



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:08 PM GMT

PDB ID : 4QYQ
Title : Crystal structure of the complex of goat lactoperoxidase with an antithyroid agent propylthiouracil at 2.5 Å resolution
Authors : Singh, R.P.; Singh, A.; Kushwaha, G.S.; Singh, A.K.; Sinha, M.; Tyagi, T.K.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on : 2014-07-25
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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

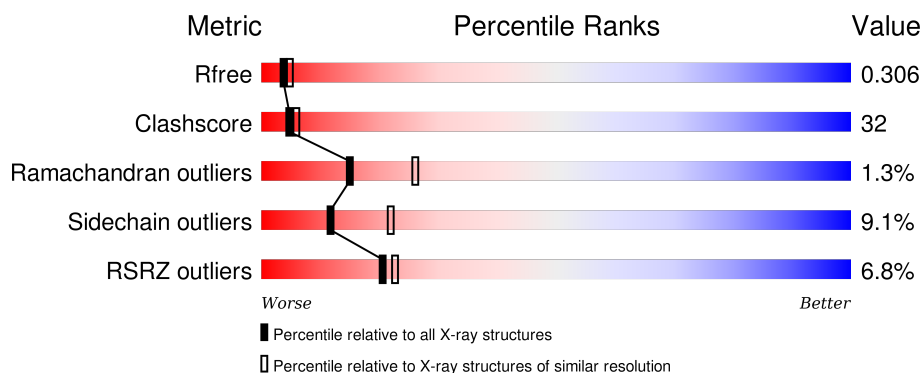
1 Overall quality at a glance ⓘ

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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (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	595	<div> <div>5%</div> <div>50%</div> <div>45%</div> <div>5%</div> </div>
1	B	595	<div> <div>6%</div> <div>54%</div> <div>42%</div> <div>.</div> </div>
1	C	595	<div> <div>9%</div> <div>51%</div> <div>45%</div> <div>5%</div> </div>
1	D	595	<div> <div>7%</div> <div>46%</div> <div>49%</div> <div>5%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	HEM	C	605	-	-	X	-
6	3CJ	A	607	-	-	X	-
6	3CJ	B	607	-	-	X	-
6	3CJ	C	607	-	-	X	X
6	3CJ	D	607	-	-	X	X
7	NO3	A	608	-	-	-	X
7	NO3	A	610	-	-	-	X
7	NO3	B	610	-	-	-	X
7	NO3	C	608	-	-	-	X
7	NO3	C	610	-	-	X	X
7	NO3	D	608	-	-	X	-
7	NO3	D	609	-	-	X	-
7	NO3	D	610	-	-	X	X

2 Entry composition [i](#)

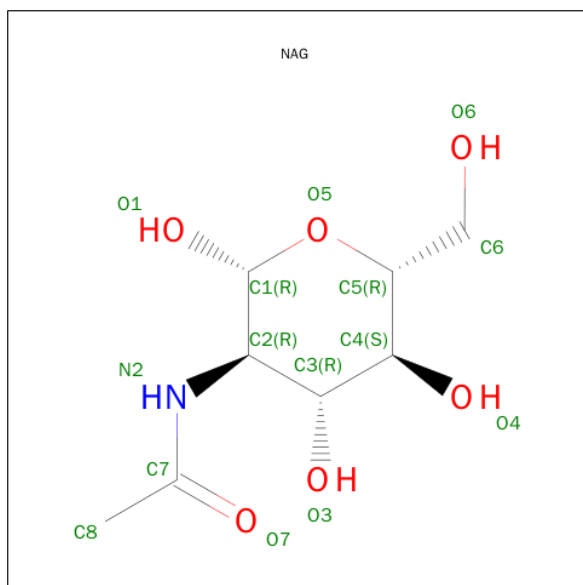
There are 8 unique types of molecules in this entry. The entry contains 20192 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Lactoperoxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	S	0	0	0
			4753	3021	844	862	26			
1	B	595	Total	C	N	O	S	0	0	0
			4753	3021	844	862	26			
1	C	595	Total	C	N	O	S	0	0	0
			4753	3021	844	862	26			
1	D	595	Total	C	N	O	S	0	0	0
			4753	3021	844	862	26			

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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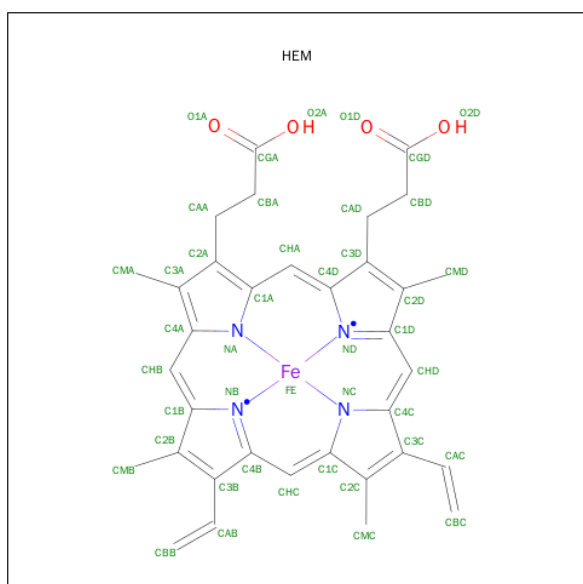
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	B	2	Total	C	N	O	0	0
			28	16	2	10		
3	C	2	Total	C	N	O	0	0
			28	16	2	10		
3	D	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).

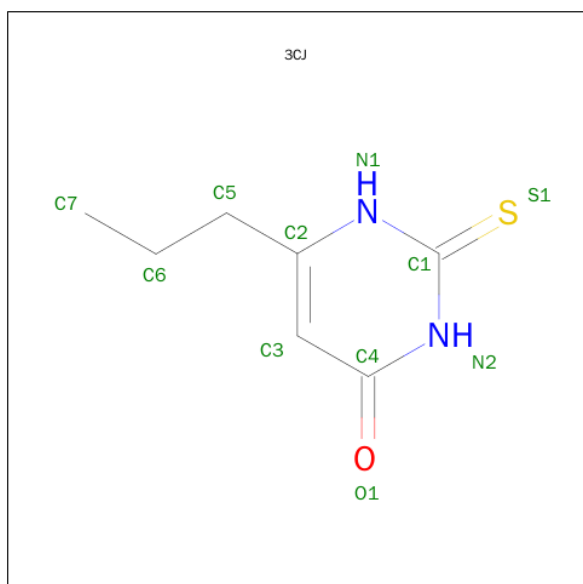


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Ca	0	0
			1	1		
5	A	1	Total	Ca	0	0
			1	1		
5	D	1	Total	Ca	0	0
			1	1		
5	C	1	Total	Ca	0	0
			1	1		

- Molecule 6 is 6-PROPYL-2-THIOXO-2,3-DIHYDROPYRIMIDIN-4(1H)-ONE (three-letter code: 3CJ) (formula: C₇H₁₀N₂OS).



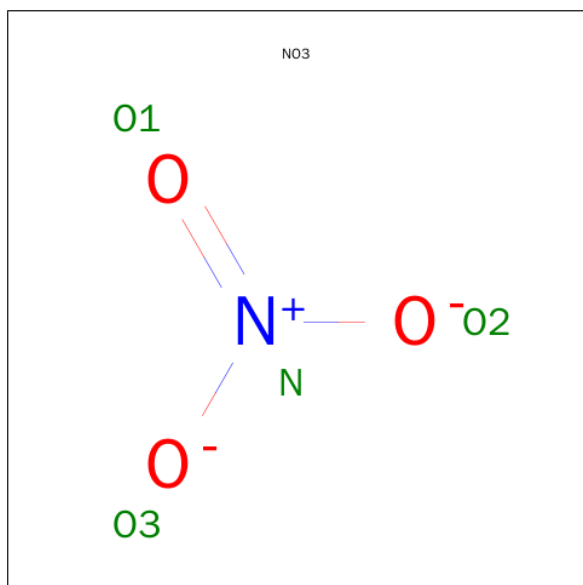
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	S	0	0
			11	7	2	1	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	S	0	0
			11	7	2	1	1		
6	C	1	Total	C	N	O	S	0	0
			11	7	2	1	1		
6	D	1	Total	C	N	O	S	0	0
			11	7	2	1	1		

- Molecule 7 is NITRATE ION (three-letter code: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	N	O	0	0
			4	1	3		
7	A	1	Total	N	O	0	0
			4	1	3		
7	A	1	Total	N	O	0	0
			4	1	3		
7	B	1	Total	N	O	0	0
			4	1	3		
7	B	1	Total	N	O	0	0
			4	1	3		
7	B	1	Total	N	O	0	0
			4	1	3		
7	C	1	Total	N	O	0	0
			4	1	3		
7	C	1	Total	N	O	0	0
			4	1	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total 4	N 1	O 3	0	0
7	D	1	Total 4	N 1	O 3	0	0
7	D	1	Total 4	N 1	O 3	0	0
7	D	1	Total 4	N 1	O 3	0	0

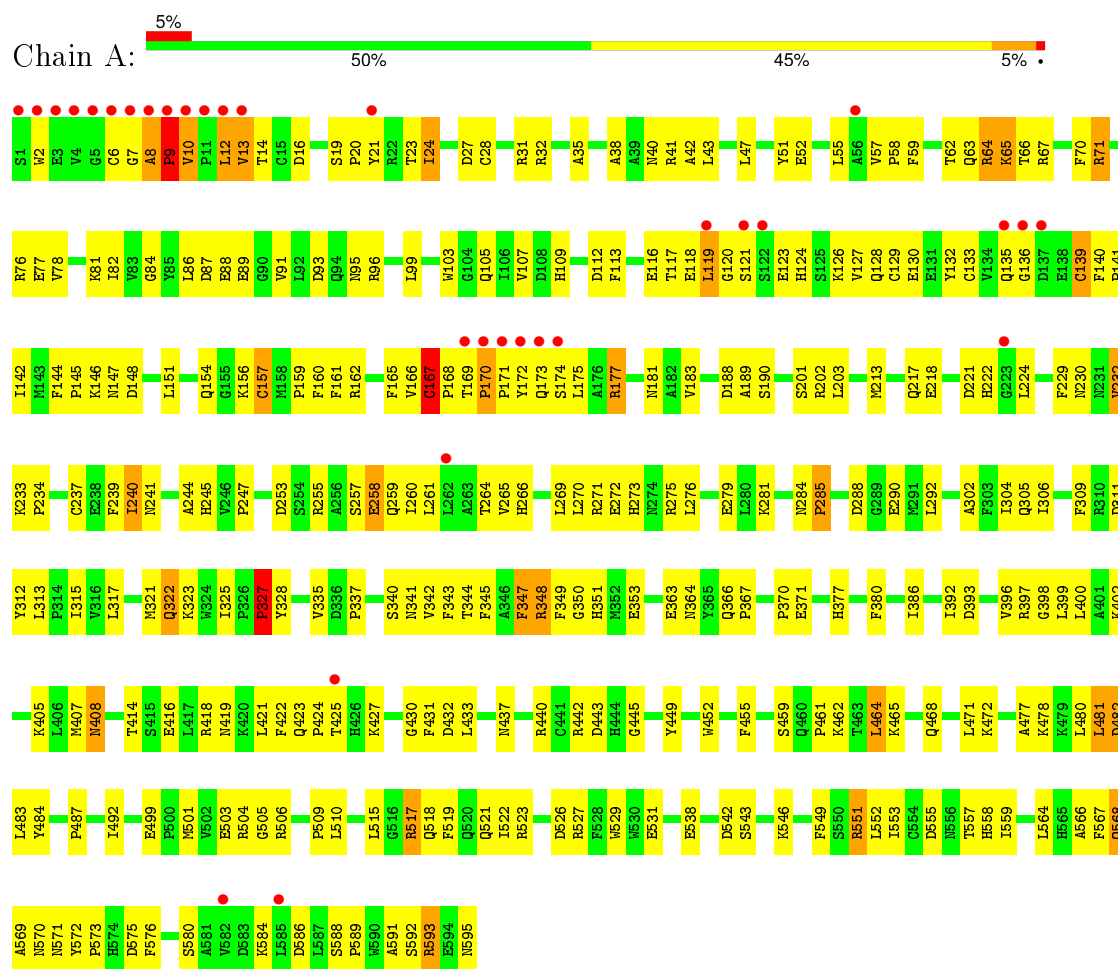
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	163	Total 163	O 163	0	0
8	B	168	Total 168	O 168	0	0
8	C	180	Total 180	O 180	0	0
8	D	177	Total 177	O 177	0	0

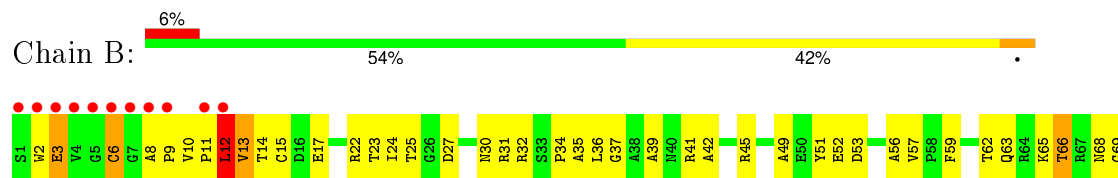
3 Residue-property plots

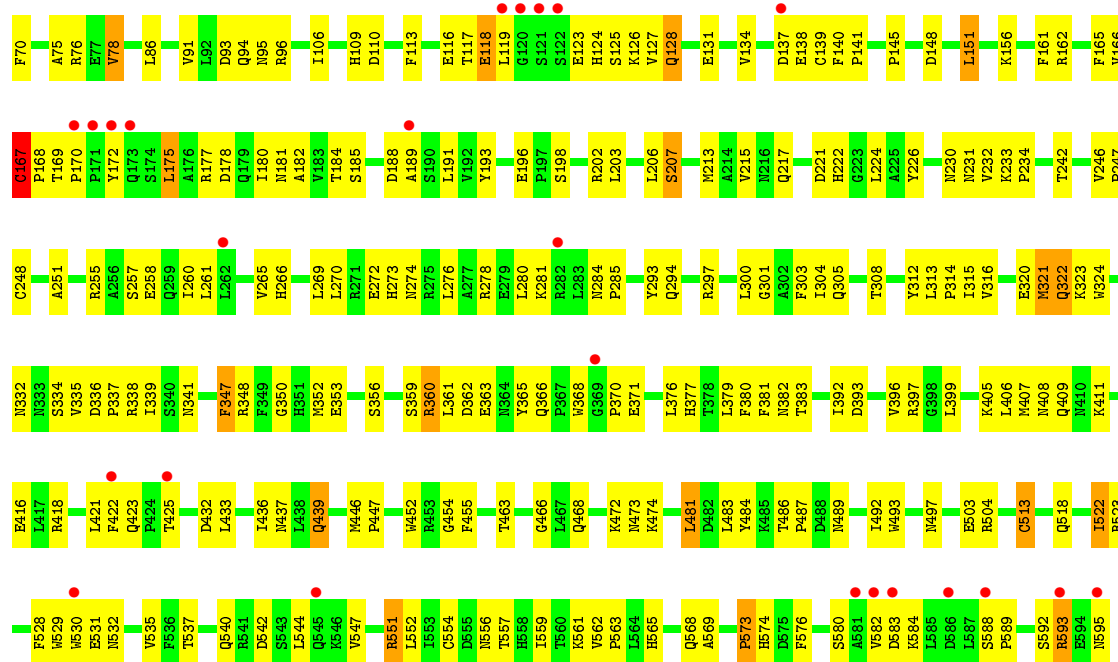
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Lactoperoxidase

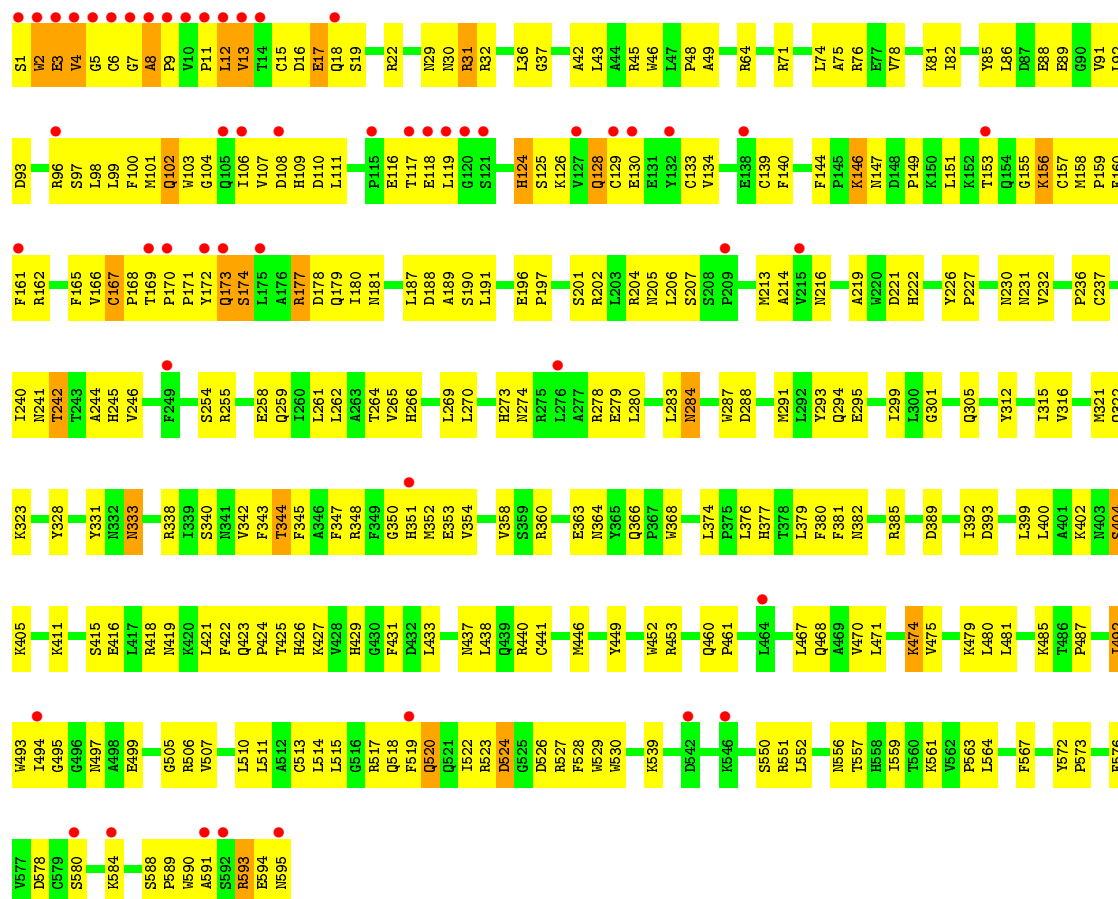


• Molecule 1: Lactoperoxidase

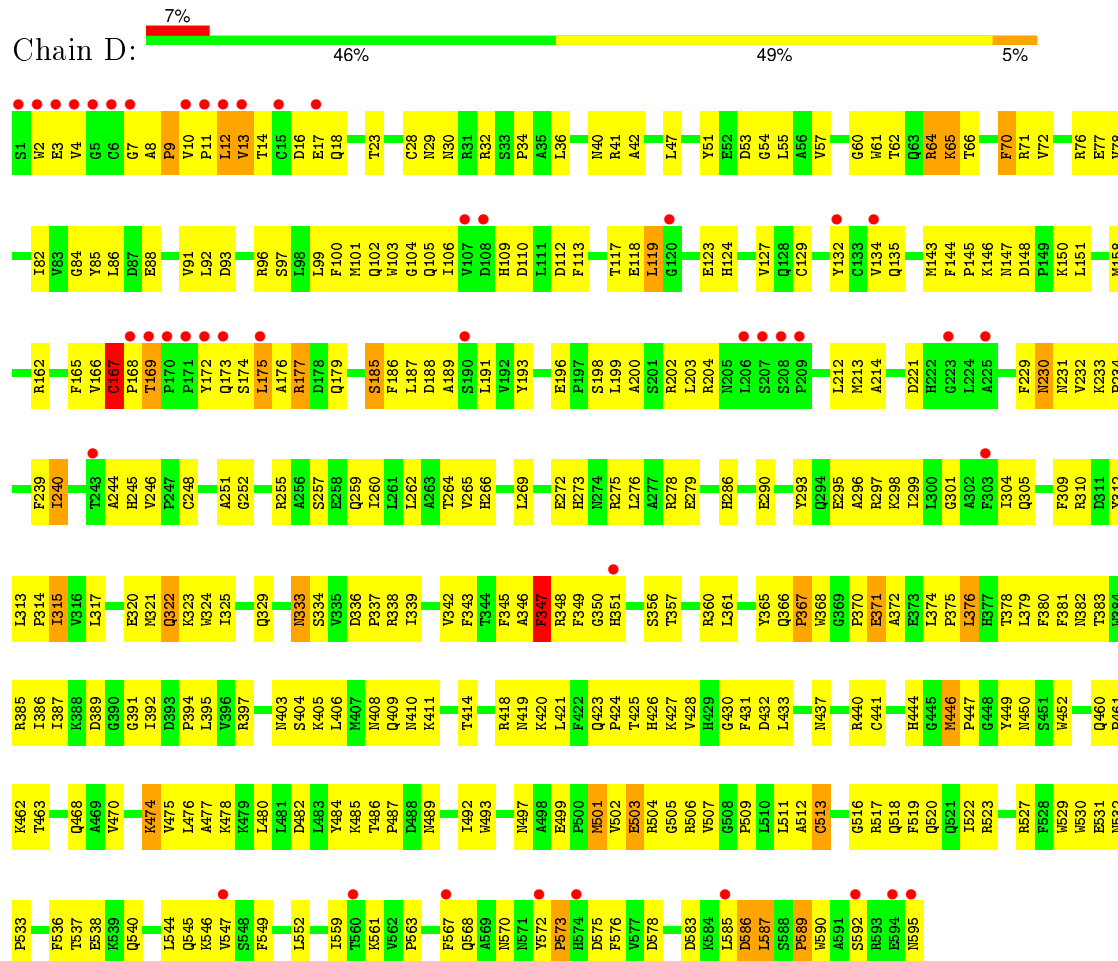




• Molecule 1: Lactoperoxidase



● Molecule 1: Lactoperoxidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	80.22Å 82.59Å 95.08Å 80.91° 73.71° 89.96°	Depositor
Resolution (Å)	42.50 – 2.50 42.46 – 2.50	Depositor EDS
% Data completeness (in resolution range)	91.7 (42.50-2.50) 87.5 (42.46-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
R, R_{free}	0.245 , 0.284 0.253 , 0.306	Depositor DCC
R_{free} test set	3683 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	41.2	Xtriage
Anisotropy	0.744	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 48.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 73032 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	20192	wwPDB-VP
Average B, all atoms (Å ²)	45.0	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 40.53 % 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 2.7003e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: HEM, CA, NO3, NAG, 3CJ

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	0.50	1/4882 (0.0%)	0.75	2/6632 (0.0%)
1	B	0.45	0/4882	0.75	1/6632 (0.0%)
1	C	0.48	0/4882	0.74	0/6632
1	D	0.50	0/4882	0.78	1/6632 (0.0%)
All	All	0.48	1/19528 (0.0%)	0.76	4/26528 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	171	PRO	N-CD	5.39	1.55	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	170	PRO	C-N-CD	5.51	139.97	128.40
1	A	349	PHE	N-CA-C	-5.38	96.49	111.00
1	B	12	LEU	CB-CG-CD2	5.22	119.87	111.00
1	D	167	CYS	CA-CB-SG	-5.20	104.64	114.00

There are no chirality outliers.

There are no planarity outliers.

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	4753	0	4646	303	0
1	B	4753	0	4644	243	0
1	C	4753	0	4649	340	0
1	D	4753	0	4647	294	0
2	A	28	0	26	0	0
2	B	28	0	26	1	0
2	C	28	0	26	0	0
2	D	28	0	26	1	0
3	A	28	0	25	1	0
3	B	28	0	25	2	0
3	C	28	0	25	1	0
3	D	28	0	25	0	0
4	A	43	0	30	14	0
4	B	43	0	30	17	0
4	C	43	0	30	28	0
4	D	43	0	30	12	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	11	0	10	12	0
6	B	11	0	10	14	0
6	C	11	0	10	20	0
6	D	11	0	10	11	0
7	A	12	0	0	1	0
7	B	12	0	0	1	0
7	C	12	0	0	4	0
7	D	12	0	0	8	0
8	A	163	0	0	14	0
8	B	168	0	0	15	0
8	C	180	0	0	21	0
8	D	177	0	0	18	0
All	All	20192	0	18950	1221	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 32.

The worst 5 of 1221 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:D:167:CYS:HB3	1:D:168:PRO:CD	1.50	1.37
1:A:167:CYS:HB2	1:A:168:PRO:CD	1.55	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:10:VAL:HG11	1:B:41:ARG:NH1	1.48	1.28
1:C:167:CYS:HB3	1:C:168:PRO:CD	1.67	1.17
1:A:62:THR:HG21	1:A:65:LYS:HB2	1.15	1.15

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	593/595 (100%)	516 (87%)	71 (12%)	6 (1%)	19	34
1	B	593/595 (100%)	518 (87%)	68 (12%)	7 (1%)	16	29
1	C	593/595 (100%)	523 (88%)	61 (10%)	9 (2%)	13	22
1	D	593/595 (100%)	516 (87%)	68 (12%)	9 (2%)	13	22
All	All	2372/2380 (100%)	2073 (87%)	268 (11%)	31 (1%)	15	26

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	ALA
1	A	13	VAL
1	A	167	CYS
1	B	167	CYS
1	C	8	ALA

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	517/517 (100%)	469 (91%)	48 (9%)	11	21
1	B	517/517 (100%)	473 (92%)	44 (8%)	13	25
1	C	517/517 (100%)	474 (92%)	43 (8%)	14	26
1	D	517/517 (100%)	463 (90%)	54 (10%)	9	16
All	All	2068/2068 (100%)	1879 (91%)	189 (9%)	12	22

5 of 189 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	522	ILE
1	C	139	CYS
1	D	428	VAL
1	B	573	PRO
1	C	6	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	135	GLN
1	C	230	ASN
1	D	329	GLN
1	C	154	GLN
1	C	250	GLN

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 ⓘ

8 carbohydrates 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
3	NAG	A	603	1,3	14,14,15	1.27	2 (14%)	15,19,21	1.64	1 (6%)
3	NAG	A	604	3	14,14,15	0.89	1 (7%)	15,19,21	2.96	5 (33%)
3	NAG	B	603	1,3	14,14,15	1.42	1 (7%)	15,19,21	2.29	6 (40%)
3	NAG	B	604	3	14,14,15	0.98	1 (7%)	15,19,21	2.10	4 (26%)
3	NAG	C	602	3	14,14,15	0.27	0	15,19,21	0.53	0
3	NAG	C	603	1,3	14,14,15	0.25	0	15,19,21	0.62	0
3	NAG	D	603	1,3	14,14,15	0.82	0	15,19,21	1.35	2 (13%)
3	NAG	D	604	3	14,14,15	0.70	0	15,19,21	1.82	4 (26%)

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
3	NAG	A	603	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	604	3	-	0/6/23/26	0/1/1/1
3	NAG	B	603	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	604	3	-	0/6/23/26	0/1/1/1
3	NAG	C	602	3	-	0/6/23/26	0/1/1/1
3	NAG	C	603	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	603	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	604	3	-	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	603	NAG	C2-N2	-2.70	1.41	1.46
3	A	603	NAG	O5-C1	-2.58	1.39	1.43
3	A	604	NAG	C2-N2	-2.41	1.42	1.46
3	B	604	NAG	C1-C2	2.04	1.55	1.52
3	B	603	NAG	C1-C2	2.96	1.56	1.52

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	603	NAG	C2-N2-C7	-4.93	116.70	123.04
3	B	604	NAG	C4-C3-C2	-4.72	103.90	111.23
3	D	604	NAG	C3-C4-C5	-4.14	102.98	110.20
3	D	603	NAG	C2-N2-C7	-3.87	118.07	123.04
3	A	604	NAG	O4-C4-C3	-3.69	102.04	110.34

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	604	NAG	1	0
3	B	603	NAG	2	0
3	B	604	NAG	2	0
3	C	603	NAG	1	0

5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 4 are monoatomic - leaving 28 for Mogul analysis.

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	NAG	A	601	1	14,14,15	0.96	0	15,19,21	2.34	7 (46%)
2	NAG	A	602	1	14,14,15	0.28	0	15,19,21	0.53	0
4	HEM	A	605	1	30,50,50	3.18	12 (40%)	24,82,82	2.77	15 (62%)
6	3CJ	A	607	-	8,11,11	2.02	2 (25%)	9,14,14	3.77	5 (55%)
7	NO3	A	608	-	3,3,3	2.30	1 (33%)	3,3,3	1.06	0
7	NO3	A	609	-	3,3,3	2.83	2 (66%)	3,3,3	0.12	0
7	NO3	A	610	-	3,3,3	2.40	2 (66%)	3,3,3	0.13	0
2	NAG	B	601	1	14,14,15	0.27	0	15,19,21	0.53	0
2	NAG	B	602	1	14,14,15	1.16	1 (7%)	15,19,21	1.75	5 (33%)
4	HEM	B	605	1	30,50,50	3.14	13 (43%)	24,82,82	2.88	16 (66%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	3CJ	B	607	-	8,11,11	2.39	2 (25%)	9,14,14	4.49	5 (55%)
7	NO3	B	608	-	3,3,3	2.39	2 (66%)	3,3,3	0.13	0
7	NO3	B	609	-	3,3,3	2.84	2 (66%)	3,3,3	0.13	0
7	NO3	B	610	-	3,3,3	2.26	2 (66%)	3,3,3	0.25	0
2	NAG	C	601	1	14,14,15	0.28	0	15,19,21	0.53	0
2	NAG	C	604	1	14,14,15	0.27	0	15,19,21	0.53	0
4	HEM	C	605	1	30,50,50	3.13	12 (40%)	24,82,82	2.74	13 (54%)
6	3CJ	C	607	-	8,11,11	2.98	3 (37%)	9,14,14	3.63	5 (55%)
7	NO3	C	608	-	3,3,3	2.39	2 (66%)	3,3,3	0.13	0
7	NO3	C	609	-	3,3,3	2.79	2 (66%)	3,3,3	0.24	0
7	NO3	C	610	-	3,3,3	2.40	2 (66%)	3,3,3	0.14	0
2	NAG	D	601	1	14,14,15	0.79	0	15,19,21	1.71	4 (26%)
2	NAG	D	602	1	14,14,15	0.28	0	15,19,21	0.53	0
4	HEM	D	605	1	30,50,50	3.37	14 (46%)	24,82,82	2.61	12 (50%)
6	3CJ	D	607	-	8,11,11	2.67	3 (37%)	9,14,14	4.69	6 (66%)
7	NO3	D	608	-	3,3,3	2.39	2 (66%)	3,3,3	0.13	0
7	NO3	D	609	-	3,3,3	2.84	2 (66%)	3,3,3	0.13	0
7	NO3	D	610	-	3,3,3	2.40	2 (66%)	3,3,3	0.13	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	NAG	A	601	1	-	0/6/23/26	0/1/1/1
2	NAG	A	602	1	-	0/6/23/26	0/1/1/1
4	HEM	A	605	1	-	0/10/54/54	0/0/8/8
6	3CJ	A	607	-	-	0/3/3/3	0/1/1/1
7	NO3	A	608	-	-	0/0/0/0	0/0/0/0
7	NO3	A	609	-	-	0/0/0/0	0/0/0/0
7	NO3	A	610	-	-	0/0/0/0	0/0/0/0
2	NAG	B	601	1	-	0/6/23/26	0/1/1/1
2	NAG	B	602	1	-	0/6/23/26	0/1/1/1
4	HEM	B	605	1	-	0/10/54/54	0/0/8/8
6	3CJ	B	607	-	-	0/3/3/3	0/1/1/1
7	NO3	B	608	-	-	0/0/0/0	0/0/0/0
7	NO3	B	609	-	-	0/0/0/0	0/0/0/0
7	NO3	B	610	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	601	1	-	0/6/23/26	0/1/1/1
2	NAG	C	604	1	-	0/6/23/26	0/1/1/1
4	HEM	C	605	1	-	0/10/54/54	0/0/8/8
6	3CJ	C	607	-	-	0/3/3/3	0/1/1/1
7	NO3	C	608	-	-	0/0/0/0	0/0/0/0
7	NO3	C	609	-	-	0/0/0/0	0/0/0/0
7	NO3	C	610	-	-	0/0/0/0	0/0/0/0
2	NAG	D	601	1	-	0/6/23/26	0/1/1/1
2	NAG	D	602	1	-	0/6/23/26	0/1/1/1
4	HEM	D	605	1	-	0/10/54/54	0/0/8/8
6	3CJ	D	607	-	-	0/3/3/3	0/1/1/1
7	NO3	D	608	-	-	0/0/0/0	0/0/0/0
7	NO3	D	609	-	-	0/0/0/0	0/0/0/0
7	NO3	D	610	-	-	0/0/0/0	0/0/0/0

The worst 5 of 85 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	605	HEM	C2C-C1C	-9.44	1.34	1.52
4	A	605	HEM	C3B-C4B	-8.88	1.43	1.51
4	D	605	HEM	C3B-C4B	-8.72	1.44	1.51
4	C	605	HEM	C3B-C4B	-8.05	1.44	1.51
4	B	605	HEM	C2D-C3D	-7.98	1.30	1.54

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	607	3CJ	C3-C2-N1	-5.70	116.53	122.96
4	B	605	HEM	C3B-CAB-CBB	-5.33	116.28	124.46
6	A	607	3CJ	C3-C2-N1	-4.42	117.98	122.96
2	A	601	NAG	C4-C3-C2	-4.12	104.83	111.23
2	D	601	NAG	C2-N2-C7	-4.11	117.76	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

18 monomers are involved in 104 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	605	HEM	14	0
6	A	607	3CJ	12	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	609	NO3	1	0
2	B	601	NAG	1	0
4	B	605	HEM	17	0
6	B	607	3CJ	14	0
7	B	608	NO3	1	0
4	C	605	HEM	28	0
6	C	607	3CJ	20	0
7	C	608	NO3	1	0
7	C	609	NO3	1	0
7	C	610	NO3	2	0
2	D	602	NAG	1	0
4	D	605	HEM	12	0
6	D	607	3CJ	11	0
7	D	608	NO3	2	0
7	D	609	NO3	2	0
7	D	610	NO3	4	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	595/595 (100%)	0.29	32 (5%)	29 33	16, 42, 76, 100	0
1	B	595/595 (100%)	0.31	35 (5%)	26 29	20, 43, 76, 100	0
1	C	595/595 (100%)	0.48	52 (8%)	13 13	20, 43, 83, 100	0
1	D	595/595 (100%)	0.40	44 (7%)	17 19	14, 41, 79, 100	0
All	All	2380/2380 (100%)	0.37	163 (6%)	20 23	14, 42, 79, 100	0

The worst 5 of 163 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	4	VAL	20.3
1	C	6	CYS	15.1
1	A	171	PRO	11.8
1	D	2	TRP	11.6
1	D	7	GLY	11.4

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](#)

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
3	NAG	C	603	14/15	0.86	0.25	1.87	20,20,20,20	0
3	NAG	B	603	14/15	0.84	0.20	0.36	36,50,59,66	0
3	NAG	A	603	14/15	0.93	0.14	-0.52	33,41,52,54	0
3	NAG	D	603	14/15	0.95	0.12	-0.87	70,79,82,85	0
3	NAG	A	604	14/15	0.87	0.20	-	43,50,51,52	14
3	NAG	B	604	14/15	0.78	0.27	-	45,53,55,58	14
3	NAG	D	604	14/15	0.86	0.20	-	61,67,70,70	14
3	NAG	C	602	14/15	0.84	0.21	-	49,56,63,63	14

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. 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
7	NO3	D	610	4/4	0.94	0.46	10.59	23,23,26,30	0
7	NO3	C	608	4/4	0.92	0.56	8.85	24,27,29,31	0
7	NO3	B	610	4/4	0.91	0.66	7.74	24,24,24,28	0
7	NO3	A	610	4/4	0.96	0.40	6.48	23,24,26,27	0
7	NO3	C	610	4/4	0.85	0.27	4.85	24,28,29,30	0
7	NO3	A	608	4/4	0.96	0.30	3.89	23,23,24,26	0
6	3CJ	D	607	11/11	0.79	0.41	3.15	31,48,60,60	0
6	3CJ	C	607	11/11	0.72	0.36	2.30	74,84,92,93	0
7	NO3	D	608	4/4	0.95	0.23	1.98	21,24,24,26	0
7	NO3	B	608	4/4	0.89	0.20	1.83	22,25,27,28	0
2	NAG	B	602	14/15	0.90	0.16	1.25	55,63,73,75	0
6	3CJ	B	607	11/11	0.79	0.24	1.02	42,47,53,54	0
4	HEM	B	605	43/43	0.94	0.22	0.78	31,41,53,62	0
2	NAG	C	604	14/15	0.87	0.21	0.70	48,55,60,61	0
4	HEM	A	605	43/43	0.95	0.21	0.63	26,37,45,49	0
5	CA	C	606	1/1	0.95	0.22	0.56	46,46,46,46	0
6	3CJ	A	607	11/11	0.90	0.22	0.29	47,53,56,60	0
5	CA	A	606	1/1	0.91	0.17	0.23	43,43,43,43	0
5	CA	D	606	1/1	0.97	0.23	0.14	36,36,36,36	0
2	NAG	C	601	14/15	0.66	0.38	-0.05	78,86,89,90	0
2	NAG	A	602	14/15	0.94	0.13	-0.43	38,46,51,54	0
4	HEM	D	605	43/43	0.95	0.16	-0.60	13,22,35,44	0
5	CA	B	606	1/1	0.93	0.14	-0.62	44,44,44,44	0
2	NAG	D	602	14/15	0.83	0.17	-0.78	46,54,59,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	D	601	14/15	0.84	0.20	-0.81	52,60,65,66	0
4	HEM	C	605	43/43	0.95	0.15	-0.89	31,41,45,52	0
7	NO3	A	609	4/4	0.97	0.18	-	24,26,28,32	0
7	NO3	B	609	4/4	0.90	0.38	-	26,26,27,29	0
7	NO3	C	609	4/4	0.86	0.45	-	24,24,27,31	0
7	NO3	D	609	4/4	0.89	0.37	-	25,26,27,28	0
2	NAG	B	601	14/15	0.82	0.26	-	64,73,77,81	0
2	NAG	A	601	14/15	0.80	0.18	-	64,79,81,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.