



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 17, 2017 – 07:22 PM EDT

PDB ID : 5TI9
Title : Crystal structure of human TDO in complex with Trp and dioxygen, Northeast Structural Genomics Consortium Target HR6161
Authors : Forouhar, F.; Lewis-Ballester, A.; Lew, S.; Karkashon, S.; Seetharaman, J.; Yeh, S.R.; Tong, L.
Deposited on : unknown
Resolution : 2.50 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 : rb-20029824
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) : rb-20029824

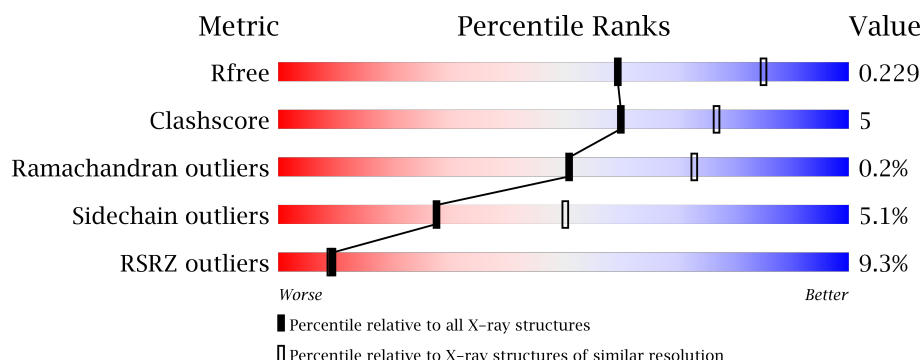
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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	380	<div> <div>9%</div> <div>80% 11% • 8%</div> </div>
1	B	380	<div> <div>6%</div> <div>75% 12% • 12%</div> </div>
1	C	380	<div> <div>13%</div> <div>68% 16% • 14%</div> </div>
1	D	380	<div> <div>6%</div> <div>74% 13% • 13%</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PO4	B	405	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12070 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 Tryptophan 2,3-dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	0	0
			2948	1891	518	528	11			
1	B	336	Total	C	N	O	S	0	0	0
			2814	1803	491	509	11			
1	C	326	Total	C	N	O	S	0	0	0
			2744	1768	480	486	10			
1	D	332	Total	C	N	O	S	0	0	0
			2818	1811	495	501	11			

There are 32 discrepancies between the modelled and reference sequences:

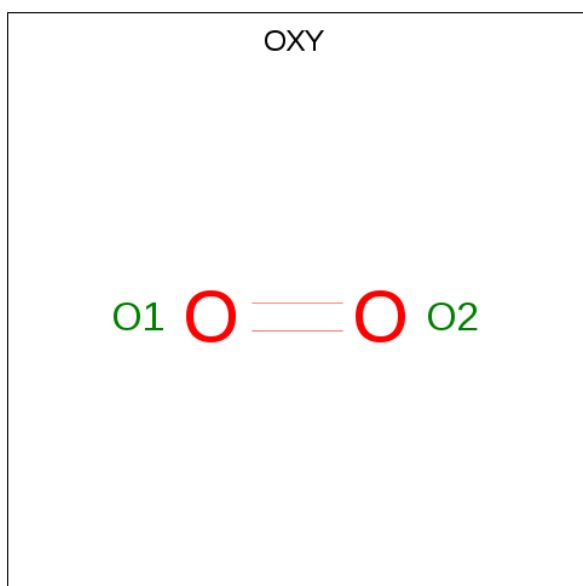
Chain	Residue	Modelled	Actual	Comment	Reference
A	17	MET	-	initiating methionine	UNP P48775
A	390	GLU	-	expression tag	UNP P48775
A	391	HIS	-	expression tag	UNP P48775
A	392	HIS	-	expression tag	UNP P48775
A	393	HIS	-	expression tag	UNP P48775
A	394	HIS	-	expression tag	UNP P48775
A	395	HIS	-	expression tag	UNP P48775
A	396	HIS	-	expression tag	UNP P48775
B	17	MET	-	initiating methionine	UNP P48775
B	390	GLU	-	expression tag	UNP P48775
B	391	HIS	-	expression tag	UNP P48775
B	392	HIS	-	expression tag	UNP P48775
B	393	HIS	-	expression tag	UNP P48775
B	394	HIS	-	expression tag	UNP P48775
B	395	HIS	-	expression tag	UNP P48775
B	396	HIS	-	expression tag	UNP P48775
C	17	MET	-	initiating methionine	UNP P48775
C	390	GLU	-	expression tag	UNP P48775
C	391	HIS	-	expression tag	UNP P48775
C	392	HIS	-	expression tag	UNP P48775
C	393	HIS	-	expression tag	UNP P48775

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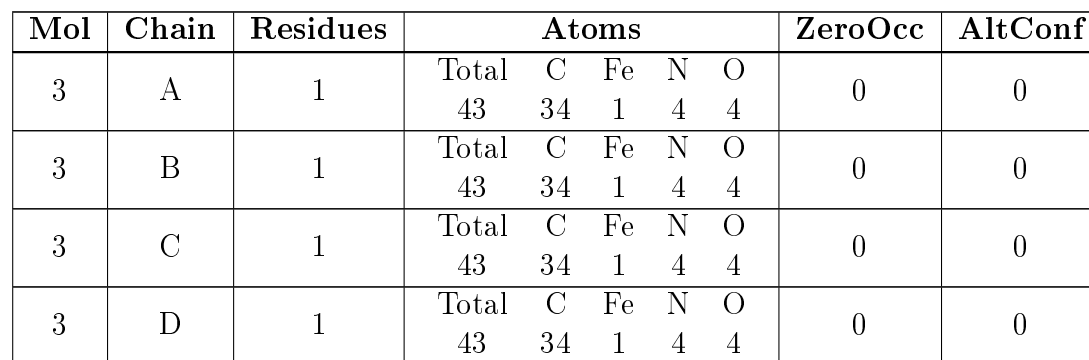
Chain	Residue	Modelled	Actual	Comment	Reference
C	394	HIS	-	expression tag	UNP P48775
C	395	HIS	-	expression tag	UNP P48775
C	396	HIS	-	expression tag	UNP P48775
D	17	MET	-	initiating methionine	UNP P48775
D	390	GLU	-	expression tag	UNP P48775
D	391	HIS	-	expression tag	UNP P48775
D	392	HIS	-	expression tag	UNP P48775
D	393	HIS	-	expression tag	UNP P48775
D	394	HIS	-	expression tag	UNP P48775
D	395	HIS	-	expression tag	UNP P48775
D	396	HIS	-	expression tag	UNP P48775

- Molecule 2 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O₂).



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

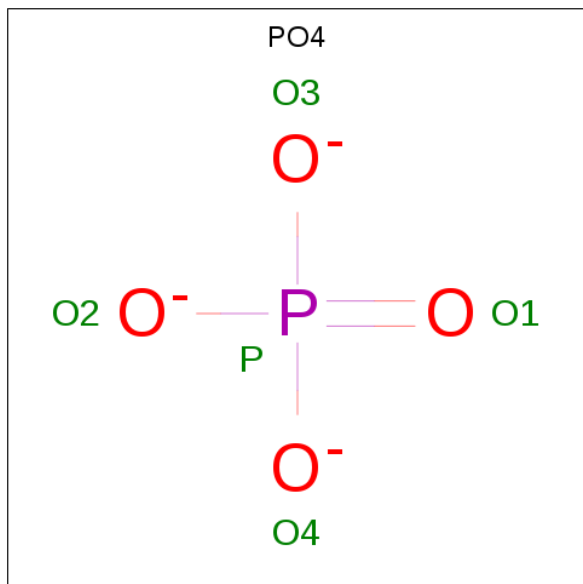
- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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- Chemical structure of Tryptophan (TRP) showing the indole ring system and the side chain. The structure is labeled with green text for atoms and blue text for functional groups. The indole ring is composed of a benzene ring fused to a pyrrole ring. The side chain is a 2-amino-3-(indol-3-yl)propanoic acid derivative. The labels are as follows:
- NE1: Nitrogen atom of the indole ring.
 - CH2: Methylene group of the side chain.
 - CH3: Methyl group of the side chain.
 - CD1: Carbon atom of the indole ring.
 - CD2: Carbon atom of the indole ring.
 - CG: Carbon atom of the side chain.
 - CB: Carbon atom of the side chain.
 - CA(S): Carbon atom of the side chain.
 - C: Carbon atom of the carboxyl group.
 - O: Oxygen atom of the carboxyl group.
 - OH_{OXT}: Hydroxyl group of the carboxyl group.
 - N: Nitrogen atom of the amino group.
 - NH₂: Amino group.

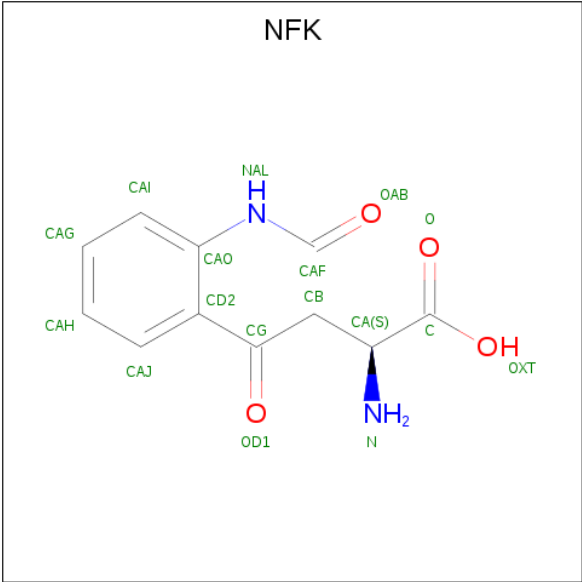
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			15	11	2	2		
4	A	1	Total	C	N	O	0	0
			15	11	2	2		
4	B	1	Total	C	N	O	0	0
			15	11	2	2		
4	B	1	Total	C	N	O	0	0
			15	11	2	2		
4	C	1	Total	C	N	O	0	0
			15	11	2	2		
4	D	1	Total	C	N	O	0	0
			15	11	2	2		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is N'-Formylkynurenine (three-letter code: NFK) (formula: C₁₁H₁₂N₂O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	N	O	0	0
			17	11	2	4		
6	D	1	Total	C	N	O	0	0
			17	11	2	4		

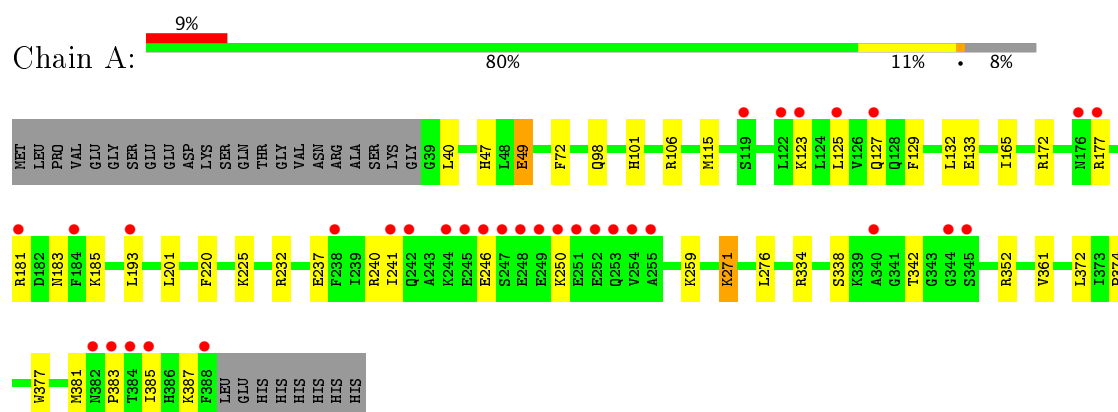
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	108	Total	O	0	0
			108	108		
7	B	134	Total	O	0	0
			134	134		
7	C	81	Total	O	0	0
			81	81		
7	D	113	Total	O	0	0
			113	113		

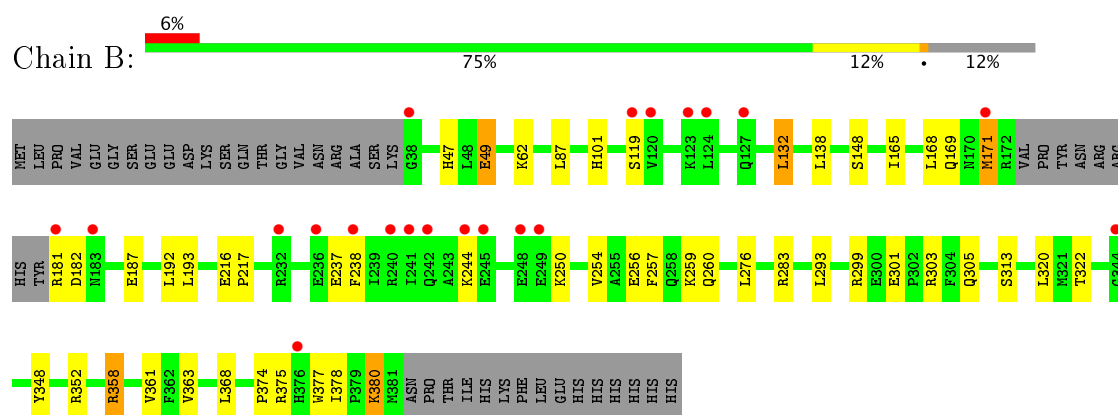
3 Residue-property plots [i](#)

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.

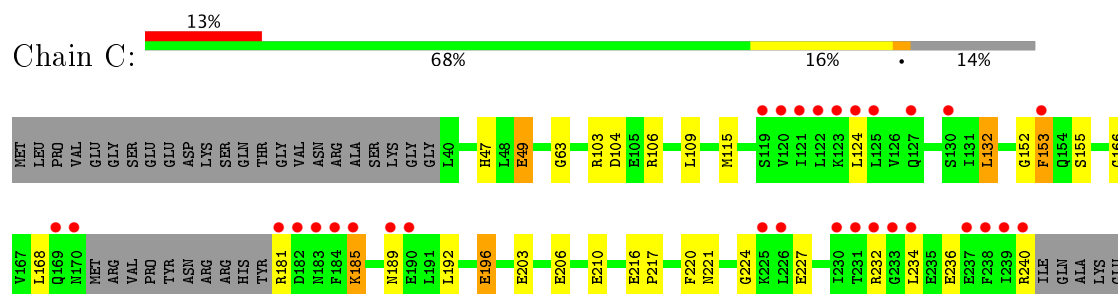
• Molecule 1: Tryptophan 2,3-dioxygenase

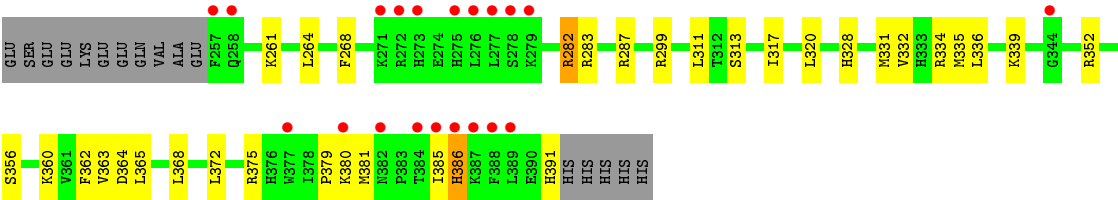


• Molecule 1: Tryptophan 2,3-dioxygenase

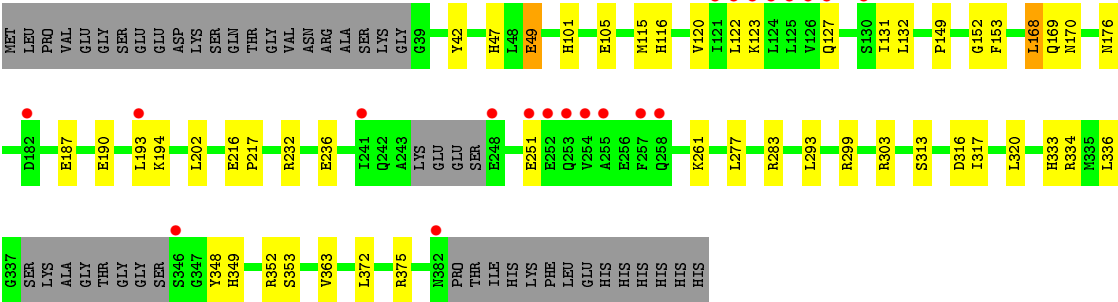


• Molecule 1: Tryptophan 2,3-dioxygenase





● Molecule 1: Tryptophan 2,3-dioxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	143.60 Å 154.01 Å 87.80 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.93 – 2.50 48.34 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (33.93-2.50) 99.7 (48.34-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.92 (at 2.48 Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.159 , 0.230 0.159 , 0.229	Depositor DCC
R_{free} test set	6848 reflections (10.09%)	DCC
Wilson B-factor (Å ²)	45.4	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 69.4	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	12070	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, PO4, NFK, OXY

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	0.53	0/3017	0.63	0/4060
1	B	0.53	0/2875	0.65	0/3864
1	C	0.48	0/2808	0.60	0/3778
1	D	0.51	0/2882	0.63	0/3877
All	All	0.51	0/11582	0.63	0/15579

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2948	0	2933	21	0
1	B	2814	0	2802	29	0
1	C	2744	0	2738	47	0
1	D	2818	0	2803	26	0
2	A	2	0	0	1	0
2	B	2	0	0	0	0
3	A	43	0	30	1	0
3	B	43	0	30	1	0
3	C	43	0	30	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	43	0	30	2	0
4	A	30	0	18	4	0
4	B	30	0	18	0	0
4	C	15	0	9	0	0
4	D	15	0	9	1	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
6	C	17	0	0	1	0
6	D	17	0	0	2	0
7	A	108	0	0	3	0
7	B	134	0	0	3	0
7	C	81	0	0	4	0
7	D	113	0	0	2	0
All	All	12070	0	11450	122	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 122 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:166:GLY:O	1:C:283:ARG:NH2	2.10	0.83
1:A:172:ARG:HB2	1:A:177:ARG:HB3	1.68	0.75
1:C:339:LYS:O	7:C:501:HOH:O	2.11	0.69
1:C:234:LEU:HD13	1:C:261:LYS:HG3	1.74	0.68
1:D:261:LYS:NZ	7:D:501:HOH:O	2.29	0.66

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	348/380 (92%)	333 (96%)	14 (4%)	1 (0%)	44	66
1	B	332/380 (87%)	325 (98%)	6 (2%)	1 (0%)	44	66
1	C	320/380 (84%)	307 (96%)	12 (4%)	1 (0%)	44	66
1	D	326/380 (86%)	317 (97%)	9 (3%)	0	100	100
All	All	1326/1520 (87%)	1282 (97%)	41 (3%)	3 (0%)	51	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	183	ASN
1	B	171	MET
1	C	379	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	322/348 (92%)	307 (95%)	15 (5%)	30	54
1	B	307/348 (88%)	290 (94%)	17 (6%)	25	46
1	C	301/348 (86%)	289 (96%)	12 (4%)	36	62
1	D	308/348 (88%)	289 (94%)	19 (6%)	21	39
All	All	1238/1392 (89%)	1175 (95%)	63 (5%)	28	50

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	322	THR
1	C	185	LYS
1	D	349	HIS
1	B	358	ARG
1	B	380	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	197	GLN
1	D	183	ASN
1	D	327	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

16 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	OXY	A	401	3	1,1,1	0.25	0	0,0,0	0.00	-
3	HEM	A	402	1,2	28,50,50	2.19	6 (21%)	17,82,82	1.99	6 (35%)
4	TRP	A	403	-	11,16,16	0.81	0	11,22,22	0.91	0
4	TRP	A	404	-	11,16,16	0.67	0	11,22,22	0.81	0
5	PO4	A	405	-	4,4,4	0.68	0	6,6,6	0.44	0
2	OXY	B	401	3	1,1,1	0.31	0	0,0,0	0.00	-
3	HEM	B	402	1,2	28,50,50	2.15	6 (21%)	17,82,82	2.11	5 (29%)
4	TRP	B	403	-	11,16,16	0.81	0	11,22,22	0.97	0
4	TRP	B	404	-	11,16,16	0.79	0	11,22,22	0.93	0
5	PO4	B	405	-	4,4,4	0.70	0	6,6,6	0.45	0
3	HEM	C	401	1,6	28,50,50	2.11	7 (25%)	17,82,82	2.49	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NFK	C	402	3	12,17,17	2.04	1 (8%)	17,22,22	2.70	4 (23%)
4	TRP	C	403	-	11,16,16	0.73	0	11,22,22	0.90	0
3	HEM	D	401	1,6	28,50,50	2.18	8 (28%)	17,82,82	1.93	6 (35%)
6	NFK	D	402	3	12,17,17	1.29	2 (16%)	17,22,22	3.04	6 (35%)
4	TRP	D	403	-	11,16,16	0.79	0	11,22,22	0.83	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	OXY	A	401	3	-	0/0/0/0	0/0/0/0
3	HEM	A	402	1,2	-	0/6/54/54	0/0/8/8
4	TRP	A	403	-	-	0/3/8/8	0/2/2/2
4	TRP	A	404	-	-	0/3/8/8	0/2/2/2
5	PO4	A	405	-	-	0/0/0/0	0/0/0/0
2	OXY	B	401	3	-	0/0/0/0	0/0/0/0
3	HEM	B	402	1,2	-	0/6/54/54	0/0/8/8
4	TRP	B	403	-	-	0/3/8/8	0/2/2/2
4	TRP	B	404	-	-	0/3/8/8	0/2/2/2
5	PO4	B	405	-	-	0/0/0/0	0/0/0/0
3	HEM	C	401	1,6	-	0/6/54/54	0/0/8/8
6	NFK	C	402	3	-	0/11/15/15	0/1/1/1
4	TRP	C	403	-	-	0/3/8/8	0/2/2/2
3	HEM	D	401	1,6	-	0/6/54/54	0/0/8/8
6	NFK	D	402	3	-	0/11/15/15	0/1/1/1
4	TRP	D	403	-	-	0/3/8/8	0/2/2/2

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402	HEM	C3C-C2C	-5.59	1.33	1.40
3	B	402	HEM	C3C-C2C	-5.07	1.33	1.40
3	C	401	HEM	C3C-C2C	-4.64	1.34	1.40
3	C	401	HEM	C3B-C2B	-4.15	1.34	1.40
3	A	402	HEM	C3B-C2B	-4.09	1.35	1.40

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	HEM	CBD-CAD-C3D	-7.55	98.06	112.47
6	D	402	NFK	CAO-NAL-CAF	-7.24	113.55	126.89
6	C	402	NFK	CAO-CD2-CG	-6.94	117.39	122.32
6	C	402	NFK	CAO-NAL-CAF	-6.23	115.42	126.89
3	B	402	HEM	CBD-CAD-C3D	-5.59	101.81	112.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	OXY	1	0
3	A	402	HEM	1	0
4	A	403	TRP	3	0
4	A	404	TRP	1	0
3	B	402	HEM	1	0
3	C	401	HEM	3	0
6	C	402	NFK	1	0
3	D	401	HEM	2	0
6	D	402	NFK	2	0
4	D	403	TRP	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	350/380 (92%)	0.20	33 (9%) 9 9	30, 49, 102, 146	0
1	B	336/380 (88%)	0.14	21 (6%) 21 21	28, 44, 89, 127	0
1	C	326/380 (85%)	0.62	50 (15%) 2 2	33, 56, 113, 150	0
1	D	332/380 (87%)	0.21	21 (6%) 21 21	30, 50, 94, 155	0
All	All	1344/1520 (88%)	0.29	125 (9%) 9 9	28, 49, 103, 155	0

The worst 5 of 125 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	385	ILE	7.1
1	C	239	ILE	7.0
1	C	238	PHE	6.2
1	C	169	GLN	5.1
1	A	248	GLU	5.0

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 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
5	PO4	B	405	5/5	0.93	0.48	2.58	106,117,121,122	0
4	TRP	A	403	15/15	0.96	0.26	1.73	63,69,74,75	0
4	TRP	D	403	15/15	0.97	0.19	1.71	39,49,57,60	0
6	NFK	C	402	17/17	0.97	0.22	1.62	60,79,94,101	0
5	PO4	A	405	5/5	0.93	0.39	1.26	105,108,112,118	0
6	NFK	D	402	17/17	0.97	0.17	0.78	47,70,98,99	0
4	TRP	C	403	15/15	0.97	0.14	0.52	45,51,63,72	0
4	TRP	B	403	15/15	0.94	0.15	-0.13	43,54,61,63	0
4	TRP	B	404	15/15	0.97	0.13	-0.14	38,41,52,53	0
3	HEM	D	401	43/43	0.99	0.13	-0.69	26,46,61,66	0
3	HEM	A	402	43/43	0.96	0.14	-0.70	30,44,57,59	0
3	HEM	C	401	43/43	0.96	0.13	-0.80	42,49,61,65	0
4	TRP	A	404	15/15	0.97	0.12	-0.83	33,41,53,60	0
3	HEM	B	402	43/43	0.98	0.12	-0.87	31,43,52,61	0
2	OXY	A	401	2/2	1.00	0.10	-1.49	73,73,73,76	0
2	OXY	B	401	2/2	0.99	0.11	-	54,54,54,56	0

6.5 Other polymers ⓘ

There are no such residues in this entry.