



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:01 PM GMT

PDB ID : 1DNW
Title : HUMAN MYELOPEROXIDASE-CYANIDE-THIOCYANATE COMPLEX
Authors : Blair-Johnson, M.; Fiedler, T.J.; Fenna, R.E.
Deposited on : 1999-12-16
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

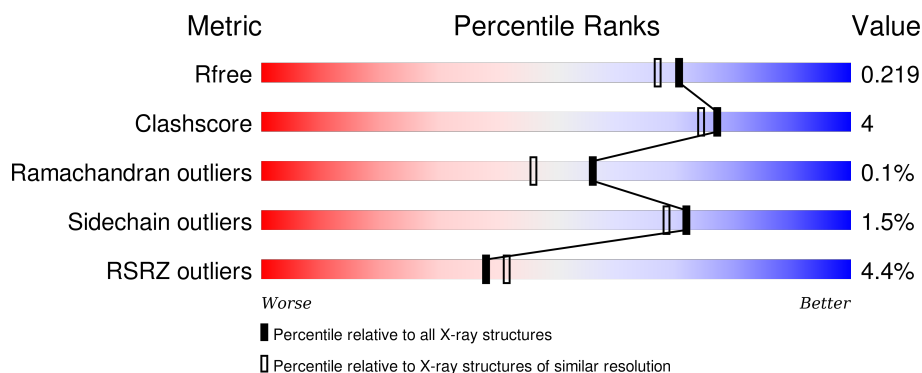
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (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	104	<div> <div>7%</div> <div>93%</div> <div>7%</div> </div>
1	B	104	<div> <div>94%</div> <div>6%</div> </div>
2	C	466	<div> <div>3%</div> <div>89%</div> <div>11%</div> </div>
2	D	466	<div> <div>6%</div> <div>89%</div> <div>10%</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
10	ACY	C	19	-	-	-	X
3	NAG	D	630	-	-	-	X
4	BMA	D	642	-	-	-	X
6	SCN	B	107	-	-	X	-
8	CYN	A	107	-	-	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 10349 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 MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	104	Total	C	N	O	S	0	0	0
			838	529	148	156	5			
1	B	104	Total	C	N	O	S	0	0	0
			838	529	148	156	5			

- Molecule 2 is a protein called MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	466	Total	C	N	O	S	0	0	0
			3733	2351	687	668	27			
2	D	466	Total	C	N	O	S	0	0	0
			3733	2351	687	668	27			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	150	CSO	CYS	MODIFIED RESIDUE	UNP P05164
D	150	CSO	CYS	MODIFIED RESIDUE	UNP P05164

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

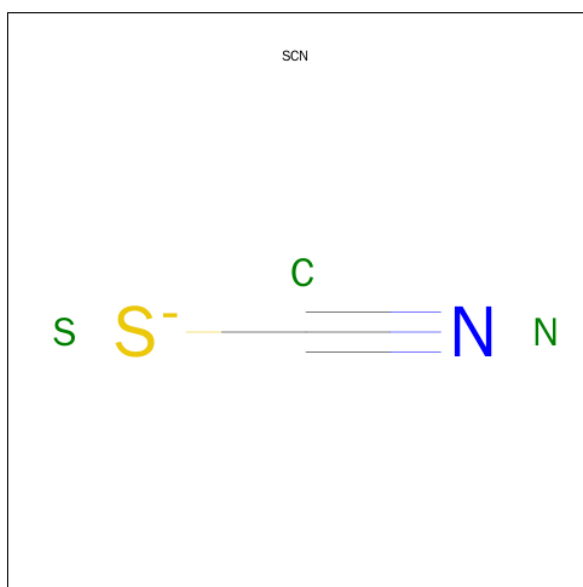
- Molecule 4 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	6	Total	C	N	O	0	0
			71	40	2	29		
4	D	6	Total	C	N	O	0	0
			71	40	2	29		

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

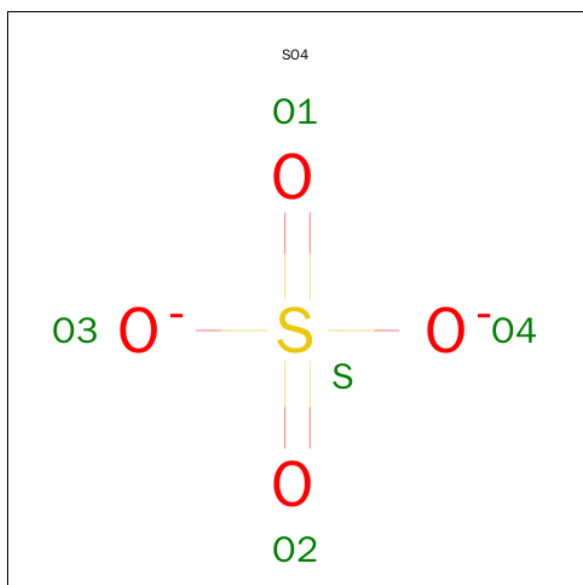
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total	Ca	0	0
			1	1		
5	C	1	Total	Ca	0	0
			1	1		

- Molecule 6 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



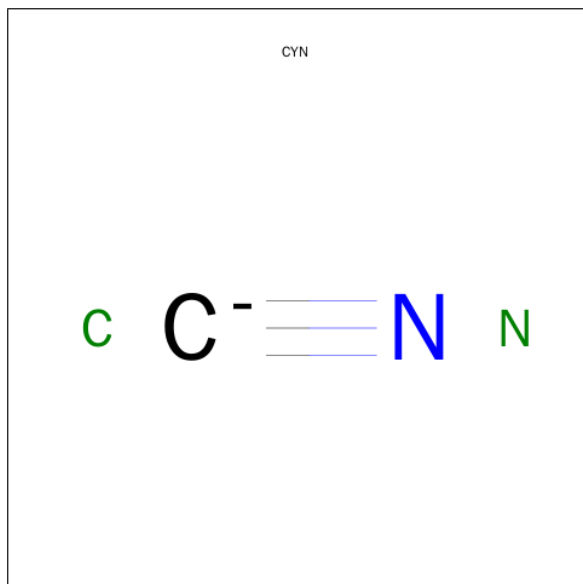
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	S	0	0
			3	1	1	1		
6	C	1	Total	C	N	S	0	0
			3	1	1	1		
6	B	1	Total	C	N	S	0	0
			3	1	1	1		
6	B	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 7 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



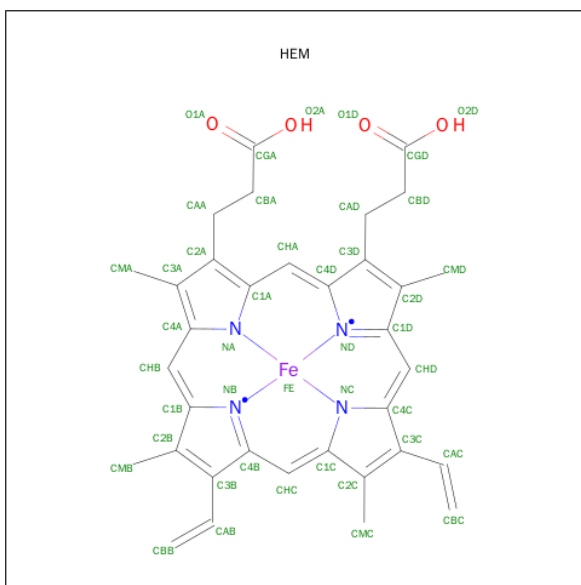
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total O S 5 4 1	0	0
7	C	1	Total O S 5 4 1	0	0
7	B	1	Total O S 5 4 1	0	0

- Molecule 8 is CYANIDE ION (three-letter code: CYN) (formula: CN).



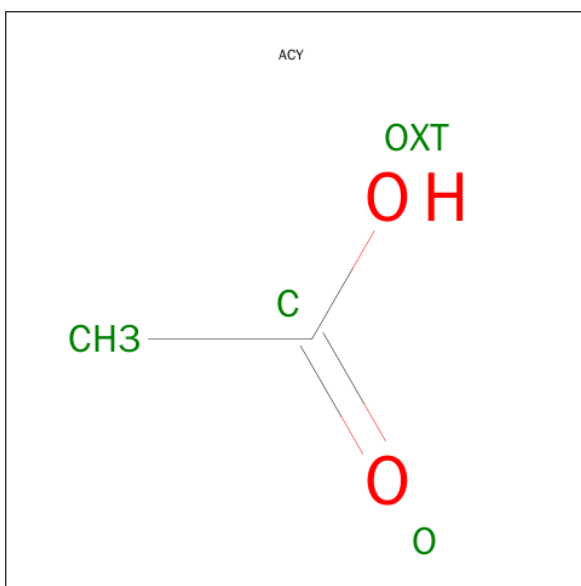
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C N 2 1 1	0	0
8	C	1	Total C N 2 1 1	0	0
8	B	1	Total C N 2 1 1	0	0
8	D	1	Total C N 2 1 1	0	0

- Molecule 9 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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

- Molecule 10 is ACETIC ACID (three-letter code: ACY) (formula: $\text{C}_2\text{H}_4\text{O}_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	C	1	Total C O 4 2 2	0	0
10	C	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	C	1	Total 4	C 2	O 2	0	0
10	D	1	Total 4	C 2	O 2	0	0
10	D	1	Total 4	C 2	O 2	0	0
10	D	1	Total 4	C 2	O 2	0	0

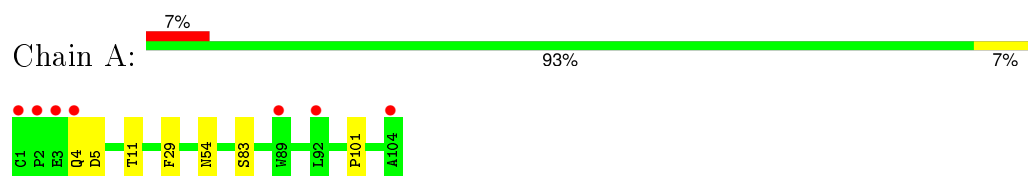
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	95	Total 95	O 95	0	0
11	B	100	Total 100	O 100	0	0
11	C	338	Total 338	O 338	0	0
11	D	329	Total 329	O 329	0	0

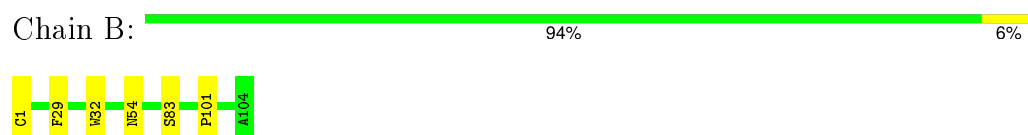
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

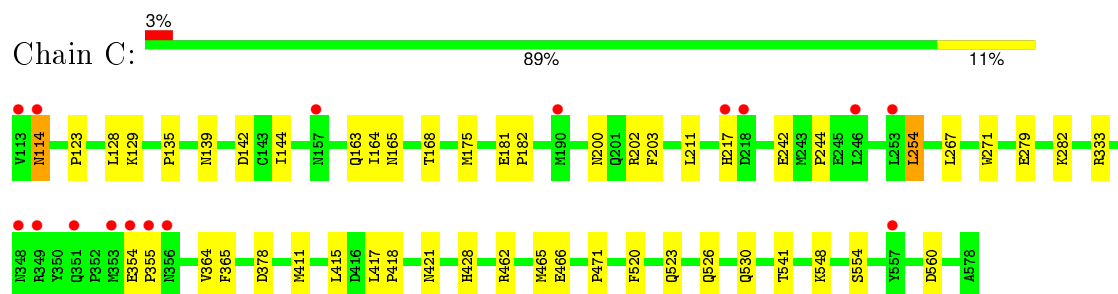
- Molecule 1: MYELOPEROXIDASE



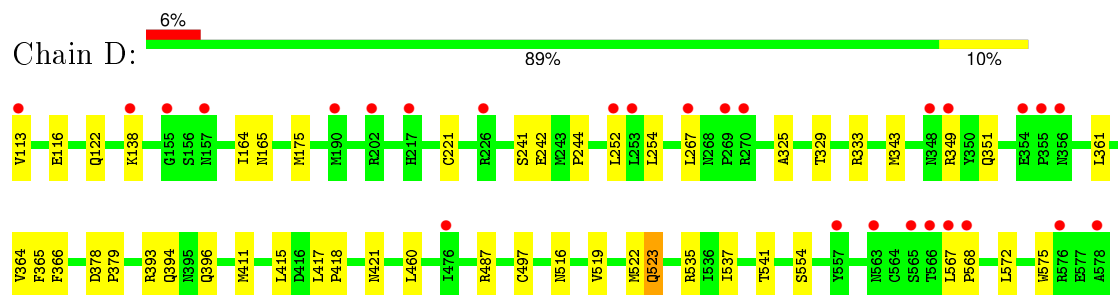
- Molecule 1: MYELOPEROXIDASE



- Molecule 2: MYELOPEROXIDASE



- Molecule 2: MYELOPEROXIDASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	111.26 Å 63.77 Å 92.60 Å 90.00° 97.51° 90.00°	Depositor
Resolution (Å)	10.00 – 1.90 29.38 – 1.90	Depositor EDS
% Data completeness (in resolution range)	93.4 (10.00-1.90) 92.3 (29.38-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.74 (at 1.91 Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.197 , 0.224 0.191 , 0.219	Depositor DCC
R_{free} test set	4646 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	17.1	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 62.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 93125 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10349	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CSO, SCN, NAG, CA, BMA, SO4, HEM, ACY, MAN, CYN, FUC

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	0.42	0/863	0.74	0/1174
1	B	0.41	0/863	0.72	0/1174
2	C	0.39	0/3811	0.66	0/5168
2	D	0.41	0/3811	0.64	0/5168
All	All	0.40	0/9348	0.67	0/12684

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	838	0	798	5	0
1	B	838	0	798	6	0
2	C	3733	0	3724	32	0
2	D	3733	0	3724	32	0
3	C	28	0	26	0	0
3	D	28	0	26	0	0
4	C	71	0	61	0	0
4	D	71	0	61	0	0
5	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	1	0	0	0	0
6	A	3	0	0	0	0
6	B	6	0	0	2	0
6	C	3	0	0	1	0
7	A	5	0	0	0	0
7	B	5	0	0	0	0
7	C	5	0	0	0	0
8	A	2	0	0	1	0
8	B	2	0	0	1	0
8	C	2	0	0	0	0
8	D	2	0	0	0	0
9	B	43	0	30	1	0
9	C	43	0	30	1	0
10	C	12	0	9	0	0
10	D	12	0	9	1	0
11	A	95	0	0	1	0
11	B	100	0	0	1	0
11	C	338	0	0	3	0
11	D	329	0	0	1	0
All	All	10349	0	9296	69	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 4.

All (69) 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)
2:C:333:ARG:HH21	2:C:421:ASN:HD22	1.31	0.75
2:C:333:ARG:HH21	2:C:421:ASN:ND2	1.85	0.74
11:A:193:HOH:O	2:C:129:LYS:HD3	1.92	0.69
2:C:200:ASN:HD22	2:C:203:PHE:H	1.41	0.67
6:C:9:SCN:S	11:C:866:HOH:O	2.54	0.66
2:D:244:PRO:HB2	2:D:343:MET:SD	2.39	0.63
2:D:349:ARG:HG3	2:D:351:GLN:HG2	1.82	0.62
2:C:211:LEU:HD23	2:C:254:LEU:HD13	1.82	0.61
2:C:200:ASN:ND2	2:C:203:PHE:H	2.01	0.58
2:D:241:SER:O	2:D:366:PHE:HA	2.04	0.58
1:A:4:GLN:HG2	1:A:5:ASP:N	2.18	0.57
2:C:200:ASN:ND2	2:C:202:ARG:H	2.02	0.57
2:C:354:GLU:HB3	2:C:355:PRO:HA	1.87	0.56
2:C:135:PRO:HG2	11:C:905:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:271:TRP:CZ3	2:C:279:GLU:HG3	2.44	0.53
2:D:244:PRO:HD3	2:D:364:VAL:O	2.07	0.53
2:D:113:VAL:HG21	2:D:122:GLN:HB2	1.89	0.53
1:B:83:SER:HB3	2:D:554:SER:O	2.10	0.52
1:A:83:SER:HB3	2:C:554:SER:O	2.09	0.52
2:C:244:PRO:HD3	2:C:364:VAL:O	2.08	0.52
2:D:393:ARG:HB2	2:D:396:GLN:HB2	1.91	0.52
2:C:200:ASN:HD22	2:C:202:ARG:H	1.56	0.51
2:D:333:ARG:HH21	2:D:421:ASN:ND2	2.09	0.51
6:B:107:SCN:C	2:D:242:GLU:HG3	2.41	0.50
2:C:417:LEU:HB3	2:C:418:PRO:HD3	1.92	0.50
2:D:417:LEU:HB3	2:D:418:PRO:HD3	1.94	0.50
6:B:107:SCN:N	8:B:108:CYN:N	2.60	0.50
2:D:349:ARG:HE	2:D:351:GLN:HG3	1.76	0.50
1:B:101:PRO:HD2	2:D:164:ILE:O	2.12	0.49
2:D:572:LEU:O	2:D:575:TRP:HB2	2.13	0.49
1:A:101:PRO:HD2	2:C:164:ILE:O	2.13	0.49
2:C:465:MET:HE1	2:C:471:PRO:HG3	1.94	0.49
2:C:333:ARG:HD3	2:C:421:ASN:ND2	2.28	0.49
1:A:29:PHE:CE2	2:C:165:ASN:HB2	2.47	0.48
2:D:411:MET:CE	2:D:415:LEU:HD21	2.43	0.48
8:A:107:CYN:C	9:C:14:HEM:ND	2.77	0.48
2:D:252:LEU:HD11	2:D:537:ILE:HA	1.96	0.48
9:B:109:HEM:HBB2	2:D:242:GLU:OE1	2.14	0.47
1:B:29:PHE:CZ	2:D:329:THR:HG21	2.50	0.47
2:C:128:LEU:HB2	2:C:144:ILE:HB	1.96	0.47
2:D:116:GLU:OE1	2:D:411:MET:HE3	2.14	0.47
2:D:535:ARG:NH2	2:D:567:LEU:O	2.49	0.45
1:A:11:THR:O	2:C:168:THR:HG22	2.16	0.45
2:D:394:GLN:HB3	2:D:460:LEU:HD22	1.99	0.45
2:D:523:GLN:H	2:D:523:GLN:CD	2.21	0.45
2:C:462:ARG:O	2:C:466:GLU:HG2	2.18	0.44
2:D:522:MET:HG3	10:D:17:ACY:H1	2.00	0.44
2:D:411:MET:HE2	2:D:415:LEU:HD21	1.99	0.44
2:D:378:ASP:HB2	2:D:379:PRO:HD3	2.00	0.44
2:C:378:ASP:OD1	2:C:541:THR:HB	2.18	0.44
1:B:32:TRP:CE2	2:D:325:ALA:HB2	2.53	0.43
2:C:282:LYS:HG2	2:C:520:PHE:CZ	2.54	0.43
2:D:361:LEU:O	2:D:364:VAL:HG22	2.19	0.42
2:C:548:LYS:HD2	2:C:560:ASP:HA	2.00	0.42
2:C:526:GLN:NE2	2:C:530:GLN:HE21	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:139:ASN:HB2	2:C:142:ASP:OD1	2.19	0.42
2:D:221:CYS:HA	2:D:366:PHE:O	2.19	0.42
2:D:568:PRO:HG2	11:D:913:HOH:O	2.19	0.42
2:C:114:ASN:HA	11:C:879:HOH:O	2.20	0.42
1:B:1:CYS:HB2	11:B:759:HOH:O	2.20	0.41
2:C:333:ARG:NH2	2:C:421:ASN:HD22	2.08	0.41
2:D:242:GLU:O	2:D:365:PHE:HA	2.20	0.41
2:C:242:GLU:O	2:C:365:PHE:HA	2.20	0.41
2:D:516:ASN:HB3	2:D:519:VAL:CG2	2.50	0.41
2:C:163:GLN:HG2	2:C:428:HIS:NE2	2.35	0.41
2:C:181:GLU:HB2	2:C:182:PRO:HD3	2.02	0.41
2:C:411:MET:HE3	2:C:415:LEU:HD21	2.02	0.41
1:B:29:PHE:CE2	2:D:165:ASN:HB2	2.56	0.41
2:D:378:ASP:OD1	2:D:541:THR:HB	2.21	0.41

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	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
1	B	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
2	C	463/466 (99%)	451 (97%)	11 (2%)	1 (0%)	52	42
2	D	463/466 (99%)	450 (97%)	13 (3%)	0	100	100
All	All	1130/1140 (99%)	1101 (97%)	28 (2%)	1 (0%)	56	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	114	ASN

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	90/90 (100%)	89 (99%)	1 (1%)	80	79
1	B	90/90 (100%)	89 (99%)	1 (1%)	80	79
2	C	410/410 (100%)	404 (98%)	6 (2%)	72	69
2	D	410/410 (100%)	403 (98%)	7 (2%)	68	64
All	All	1000/1000 (100%)	985 (98%)	15 (2%)	72	69

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
2	C	123	PRO
2	C	175	MET
2	C	217	HIS
2	C	254	LEU
2	C	267	LEU
2	C	523	GLN
1	B	54	ASN
2	D	138	LYS
2	D	175	MET
2	D	254	LEU
2	D	267	LEU
2	D	487	ARG
2	D	497	CYS
2	D	523	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
2	C	122	GLN
2	C	200	ASN
2	C	421	ASN

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Mol	Chain	Res	Type
2	C	526	GLN
1	B	54	ASN
2	D	140	GLN
2	D	549	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	$\# Z > 2$
2	CSO	C	150	2	3,6,7	0.63	0	1,6,8	1.98	0
2	CSO	D	150	2	3,6,7	0.57	0	1,6,8	1.83	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	CSO	C	150	2	-	0/1/5/7	0/0/0/0
2	CSO	D	150	2	-	0/1/5/7	0/0/0/0

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.

5.5 Carbohydrates

12 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	$\# Z > 2$
4	NAG	C	640	2,4	14,14,15	0.56	0	15,19,21	0.90	0
4	NAG	C	641	4	14,14,15	0.40	0	15,19,21	0.74	0
4	BMA	C	642	4	11,11,12	0.36	0	14,15,17	0.49	0
4	MAN	C	643	4	11,11,12	0.49	0	14,15,17	0.65	0
4	MAN	C	644	4	11,11,12	0.42	0	14,15,17	0.60	0
4	FUC	C	645	4	10,10,11	0.41	0	14,14,16	0.62	0
4	NAG	D	640	2,4	14,14,15	0.48	0	15,19,21	0.86	0
4	NAG	D	641	4	14,14,15	0.44	0	15,19,21	1.06	2 (13%)
4	BMA	D	642	4	11,11,12	0.46	0	14,15,17	0.62	0
4	MAN	D	643	4	11,11,12	0.43	0	14,15,17	0.72	0
4	MAN	D	644	4	11,11,12	0.46	0	14,15,17	0.60	0
4	FUC	D	645	4	10,10,11	0.47	0	14,14,16	0.71	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
4	NAG	C	640	2,4	-	0/6/23/26	0/1/1/1
4	NAG	C	641	4	-	0/6/23/26	0/1/1/1
4	BMA	C	642	4	-	0/2/19/22	0/1/1/1
4	MAN	C	643	4	-	0/2/19/22	0/1/1/1
4	MAN	C	644	4	-	0/2/19/22	0/1/1/1
4	FUC	C	645	4	-	0/0/17/20	0/1/1/1
4	NAG	D	640	2,4	-	0/6/23/26	0/1/1/1
4	NAG	D	641	4	-	0/6/23/26	0/1/1/1
4	BMA	D	642	4	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MAN	D	643	4	-	0/2/19/22	0/1/1/1
4	MAN	D	644	4	-	0/2/19/22	0/1/1/1
4	FUC	D	645	4	-	0/0/17/20	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	641	NAG	C4-C3-C2	-2.62	107.16	111.23
4	D	641	NAG	C2-N2-C7	-2.59	119.71	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry [i](#)

Of 25 ligands modelled in this entry, 2 are monoatomic - leaving 23 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	$\# Z > 2$
6	SCN	A	105	-	2,2,2	1.12	0	1,1,1	0.51	0
7	SO4	A	106	-	4,4,4	0.30	0	6,6,6	0.08	0
8	CYN	A	107	9	0,1,1	0.00	-	0,0,0	0.00	-
6	SCN	B	105	-	2,2,2	1.15	0	1,1,1	0.55	0
7	SO4	B	106	-	4,4,4	1.01	0	6,6,6	0.08	0
6	SCN	B	107	-	2,2,2	1.14	0	1,1,1	0.51	0
8	CYN	B	108	9	0,1,1	0.00	-	0,0,0	0.00	-
9	HEM	B	109	1,8,2	30,50,50	2.46	10 (33%)	24,82,82	2.63	8 (33%)
7	SO4	C	13	-	4,4,4	0.36	0	6,6,6	0.18	0
9	HEM	C	14	1,8,2	30,50,50	2.65	9 (30%)	24,82,82	2.51	7 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	ACY	C	19	-	1,3,3	2.22	1 (100%)	0,3,3	0.00	-
10	ACY	C	20	-	1,3,3	3.09	1 (100%)	0,3,3	0.00	-
10	ACY	C	21	-	1,3,3	2.27	1 (100%)	0,3,3	0.00	-
8	CYN	C	6	-	0,1,1	0.00	-	0,0,0	0.00	-
3	NAG	C	620	2	14,14,15	0.46	0	15,19,21	1.02	1 (6%)
3	NAG	C	630	2	14,14,15	0.43	0	15,19,21	0.79	1 (6%)
6	SCN	C	9	-	2,2,2	1.12	0	1,1,1	0.48	0
10	ACY	D	16	-	1,3,3	3.05	1 (100%)	0,3,3	0.00	-
10	ACY	D	17	-	1,3,3	3.54	1 (100%)	0,3,3	0.00	-
10	ACY	D	18	-	1,3,3	2.53	1 (100%)	0,3,3	0.00	-
8	CYN	D	5	-	0,1,1	0.00	-	0,0,0	0.00	-
3	NAG	D	620	2	14,14,15	0.51	0	15,19,21	0.87	0
3	NAG	D	630	2	14,14,15	0.53	0	15,19,21	0.68	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
6	SCN	A	105	-	-	0/0/0/0	0/0/0/0
7	SO4	A	106	-	-	0/0/0/0	0/0/0/0
8	CYN	A	107	9	-	0/0/0/0	0/0/0/0
6	SCN	B	105	-	-	0/0/0/0	0/0/0/0
7	SO4	B	106	-	-	0/0/0/0	0/0/0/0
6	SCN	B	107	-	-	0/0/0/0	0/0/0/0
8	CYN	B	108	9	-	0/0/0/0	0/0/0/0
9	HEM	B	109	1,8,2	-	0/10/54/54	0/0/8/8
7	SO4	C	13	-	-	0/0/0/0	0/0/0/0
9	HEM	C	14	1,8,2	-	0/10/54/54	0/0/8/8
10	ACY	C	19	-	-	0/0/0/0	0/0/0/0
10	ACY	C	20	-	-	0/0/0/0	0/0/0/0
10	ACY	C	21	-	-	0/0/0/0	0/0/0/0
8	CYN	C	6	-	-	0/0/0/0	0/0/0/0
3	NAG	C	620	2	-	0/6/23/26	0/1/1/1
3	NAG	C	630	2	-	0/6/23/26	0/1/1/1
6	SCN	C	9	-	-	0/0/0/0	0/0/0/0
10	ACY	D	16	-	-	0/0/0/0	0/0/0/0
10	ACY	D	17	-	-	0/0/0/0	0/0/0/0
10	ACY	D	18	-	-	0/0/0/0	0/0/0/0
8	CYN	D	5	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	D	620	2	-	0/6/23/26	0/1/1/1
3	NAG	D	630	2	-	0/6/23/26	0/1/1/1

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	14	HEM	C3B-C4B	-6.57	1.46	1.51
9	C	14	HEM	C3C-CAC	-6.05	1.40	1.51
9	B	109	HEM	C3C-CAC	-5.83	1.40	1.51
9	C	14	HEM	C2D-C3D	-5.61	1.37	1.54
9	B	109	HEM	C2D-C3D	-5.56	1.37	1.54
9	C	14	HEM	C3B-CAB	-5.48	1.41	1.51
9	B	109	HEM	C3B-CAB	-5.45	1.41	1.51
9	C	14	HEM	C3D-C4D	-5.31	1.44	1.51
9	B	109	HEM	C3B-C4B	-4.69	1.47	1.51
9	B	109	HEM	C2C-C1C	-4.13	1.44	1.52
9	B	109	HEM	C3D-C4D	-3.56	1.47	1.51
9	C	14	HEM	C2C-C1C	-3.51	1.45	1.52
9	B	109	HEM	C1C-NC	2.02	1.38	1.36
9	C	14	HEM	CHD-C4C	2.18	1.41	1.36
10	C	19	ACY	CH3-C	2.22	1.51	1.48
10	C	21	ACY	CH3-C	2.27	1.52	1.48
9	C	14	HEM	CBC-CAC	2.36	1.43	1.29
9	C	14	HEM	CBB-CAB	2.50	1.43	1.29
9	B	109	HEM	CBC-CAC	2.52	1.43	1.29
10	D	18	ACY	CH3-C	2.53	1.52	1.48
9	B	109	HEM	C4C-NC	2.81	1.39	1.36
9	B	109	HEM	CBB-CAB	2.89	1.46	1.29
10	D	16	ACY	CH3-C	3.05	1.53	1.48
10	C	20	ACY	CH3-C	3.09	1.53	1.48
10	D	17	ACY	CH3-C	3.54	1.53	1.48

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	620	NAG	C2-N2-C7	-2.87	119.35	123.04
9	B	109	HEM	CBA-CAA-C2A	-2.31	108.39	112.53
3	C	630	NAG	C2-N2-C7	-2.15	120.28	123.04
9	B	109	HEM	C2D-C3D-C4D	2.43	105.62	101.50
9	C	14	HEM	C2D-C3D-C4D	2.44	105.64	101.50
9	C	14	HEM	C3C-CAC-CBC	2.99	129.04	124.46
9	C	14	HEM	CMD-C2D-C3D	3.07	127.91	114.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	109	HEM	CMD-C2D-C3D	3.25	128.73	114.35
9	B	109	HEM	CAD-C3D-C4D	3.40	124.47	112.47
9	C	14	HEM	CAD-C3D-C4D	3.53	124.92	112.47
9	B	109	HEM	C3C-CAC-CBC	4.66	131.60	124.46
9	B	109	HEM	CAD-C3D-C2D	5.51	129.06	113.22
9	C	14	HEM	CAD-C3D-C2D	5.57	129.24	113.22
9	B	109	HEM	CMB-C2B-C3B	5.83	131.09	116.53
9	C	14	HEM	CMB-C2B-C3B	6.02	131.56	116.53
9	C	14	HEM	CMC-C2C-C3C	6.18	131.96	116.53
9	B	109	HEM	CMC-C2C-C3C	6.28	132.20	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	107	CYN	1	0
6	B	107	SCN	2	0
8	B	108	CYN	1	0
9	B	109	HEM	1	0
9	C	14	HEM	1	0
6	C	9	SCN	1	0
10	D	17	ACY	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	104/104 (100%)	0.14	7 (6%) 21 23	6, 11, 23, 38	0
1	B	104/104 (100%)	0.04	0 100 100	7, 12, 21, 26	0
2	C	465/466 (99%)	0.19	16 (3%) 49 52	5, 13, 24, 33	0
2	D	465/466 (99%)	0.40	27 (5%) 26 29	6, 15, 27, 35	0
All	All	1138/1140 (99%)	0.26	50 (4%) 38 41	5, 13, 26, 38	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	113	VAL	9.6
2	C	355	PRO	7.2
2	D	568	PRO	6.2
2	C	217	HIS	5.4
2	D	355	PRO	5.4
2	D	578	ALA	5.3
2	D	217	HIS	5.2
1	A	3	GLU	5.1
2	D	349	ARG	4.5
2	D	113	VAL	3.7
1	A	4	GLN	3.5
2	D	226	ARG	3.5
2	D	576	ARG	3.5
1	A	1	CYS	3.3
2	C	356	ASN	3.2
2	D	567	LEU	3.2
2	C	349	ARG	3.2
2	D	190	MET	3.2
2	D	253	LEU	3.2
2	D	270	ARG	3.1
2	C	348	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
2	D	356	ASN	2.9
2	C	253	LEU	2.9
2	C	354	GLU	2.9
2	D	565	SER	2.9
2	D	269	PRO	2.9
2	D	354	GLU	2.9
2	C	353	MET	2.8
2	D	563	ASN	2.7
2	D	566	THR	2.7
2	C	190	MET	2.6
1	A	104	ALA	2.6
2	D	267	LEU	2.6
2	D	202	ARG	2.5
2	D	157	ASN	2.5
2	D	155	GLY	2.5
2	C	157	ASN	2.4
2	D	348	ASN	2.4
1	A	92	LEU	2.2
2	D	138	LYS	2.2
2	C	246	LEU	2.2
1	A	89	TRP	2.2
2	C	218	ASP	2.1
2	C	351	GLN	2.1
2	D	476	ILE	2.1
2	D	557	TYR	2.1
2	C	557	TYR	2.1
2	C	114	ASN	2.0
2	D	252	LEU	2.0
1	A	2	PRO	2.0

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

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(Å ²)	Q<0.9
2	CSO	D	150	7/8	0.94	0.11	-	7,10,10,14	0
2	CSO	C	150	7/8	0.91	0.10	-	8,9,10,12	0

6.3 Carbohydrates ⓘ

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(Å ²)	Q<0.9
4	BMA	D	642	11/12	0.96	0.12	3.83	12,13,14,17	0
4	BMA	C	642	11/12	0.95	0.10	1.03	12,13,15,19	0
4	NAG	C	641	14/15	0.95	0.09	-0.14	9,10,12,12	0
4	NAG	D	641	14/15	0.96	0.09	-0.27	9,10,13,13	0
4	MAN	C	643	11/12	0.92	0.15	-	21,23,24,24	0
4	MAN	D	643	11/12	0.90	0.19	-	20,23,25,26	0
4	NAG	C	640	14/15	0.95	0.08	-	9,11,16,17	0
4	MAN	C	644	11/12	0.95	0.09	-	13,14,15,15	0
4	FUC	C	645	10/11	0.95	0.08	-	13,15,16,16	0
4	NAG	D	640	14/15	0.95	0.10	-	11,13,18,20	0
4	FUC	D	645	10/11	0.95	0.13	-	14,15,16,18	0
4	MAN	D	644	11/12	0.92	0.11	-	14,15,16,16	0

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(Å ²)	Q<0.9
8	CYN	A	107	2/2	0.95	0.17	9.26	12,12,12,15	0
3	NAG	D	630	14/15	0.84	0.24	4.05	26,29,30,33	0
10	ACY	C	19	4/4	0.86	0.13	2.76	28,29,29,29	0
3	NAG	C	620	14/15	0.91	0.17	1.72	14,19,22,23	0
8	CYN	D	5	2/2	0.71	0.27	1.44	11,11,11,14	0
3	NAG	D	620	14/15	0.90	0.16	0.73	17,21,25,26	0
10	ACY	D	18	4/4	0.91	0.13	0.33	25,25,25,28	0
9	HEM	B	109	43/43	0.96	0.12	-0.15	6,10,14,14	0
9	HEM	C	14	43/43	0.97	0.12	-0.17	4,9,10,12	0
6	SCN	B	105	3/3	0.99	0.12	-0.59	5,5,5,10	0
6	SCN	C	9	3/3	0.96	0.11	-0.59	19,19,20,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	SCN	B	107	3/3	0.97	0.09	-0.75	26,26,26,28	0
8	CYN	C	6	2/2	0.90	0.10	-0.85	21,21,21,24	0
6	SCN	A	105	3/3	0.97	0.09	-1.29	3,3,4,12	0
5	CA	C	1	1/1	1.00	0.05	-2.68	7,7,7,7	0
5	CA	D	2	1/1	0.99	0.06	-3.50	8,8,8,8	0
10	ACY	C	20	4/4	0.92	0.17	-	26,26,26,26	0
7	SO4	C	13	5/5	0.94	0.13	-	27,27,29,29	0
10	ACY	D	16	4/4	0.92	0.18	-	29,29,29,31	0
7	SO4	A	106	5/5	0.99	0.09	-	25,26,27,28	0
8	CYN	B	108	2/2	0.96	0.15	-	18,18,18,18	0
10	ACY	C	21	4/4	0.92	0.15	-	26,26,27,27	0
10	ACY	D	17	4/4	0.73	0.38	-	33,36,36,38	0
7	SO4	B	106	5/5	0.81	0.48	-	55,55,56,57	0
3	NAG	C	630	14/15	0.89	0.22	-	22,25,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.