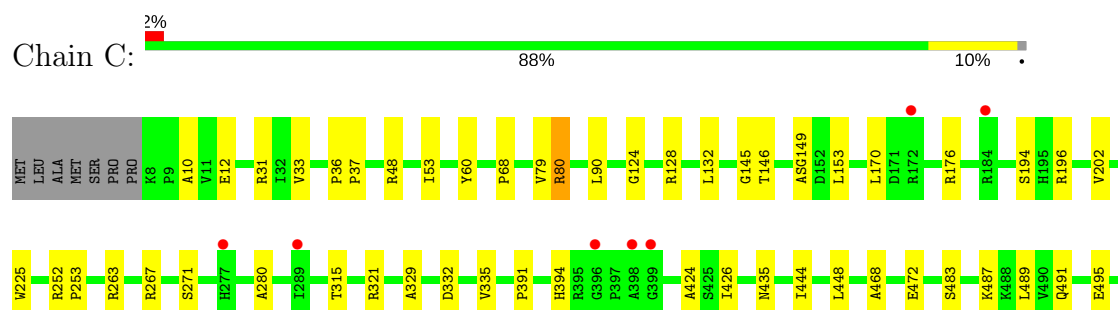
• Molecule 1: Putative histidine ammonia-lyase

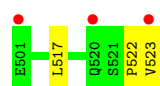


• Molecule 1: Putative histidine ammonia-lyase

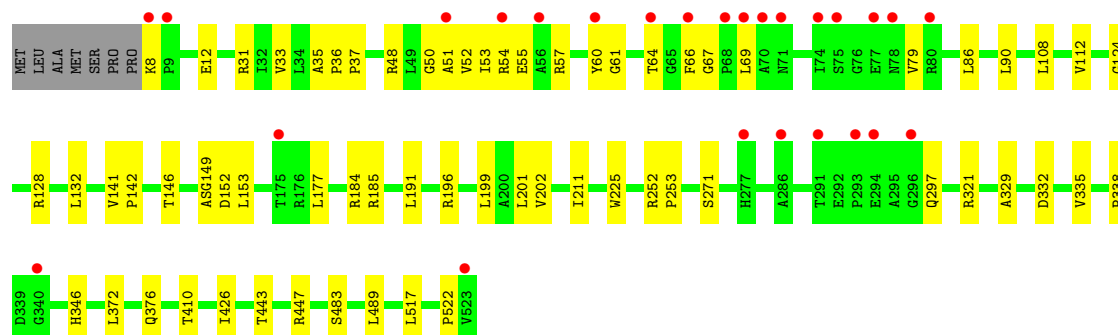
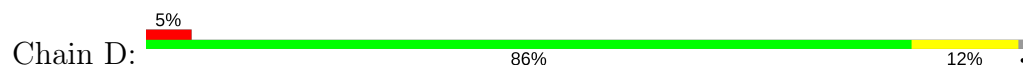


• Molecule 1: Putative histidine ammonia-lyase

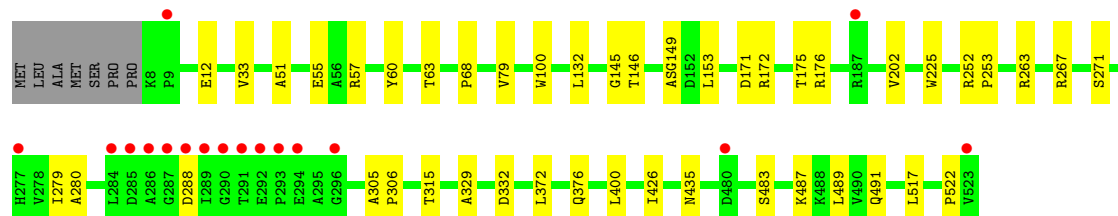
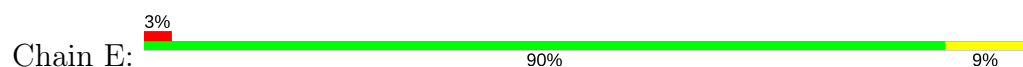




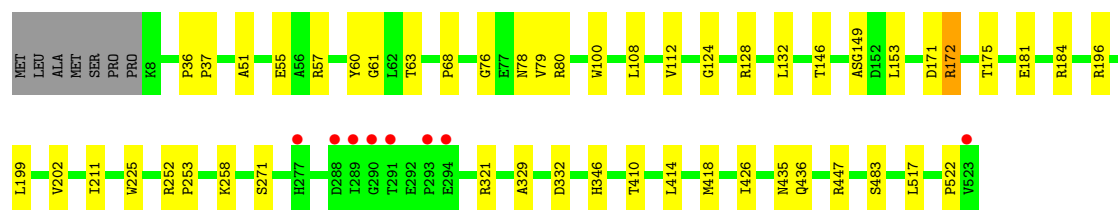
• Molecule 1: Putative histidine ammonia-lyase



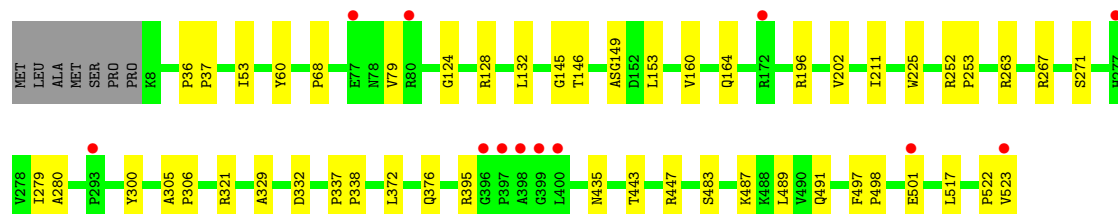
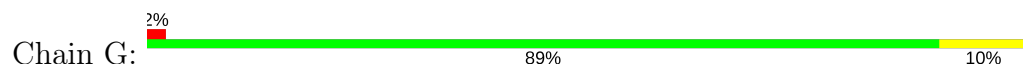
• Molecule 1: Putative histidine ammonia-lyase



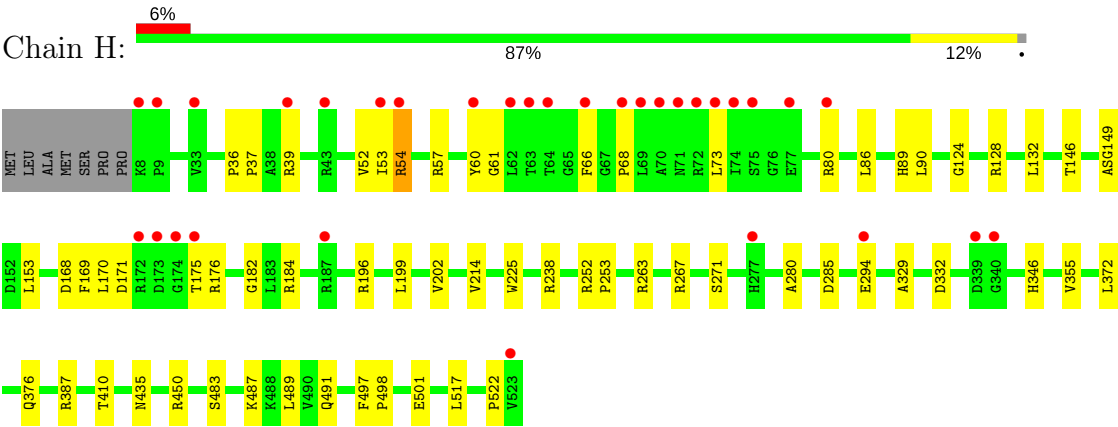
• Molecule 1: Putative histidine ammonia-lyase



• Molecule 1: Putative histidine ammonia-lyase



● Molecule 1: Putative histidine ammonia-lyase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.61Å 154.90Å 164.16Å 90.00° 94.06° 90.00°	Depositor
Resolution (Å)	500.00 – 1.90 37.68 – 1.85	Depositor EDS
% Data completeness (in resolution range)	98.9 (500.00-1.90) 98.6 (37.68-1.85)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 1.85Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.175 , 0.198 0.175 , 0.197	Depositor DCC
R_{free} test set	17030 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.233	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	33789	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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: DHC, MDO

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	0.27	0/3862	0.55	0/5253
1	B	0.28	0/3862	0.55	0/5253
1	C	0.28	0/3854	0.56	0/5242
1	D	0.28	0/3854	0.56	0/5242
1	E	0.28	0/3854	0.56	0/5242
1	F	0.29	0/3854	0.57	0/5242
1	G	0.29	0/3854	0.57	0/5242
1	H	0.27	0/3854	0.54	0/5242
All	All	0.28	0/30848	0.56	0/41958

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	2
1	B	0	2
1	C	0	2
1	D	0	2
1	E	0	2
1	F	0	2
1	G	0	2
1	H	0	2
All	All	0	16

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	149	MDO	Mainchain,Peptide
1	B	149	MDO	Mainchain,Peptide
1	C	149	MDO	Mainchain,Peptide
1	D	149	MDO	Mainchain,Peptide
1	E	149	MDO	Mainchain

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	3813	0	3864	34	0
1	B	3813	0	3864	49	0
1	C	3806	0	3856	42	0
1	D	3806	0	3856	45	0
1	E	3806	0	3856	32	0
1	F	3806	0	3856	37	0
1	G	3806	0	3856	31	0
1	H	3806	0	3856	53	0
2	A	13	0	7	0	0
2	B	13	0	7	1	0
2	C	13	0	6	1	0
2	D	13	0	5	1	0
2	E	13	0	6	1	0
2	F	13	0	6	1	0
2	G	13	0	6	1	0
2	H	13	0	6	1	0
3	A	360	0	0	3	0
3	B	369	0	0	5	0
3	C	407	0	0	5	0
3	D	404	0	0	6	0
3	E	382	0	0	5	0
3	F	491	0	0	4	0
3	G	431	0	0	2	0
3	H	379	0	0	5	0
All	All	33789	0	30913	293	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 5.

The worst 5 of 293 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:153:LEU:HD22	1:F:202:VAL:HG12	1.63	0.80
1:D:153:LEU:HD22	1:D:202:VAL:HG12	1.64	0.79
1:E:487:LYS:O	1:E:491:GLN:HG3	1.83	0.78
1:B:153:LEU:HD22	1:B:202:VAL:HG12	1.70	0.74
1:B:487:LYS:O	1:B:491:GLN:HG3	1.87	0.74

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	512/521 (98%)	501 (98%)	9 (2%)	2 (0%)	38	26
1	B	512/521 (98%)	505 (99%)	6 (1%)	1 (0%)	51	41
1	C	511/521 (98%)	505 (99%)	5 (1%)	1 (0%)	51	41
1	D	511/521 (98%)	501 (98%)	9 (2%)	1 (0%)	51	41
1	E	511/521 (98%)	503 (98%)	7 (1%)	1 (0%)	51	41
1	F	511/521 (98%)	504 (99%)	6 (1%)	1 (0%)	51	41
1	G	511/521 (98%)	504 (99%)	6 (1%)	1 (0%)	51	41
1	H	511/521 (98%)	501 (98%)	9 (2%)	1 (0%)	51	41
All	All	4090/4168 (98%)	4024 (98%)	57 (1%)	9 (0%)	51	41

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	253	PRO
1	F	253	PRO
1	A	8	LYS
1	C	253	PRO

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Mol	Chain	Res	Type
1	D	253	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	384/389 (99%)	383 (100%)	1 (0%)	94	94
1	B	384/389 (99%)	381 (99%)	3 (1%)	85	85
1	C	383/389 (98%)	381 (100%)	2 (0%)	91	91
1	D	383/389 (98%)	382 (100%)	1 (0%)	94	94
1	E	383/389 (98%)	382 (100%)	1 (0%)	94	94
1	F	383/389 (98%)	381 (100%)	2 (0%)	91	91
1	G	383/389 (98%)	381 (100%)	2 (0%)	91	91
1	H	383/389 (98%)	381 (100%)	2 (0%)	91	91
All	All	3066/3112 (98%)	3052 (100%)	14 (0%)	91	91

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	332	ASP
1	E	332	ASP
1	G	443	THR
1	C	332	ASP
1	G	332	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	491	GLN
1	D	516	HIS
1	F	491	GLN
1	D	394	HIS

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Mol	Chain	Res	Type
1	G	394	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 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	MDO	A	149	1	12,13,14	2.17	4 (33%)	12,18,20	4.63	5 (41%)
1	MDO	B	149	1	12,13,14	2.22	4 (33%)	12,18,20	4.51	5 (41%)
1	MDO	C	149	1	12,13,14	2.20	4 (33%)	12,18,20	4.39	5 (41%)
1	MDO	D	149	1	12,13,14	2.22	4 (33%)	12,18,20	4.47	5 (41%)
1	MDO	E	149	1	12,13,14	2.16	4 (33%)	12,18,20	4.51	5 (41%)
1	MDO	F	149	1	12,13,14	2.19	4 (33%)	12,18,20	4.51	5 (41%)
1	MDO	G	149	1	12,13,14	2.16	4 (33%)	12,18,20	4.57	5 (41%)
1	MDO	H	149	1	12,13,14	2.20	3 (25%)	12,18,20	4.53	5 (41%)

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	MDO	A	149	1	-	0/4/23/24	0/1/1/1
1	MDO	B	149	1	-	0/4/23/24	0/1/1/1
1	MDO	C	149	1	-	0/4/23/24	0/1/1/1
1	MDO	D	149	1	-	0/4/23/24	0/1/1/1
1	MDO	E	149	1	-	0/4/23/24	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MDO	F	149	1	-	0/4/23/24	0/1/1/1
1	MDO	G	149	1	-	0/4/23/24	0/1/1/1
1	MDO	H	149	1	-	0/4/23/24	0/1/1/1

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	149	MDO	C2-N3	-3.57	1.31	1.39
1	B	149	MDO	C2-N3	-3.50	1.31	1.39
1	E	149	MDO	C2-N3	-3.48	1.31	1.39
1	A	149	MDO	C2-N3	-3.37	1.31	1.39
1	F	149	MDO	C2-N3	-3.36	1.31	1.39

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	149	MDO	O2-C2-CA2	-5.50	128.01	130.97
1	F	149	MDO	O2-C2-CA2	-5.46	128.03	130.97
1	G	149	MDO	O2-C2-CA2	-5.45	128.03	130.97
1	D	149	MDO	O2-C2-CA2	-5.24	128.15	130.97
1	A	149	MDO	O2-C2-CA2	-5.18	128.18	130.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 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	DHC	A	701	-	10,13,13	2.70	5 (50%)	13,17,17	0.75	0
2	DHC	B	701	-	10,13,13	2.77	5 (50%)	13,17,17	0.80	0
2	DHC	C	701	-	10,13,13	2.73	6 (60%)	13,17,17	0.85	0
2	DHC	D	701	-	10,13,13	2.85	6 (60%)	13,17,17	0.71	0
2	DHC	E	701	-	10,13,13	2.78	6 (60%)	13,17,17	0.72	0
2	DHC	F	701	-	10,13,13	2.79	6 (60%)	13,17,17	0.83	0
2	DHC	G	701	-	10,13,13	2.72	6 (60%)	13,17,17	0.74	0
2	DHC	H	701	-	10,13,13	2.73	6 (60%)	13,17,17	0.76	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
2	DHC	A	701	-	-	0/3/5/5	0/1/1/1
2	DHC	B	701	-	-	0/3/5/5	0/1/1/1
2	DHC	C	701	-	-	0/3/5/5	0/1/1/1
2	DHC	D	701	-	-	0/3/5/5	0/1/1/1
2	DHC	E	701	-	-	0/3/5/5	0/1/1/1
2	DHC	F	701	-	-	0/3/5/5	0/1/1/1
2	DHC	G	701	-	-	0/3/5/5	0/1/1/1
2	DHC	H	701	-	-	0/3/5/5	0/1/1/1

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	701	DHC	C4'-C3'	2.02	1.43	1.40
2	F	701	DHC	C4'-C3'	2.12	1.43	1.40
2	C	701	DHC	C4'-C3'	2.18	1.43	1.40
2	G	701	DHC	C5'-C4'	2.18	1.43	1.39
2	D	701	DHC	C4'-C3'	2.27	1.43	1.40

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	DHC	1	0
2	C	701	DHC	1	0
2	D	701	DHC	1	0
2	E	701	DHC	1	0
2	F	701	DHC	1	0
2	G	701	DHC	1	0
2	H	701	DHC	1	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 [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	514/521 (98%)	0.12	23 (4%) 34 37	10, 20, 41, 61	0
1	B	514/521 (98%)	0.01	13 (2%) 58 62	10, 20, 38, 53	0
1	C	513/521 (98%)	0.01	10 (1%) 67 70	9, 18, 35, 48	0
1	D	513/521 (98%)	0.03	26 (5%) 29 32	8, 18, 41, 55	0
1	E	513/521 (98%)	0.03	17 (3%) 47 50	9, 18, 37, 66	0
1	F	513/521 (98%)	-0.17	8 (1%) 72 75	8, 15, 32, 46	0
1	G	513/521 (98%)	-0.05	12 (2%) 61 64	7, 17, 33, 47	0
1	H	513/521 (98%)	0.21	32 (6%) 21 24	9, 20, 43, 59	0
All	All	4106/4168 (98%)	0.02	141 (3%) 46 49	7, 18, 38, 66	0

The worst 5 of 141 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	74	ILE	10.5
1	H	74	ILE	9.7
1	E	293	PRO	9.2
1	A	286	ALA	8.9
1	E	288	ASP	8.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
1	MDO	E	149	13/14	0.92	0.15	-	13,17,22,23	0
1	MDO	F	149	13/14	0.91	0.16	-	15,19,23,27	0
1	MDO	C	149	13/14	0.91	0.17	-	13,15,20,25	0
1	MDO	A	149	13/14	0.94	0.16	-	14,19,21,24	0
1	MDO	B	149	13/14	0.89	0.15	-	19,22,27,28	0
1	MDO	H	149	13/14	0.83	0.17	-	19,23,29,30	0
1	MDO	D	149	13/14	0.92	0.16	-	18,21,29,29	0
1	MDO	G	149	13/14	0.91	0.19	-	14,17,21,22	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	DHC	A	701	13/13	0.86	0.23	3.96	34,42,46,48	0
2	DHC	E	701	13/13	0.87	0.14	1.81	24,30,34,34	0
2	DHC	G	701	13/13	0.90	0.15	1.47	24,28,36,39	0
2	DHC	B	701	13/13	0.85	0.15	1.44	27,31,37,40	0
2	DHC	D	701	13/13	0.83	0.19	1.43	34,39,44,47	0
2	DHC	C	701	13/13	0.90	0.14	1.24	21,26,33,36	0
2	DHC	H	701	13/13	0.80	0.20	1.20	33,40,49,53	0
2	DHC	F	701	13/13	0.92	0.11	0.47	24,28,32,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.