wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 04:32 PM GMT

PDB ID	:	4FAS
Title	:	Complex crystal structure of hydroxylamine oxidoreductase and NE1300 from Nitrosomonas europaea
Authors	:	Cedervall, P.E.; Wilmot, C.M.
Deposited on	:	2012-05-22
Resolution	:	2.10 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

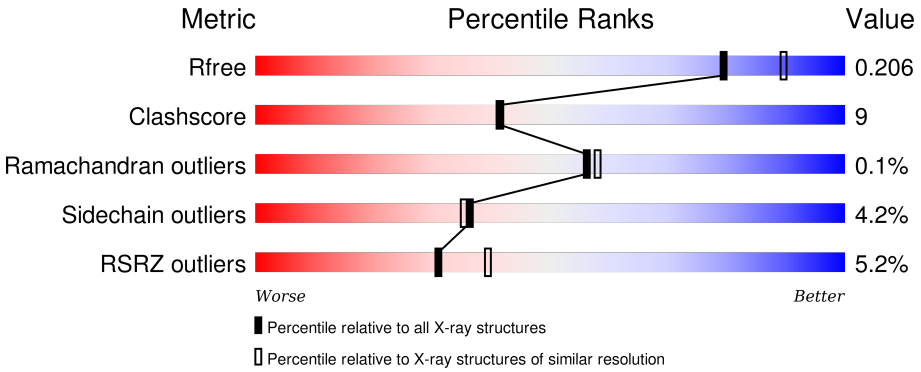
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 <=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	546	% 77% 14% • 8%
1	B	546	% 76% 14% • 8%
1	C	546	3% 78% 13% • 8%
2	D	69	30% 62% 9% 29%
2	E	69	41% 52% 16% • 29%

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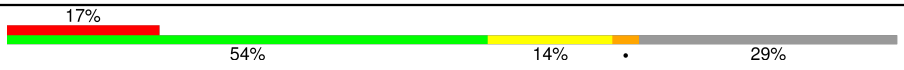
Mol	Chain	Length	Quality of chain
2	F	69	

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	NO3	B	617	-	X	-	-
10	NO3	B	618	-	X	-	-
10	NO3	C	619	-	X	-	-
10	NO3	F	101	-	X	-	-
5	PEG	A	610	-	-	-	X
5	PEG	A	611	-	-	-	X
5	PEG	A	614	-	-	-	X
5	PEG	B	610	-	-	-	X
5	PEG	B	612	-	-	-	X
5	PEG	C	610	-	-	-	X
5	PEG	C	613	-	-	-	X
6	PGE	A	615	-	-	-	X
6	PGE	C	614	-	-	-	X
7	EDO	B	616	-	-	-	X
7	EDO	B	621	-	-	-	X
9	PG4	B	614	-	-	-	X

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 15197 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.

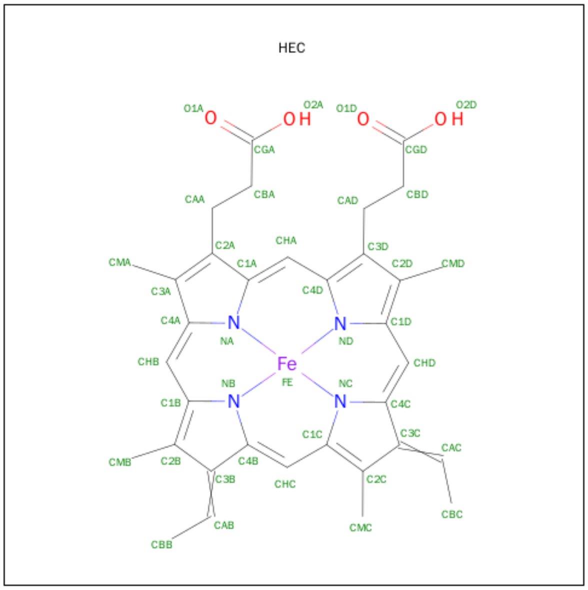
- Molecule 1 is a protein called Hydroxylamine oxidoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	502	Total	C	N	O	S	0	1	0
			4013	2495	711	775	32			
1	B	502	Total	C	N	O	S	0	1	0
			4005	2491	710	772	32			
1	C	502	Total	C	N	O	S	0	0	0
			4005	2491	710	772	32			

- Molecule 2 is a protein called NE1300.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	49	Total	C	N	O	S	0	0	0
			370	233	63	71	3			
2	E	49	Total	C	N	O	S	0	0	0
			370	233	63	71	3			
2	F	49	Total	C	N	O	S	0	0	0
			370	233	63	71	3			

- Molecule 3 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

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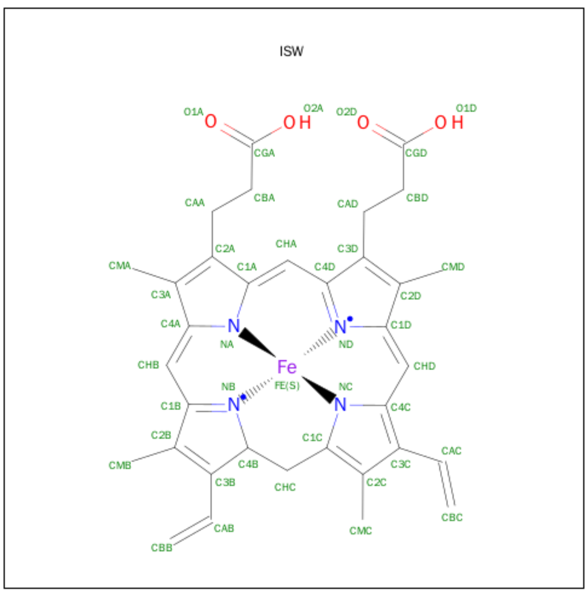
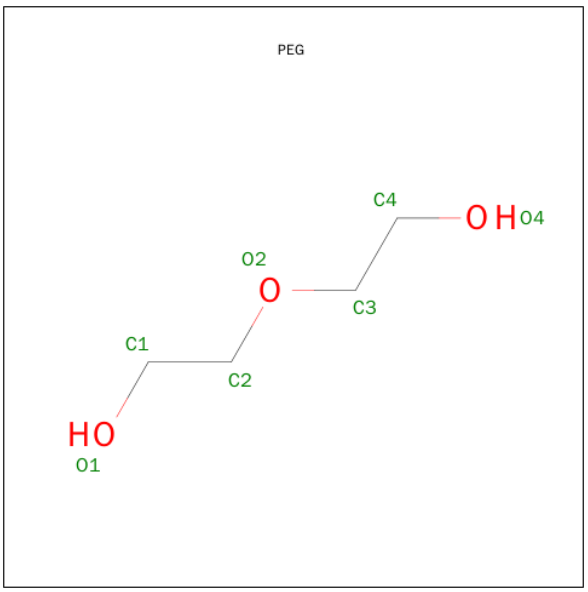
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C Fe N O 43 34 1 4 4	0	0
3	C	1	Total C Fe N O 43 34 1 4 4	0	0
3	C	1	Total C Fe N O 43 34 1 4 4	0	0
3	C	1	Total C Fe N O 43 34 1 4 4	0	0
3	C	1	Total C Fe N O 43 34 1 4 4	0	0
3	C	1	Total C Fe N O 43 34 1 4 4	0	0
3	C	1	Total C Fe N O 43 34 1 4 4	0	0

- Molecule 4 is {3,3'-[(9S)-8,13-DIETHENYL-3,7,12,17-TETRAMETHYL-9,10-DIHYDROP ORPHYRIN-2,18-DIYL-KAPPA 4 N 21 ,N 22 ,N 23 ,N 24]DIPROPANOATO(2-)}IRON (three-letter code: ISW) (formula: $C_{34}H_{34}FeN_4O_4$).



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

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



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

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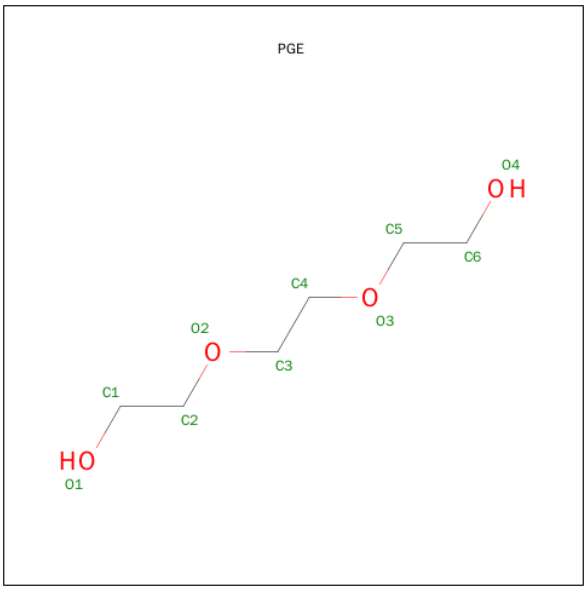
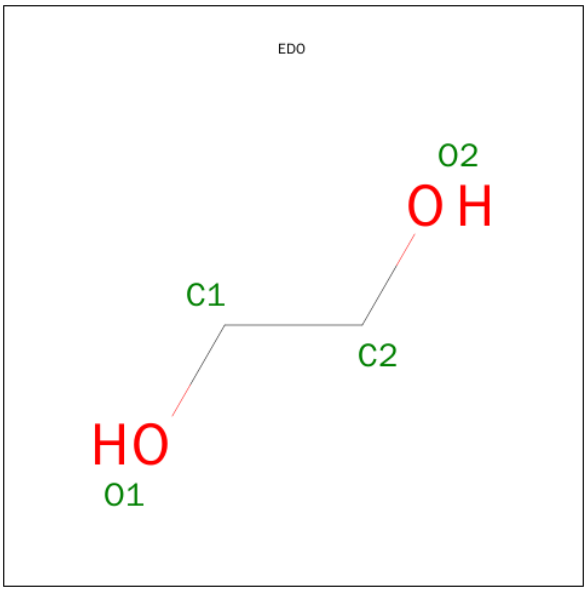
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total C O 7 4 3	0	0
5	C	1	Total C O 7 4 3	0	0
5	C	1	Total C O 7 4 3	0	0
5	F	1	Total C O 7 4 3	0	0

- Molecule 6 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 10 6 4	0	0
6	C	1	Total C O 10 6 4	0	0

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0

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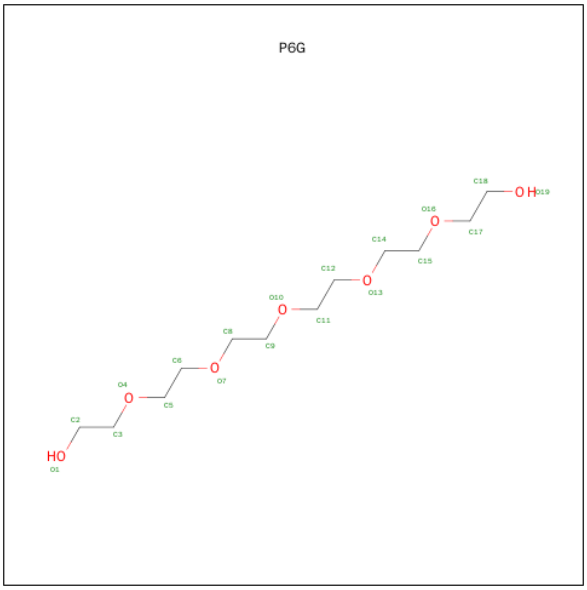
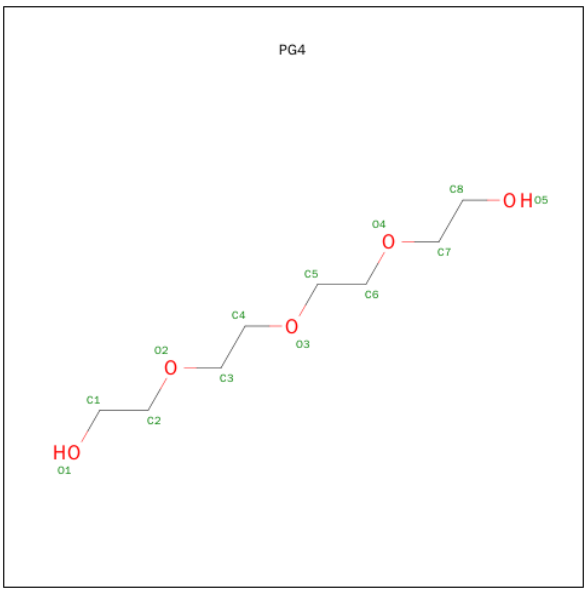
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	1	Total C O 4 2 2	0	0

- Molecule 8 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: $C_{12}H_{26}O_7$).



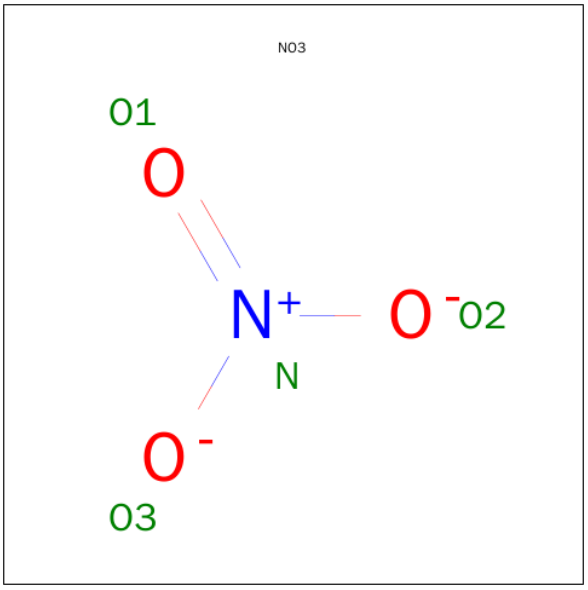
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	1	Total C O 19 12 7	0	0

- Molecule 9 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total C O 13 8 5	0	0

- Molecule 10 is NITRATE ION (three-letter code: NO3) (formula: NO_3).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	B	1	Total N O 4 1 3	0	0
10	B	1	Total N O 4 1 3	0	0
10	C	1	Total N O 4 1 3	0	0
10	F	1	Total N O 4 1 3	0	0

- Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	237	Total O 237 237	0	0
11	B	258	Total O 258 258	0	0
11	C	244	Total O 244 244	0	0
11	D	14	Total O 14 14	0	0
11	E	10	Total O 10 10	0	0

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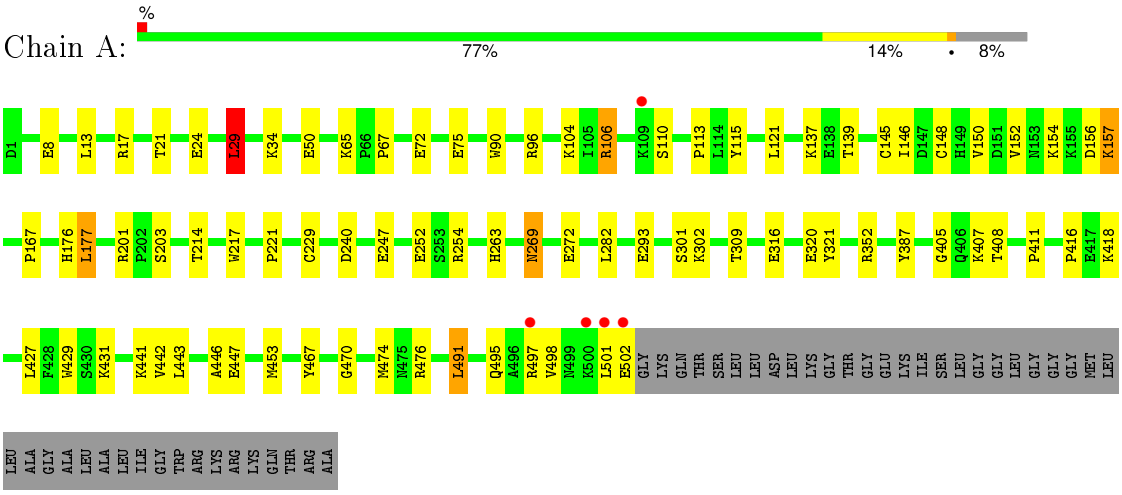
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	F	22	Total O 22 22	0	0

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.

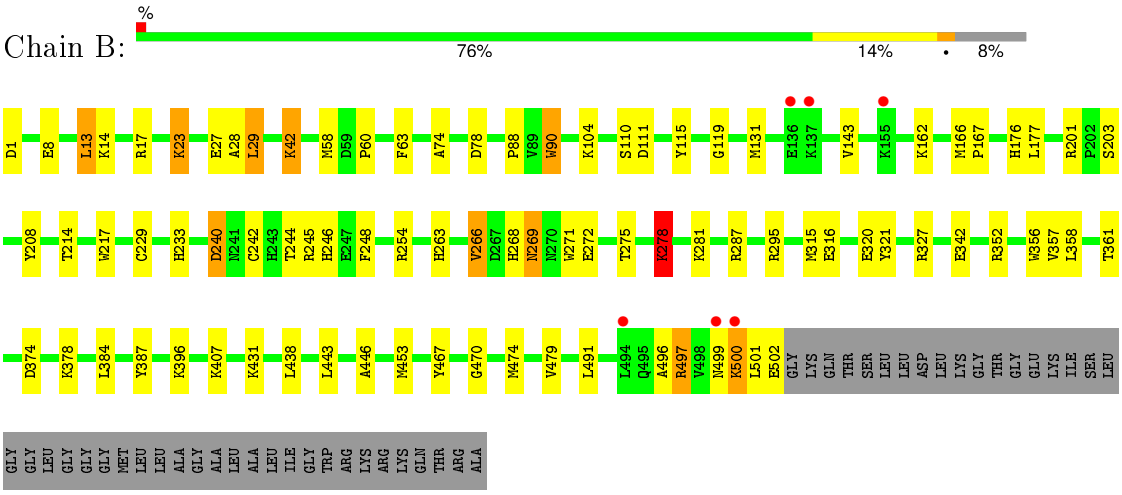
- Molecule 1: Hydroxylamine oxidoreductase

Chain A:



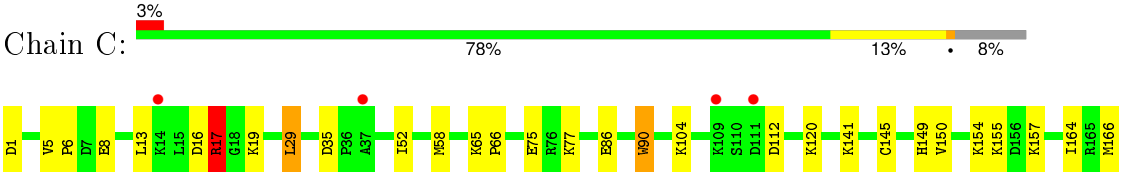
- Molecule 1: Hydroxylamine oxidoreductase

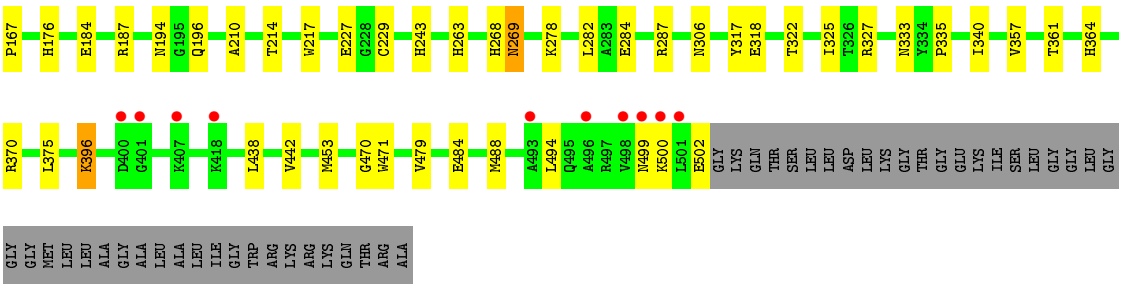
Chain B:



- Molecule 1: Hydroxylamine oxidoreductase

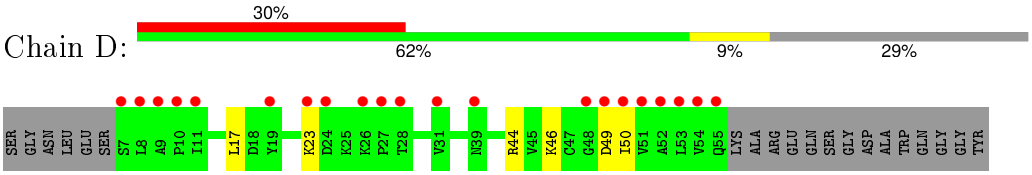
Chain C:





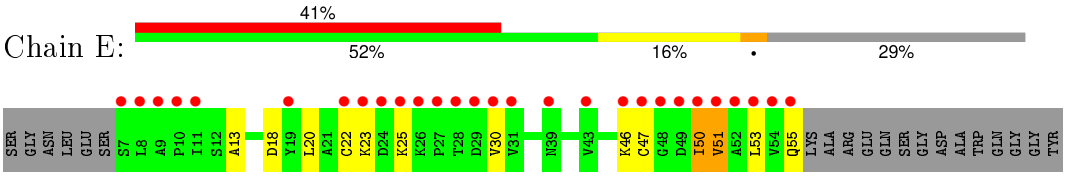
- Molecule 2: NE1300

Chain D:



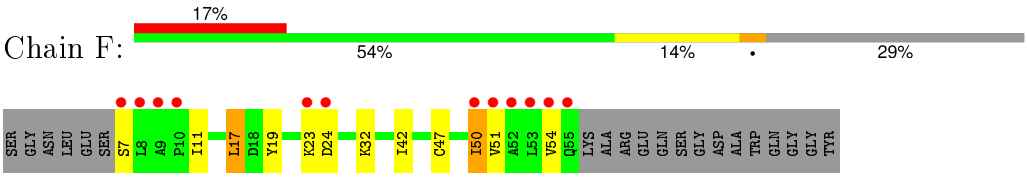
- Molecule 2: NE1300

Chain E:



- Molecule 2: NE1300

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	140.73Å 142.62Å 107.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.89 – 2.10 42.89 – 2.10	Depositor EDS
% Data completeness (in resolution range)	79.9 (42.89-2.10) 79.9 (42.89-2.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.36 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.165 , 0.206 0.166 , 0.206	Depositor DCC
R_{free} test set	5071 reflections (5.31%)	DCC
Wilson B-factor (Å^2)	23.6	Xtriage
Anisotropy	0.603	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 56.4	EDS
Estimated twinning fraction	0.015 for k,h,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 100626 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	15197	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: PGE, ISW, EDO, PG4, P6G, HEC, PEG, NO3

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	1.07	5/4116 (0.1%)	0.92	8/5578 (0.1%)
1	B	1.10	8/4108 (0.2%)	0.96	11/5567 (0.2%)
1	C	1.07	1/4108 (0.0%)	0.92	5/5567 (0.1%)
2	D	0.78	0/373	0.87	0/502
2	E	0.76	0/373	0.86	0/502
2	F	0.87	0/373	0.96	1/502 (0.2%)
All	All	1.06	14/13451 (0.1%)	0.93	25/18218 (0.1%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	272	GLU	CG-CD	5.90	1.60	1.51
1	B	266	VAL	CB-CG1	-5.85	1.40	1.52
1	B	272	GLU	CG-CD	5.78	1.60	1.51
1	B	242	CYS	CB-SG	-5.52	1.72	1.81
1	A	148	CYS	CB-SG	-5.45	1.73	1.81

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	352	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	B	295	ARG	NE-CZ-NH2	-6.06	117.27	120.30
1	C	58	MET	CG-SD-CE	5.93	109.69	100.20
1	A	254	ARG	NE-CZ-NH1	5.93	123.26	120.30
1	B	17	ARG	NE-CZ-NH2	-5.90	117.35	120.30

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	4013	0	3811	59	0
1	B	4005	0	3807	66	0
1	C	4005	0	3808	64	0
2	D	370	0	391	1	0
2	E	370	0	391	9	0
2	F	370	0	391	8	0
3	A	301	0	210	15	0
3	B	301	0	210	17	0
3	C	301	0	210	20	0
4	A	43	0	28	11	0
4	B	43	0	28	14	0
4	C	43	0	28	11	0
5	A	42	0	60	5	0
5	B	28	0	40	4	0
5	C	42	0	60	4	0
5	F	7	0	10	1	0
6	A	10	0	14	2	0
6	C	10	0	14	4	0
7	A	16	0	24	2	0
7	B	20	0	30	0	0
7	C	24	0	36	3	0
8	B	19	0	26	1	0
9	B	13	0	18	1	0
10	B	8	0	0	0	0
10	C	4	0	0	0	0
10	F	4	0	0	0	0
11	A	237	0	0	4	0
11	B	258	0	0	1	0
11	C	244	0	0	3	0
11	D	14	0	0	0	0
11	E	10	0	0	0	0
11	F	22	0	0	1	0
All	All	15197	0	13645	239	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 9.

The worst 5 of 239 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)
4:A:608:ISW:HBAA	3:B:605:HEC:O1D	1.65	0.96
4:B:608:ISW:HBAA	3:C:606:HEC:O1D	1.66	0.95
1:B:497:ARG:HH11	1:B:497:ARG:HB2	1.31	0.95
1:B:497:ARG:HH11	1:B:497:ARG:CB	1.80	0.94
5:A:614:PEG:H42	4:C:601:ISW:HMAA	1.49	0.93

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	501/546 (92%)	482 (96%)	19 (4%)	0	100	100
1	B	500/546 (92%)	483 (97%)	16 (3%)	1 (0%)	52	53
1	C	500/546 (92%)	478 (96%)	21 (4%)	1 (0%)	52	53
2	D	47/69 (68%)	45 (96%)	2 (4%)	0	100	100
2	E	47/69 (68%)	44 (94%)	3 (6%)	0	100	100
2	F	47/69 (68%)	45 (96%)	2 (4%)	0	100	100
All	All	1642/1845 (89%)	1577 (96%)	63 (4%)	2 (0%)	56	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	268	HIS
1	C	268	HIS

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	430/459 (94%)	414 (96%)	16 (4%)	41	41
1	B	429/459 (94%)	410 (96%)	19 (4%)	35	33
1	C	429/459 (94%)	416 (97%)	13 (3%)	48	51
2	D	43/57 (75%)	39 (91%)	4 (9%)	11	7
2	E	43/57 (75%)	39 (91%)	4 (9%)	11	7
2	F	43/57 (75%)	40 (93%)	3 (7%)	19	15
All	All	1417/1548 (92%)	1358 (96%)	59 (4%)	36	35

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	278	LYS
1	B	499	ASN
2	E	51	VAL
1	B	287	ARG
1	B	358	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	269	ASN
1	B	448	ASN
1	C	461	ASN
1	A	489	GLN
1	C	448	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

64 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	$\#\|Z\| > 2$
3	HEC	A	601	1	24,50,50	1.32	4 (16%)	19,82,82	2.49	5 (26%)
3	HEC	A	602	1	24,50,50	1.70	5 (20%)	19,82,82	2.91	6 (31%)
3	HEC	A	603	1	24,50,50	1.34	2 (8%)	19,82,82	2.51	5 (26%)
3	HEC	A	604	1	24,50,50	1.62	5 (20%)	19,82,82	3.40	6 (31%)
3	HEC	A	605	1	24,50,50	1.40	3 (12%)	19,82,82	2.70	8 (42%)
3	HEC	A	606	1	24,50,50	1.53	7 (29%)	19,82,82	3.08	6 (31%)
3	HEC	A	607	1	24,50,50	1.68	6 (25%)	19,82,82	3.25	10 (52%)
4	ISW	A	608	1	29,50,50	2.96	12 (41%)	23,82,82	4.29	10 (43%)
5	PEG	A	609	-	6,6,6	0.22	0	5,5,5	1.00	0
5	PEG	A	610	-	6,6,6	0.27	0	5,5,5	1.05	0
5	PEG	A	611	-	6,6,6	0.64	0	5,5,5	0.49	0
5	PEG	A	612	-	6,6,6	0.53	0	5,5,5	0.29	0
5	PEG	A	613	-	6,6,6	0.55	0	5,5,5	0.52	0
5	PEG	A	614	-	6,6,6	0.75	0	5,5,5	0.79	0
6	PGE	A	615	-	9,9,9	0.67	0	8,8,8	0.78	0
7	EDO	A	616	-	3,3,3	0.62	0	2,2,2	1.07	0
7	EDO	A	617	-	3,3,3	0.68	0	2,2,2	0.41	0
7	EDO	A	618	-	3,3,3	0.47	0	2,2,2	0.27	0
7	EDO	A	619	-	3,3,3	0.57	0	2,2,2	0.41	0
3	HEC	B	601	1	24,50,50	1.60	6 (25%)	19,82,82	2.80	7 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	HEC	B	602	1	24,50,50	1.70	4 (16%)	19,82,82	2.48	8 (42%)
3	HEC	B	603	1	24,50,50	1.48	4 (16%)	19,82,82	2.88	9 (47%)
3	HEC	B	604	1	24,50,50	1.34	5 (20%)	19,82,82	3.21	6 (31%)
3	HEC	B	605	1	24,50,50	1.52	5 (20%)	19,82,82	2.29	7 (36%)
3	HEC	B	606	1	24,50,50	1.49	5 (20%)	19,82,82	2.48	4 (21%)
3	HEC	B	607	1	24,50,50	1.58	6 (25%)	19,82,82	2.70	7 (36%)
4	ISW	B	608	1	29,50,50	3.50	13 (44%)	23,82,82	4.09	11 (47%)
5	PEG	B	609	-	6,6,6	0.46	0	5,5,5	0.88	0
5	PEG	B	610	-	6,6,6	0.50	0	5,5,5	0.48	0
5	PEG	B	611	-	6,6,6	0.34	0	5,5,5	0.94	0
5	PEG	B	612	-	6,6,6	0.69	0	5,5,5	0.67	0
8	P6G	B	613	-	18,18,18	0.49	0	17,17,17	0.74	0
9	PG4	B	614	-	12,12,12	0.62	0	11,11,11	0.91	0
7	EDO	B	615	-	3,3,3	0.63	0	2,2,2	0.10	0
7	EDO	B	616	-	3,3,3	0.50	0	2,2,2	0.49	0
10	NO3	B	617	-	3,3,3	3.14	3 (100%)	3,3,3	0.62	0
10	NO3	B	618	-	3,3,3	3.65	3 (100%)	3,3,3	0.45	0
7	EDO	B	619	-	3,3,3	0.27	0	2,2,2	0.80	0
7	EDO	B	620	-	3,3,3	0.74	0	2,2,2	0.45	0
7	EDO	B	621	-	3,3,3	0.49	0	2,2,2	0.23	0
4	ISW	C	601	1	29,50,50	3.23	16 (55%)	23,82,82	3.85	8 (34%)
3	HEC	C	602	1	24,50,50	1.42	4 (16%)	19,82,82	2.84	7 (36%)
3	HEC	C	603	1	24,50,50	1.54	5 (20%)	19,82,82	2.41	7 (36%)
3	HEC	C	604	1	24,50,50	1.49	5 (20%)	19,82,82	2.94	5 (26%)
3	HEC	C	605	1	24,50,50	1.66	4 (16%)	19,82,82	3.28	7 (36%)
3	HEC	C	606	1	24,50,50	1.27	3 (12%)	19,82,82	2.55	6 (31%)
3	HEC	C	607	1	24,50,50	1.55	4 (16%)	19,82,82	2.34	6 (31%)
3	HEC	C	608	1	24,50,50	1.33	4 (16%)	19,82,82	3.01	9 (47%)
5	PEG	C	609	-	6,6,6	0.48	0	5,5,5	0.44	0
5	PEG	C	610	-	6,6,6	0.74	0	5,5,5	0.61	0
5	PEG	C	611	-	6,6,6	0.56	0	5,5,5	0.59	0
5	PEG	C	612	-	6,6,6	0.46	0	5,5,5	0.83	0
5	PEG	C	613	-	6,6,6	0.65	0	5,5,5	0.84	0
6	PGE	C	614	-	9,9,9	0.36	0	8,8,8	1.01	0
7	EDO	C	615	-	3,3,3	0.46	0	2,2,2	0.31	0
7	EDO	C	616	-	3,3,3	0.21	0	2,2,2	0.83	0
7	EDO	C	617	-	3,3,3	0.53	0	2,2,2	0.40	0
7	EDO	C	618	-	3,3,3	0.73	0	2,2,2	0.13	0
10	NO3	C	619	-	3,3,3	3.40	3 (100%)	3,3,3	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	EDO	C	620	-	3,3,3	0.82	0	2,2,2	0.39	0
7	EDO	C	621	-	3,3,3	0.56	0	2,2,2	0.51	0
5	PEG	C	622	-	6,6,6	0.95	0	5,5,5	1.11	0
10	NO3	F	101	-	3,3,3	3.57	3 (100%)	3,3,3	0.18	0
5	PEG	F	102	-	6,6,6	0.58	0	5,5,5	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
3	HEC	A	601	1	-	0/6/54/54	0/0/8/8
3	HEC	A	602	1	-	0/6/54/54	0/0/8/8
3	HEC	A	603	1	-	0/6/54/54	0/0/8/8
3	HEC	A	604	1	-	0/6/54/54	0/0/8/8
3	HEC	A	605	1	-	0/6/54/54	0/0/8/8
3	HEC	A	606	1	-	0/6/54/54	0/0/8/8
3	HEC	A	607	1	-	0/6/54/54	0/0/8/8
4	ISW	A	608	1	-	0/8/74/74	0/0/8/8
5	PEG	A	609	-	-	0/4/4/4	0/0/0/0
5	PEG	A	610	-	-	0/4/4/4	0/0/0/0
5	PEG	A	611	-	-	0/4/4/4	0/0/0/0
5	PEG	A	612	-	-	0/4/4/4	0/0/0/0
5	PEG	A	613	-	-	0/4/4/4	0/0/0/0
5	PEG	A	614	-	-	0/4/4/4	0/0/0/0
6	PGE	A	615	-	-	0/7/7/7	0/0/0/0
7	EDO	A	616	-	-	0/1/1/1	0/0/0/0
7	EDO	A	617	-	-	0/1/1/1	0/0/0/0
7	EDO	A	618	-	-	0/1/1/1	0/0/0/0
7	EDO	A	619	-	-	0/1/1/1	0/0/0/0
3	HEC	B	601	1	-	0/6/54/54	0/0/8/8
3	HEC	B	602	1	-	0/6/54/54	0/0/8/8
3	HEC	B	603	1	-	0/6/54/54	0/0/8/8
3	HEC	B	604	1	-	0/6/54/54	0/0/8/8
3	HEC	B	605	1	-	0/6/54/54	0/0/8/8
3	HEC	B	606	1	-	0/6/54/54	0/0/8/8
3	HEC	B	607	1	-	0/6/54/54	0/0/8/8
4	ISW	B	608	1	-	0/8/74/74	0/0/8/8
5	PEG	B	609	-	-	0/4/4/4	0/0/0/0
5	PEG	B	610	-	-	0/4/4/4	0/0/0/0
5	PEG	B	611	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEG	B	612	-	-	0/4/4/4	0/0/0/0
8	P6G	B	613	-	-	0/16/16/16	0/0/0/0
9	PG4	B	614	-	-	0/10/10/10	0/0/0/0
7	EDO	B	615	-	-	0/1/1/1	0/0/0/0
7	EDO	B	616	-	-	0/1/1/1	0/0/0/0
10	NO3	B	617	-	-	0/0/0/0	0/0/0/0
10	NO3	B	618	-	-	0/0/0/0	0/0/0/0
7	EDO	B	619	-	-	0/1/1/1	0/0/0/0
7	EDO	B	620	-	-	0/1/1/1	0/0/0/0
7	EDO	B	621	-	-	0/1/1/1	0/0/0/0
4	ISW	C	601	1	-	0/8/74/74	0/0/8/8
3	HEC	C	602	1	-	0/6/54/54	0/0/8/8
3	HEC	C	603	1	-	0/6/54/54	0/0/8/8
3	HEC	C	604	1	-	0/6/54/54	0/0/8/8
3	HEC	C	605	1	-	0/6/54/54	0/0/8/8
3	HEC	C	606	1	-	0/6/54/54	0/0/8/8
3	HEC	C	607	1	-	0/6/54/54	0/0/8/8
3	HEC	C	608	1	-	0/6/54/54	0/0/8/8
5	PEG	C	609	-	-	0/4/4/4	0/0/0/0
5	PEG	C	610	-	-	0/4/4/4	0/0/0/0
5	PEG	C	611	-	-	0/4/4/4	0/0/0/0
5	PEG	C	612	-	-	0/4/4/4	0/0/0/0
5	PEG	C	613	-	-	0/4/4/4	0/0/0/0
6	PGE	C	614	-	-	0/7/7/7	0/0/0/0
7	EDO	C	615	-	-	0/1/1/1	0/0/0/0
7	EDO	C	616	-	-	0/1/1/1	0/0/0/0
7	EDO	C	617	-	-	0/1/1/1	0/0/0/0
7	EDO	C	618	-	-	0/1/1/1	0/0/0/0
10	NO3	C	619	-	-	0/0/0/0	0/0/0/0
7	EDO	C	620	-	-	0/1/1/1	0/0/0/0
7	EDO	C	621	-	-	0/1/1/1	0/0/0/0
5	PEG	C	622	-	-	0/4/4/4	0/0/0/0
10	NO3	F	101	-	-	0/0/0/0	0/0/0/0
5	PEG	F	102	-	-	0/4/4/4	0/0/0/0

The worst 5 of 149 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	602	HEC	C4B-NB	-4.73	1.30	1.36
3	A	604	HEC	C1A-NA	-4.12	1.31	1.36
3	C	605	HEC	C3C-C2C	-4.09	1.36	1.40
3	B	602	HEC	C3B-C2B	-4.02	1.36	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	607	HEC	C3B-C2B	-3.99	1.36	1.40

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	601	ISW	C3C-CAC-CBC	-10.22	105.42	126.32
4	B	608	ISW	C3C-CAC-CBC	-9.92	106.02	126.32
4	A	608	ISW	CBB-CAB-C3B	-9.47	112.28	126.36
4	A	608	ISW	C3C-CAC-CBC	-9.32	107.25	126.32
3	C	604	HEC	CBB-CAB-C3B	-9.07	107.19	127.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

39 monomers are involved in 105 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	HEC	4	0
3	A	602	HEC	4	0
3	A	603	HEC	1	0
3	A	604	HEC	3	0
3	A	605	HEC	4	0
3	A	606	HEC	1	0
4	A	608	ISW	11	0
5	A	612	PEG	1	0
5	A	613	PEG	3	0
5	A	614	PEG	1	0
6	A	615	PGE	2	0
7	A	617	EDO	1	0
7	A	619	EDO	1	0
3	B	601	HEC	3	0
3	B	602	HEC	3	0
3	B	603	HEC	4	0
3	B	604	HEC	2	0
3	B	605	HEC	4	0
3	B	606	HEC	2	0
3	B	607	HEC	1	0
4	B	608	ISW	14	0
5	B	609	PEG	3	0
5	B	612	PEG	1	0
8	B	613	P6G	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	614	PG4	1	0
4	C	601	ISW	11	0
3	C	602	HEC	5	0
3	C	603	HEC	3	0
3	C	604	HEC	1	0
3	C	605	HEC	4	0
3	C	606	HEC	5	0
3	C	607	HEC	1	0
3	C	608	HEC	2	0
5	C	610	PEG	3	0
5	C	612	PEG	1	0
6	C	614	PGE	4	0
7	C	616	EDO	1	0
7	C	617	EDO	2	0
5	F	102	PEG	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, 95^{th} 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	502/546 (91%)	-0.22	5 (0%) 84 87	17, 33, 52, 88	0
1	B	502/546 (91%)	-0.28	6 (1%) 81 85	18, 34, 53, 80	0
1	C	502/546 (91%)	-0.04	14 (2%) 56 64	18, 35, 55, 82	0
2	D	49/69 (71%)	1.91	21 (42%) 0 0	39, 58, 89, 96	0
2	E	49/69 (71%)	2.52	28 (57%) 0 0	36, 64, 94, 101	0
2	F	49/69 (71%)	1.11	12 (24%) 1 1	35, 48, 72, 84	0
All	All	1653/1845 (89%)	-0.00	86 (5%) 31 39	17, 35, 63, 101	0

The worst 5 of 86 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	53	LEU	8.0
2	F	54	VAL	7.3
2	E	54	VAL	6.8
2	E	51	VAL	6.5
2	D	54	VAL	6.4

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

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, 95^{th} 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
5	PEG	B	612	7/7	0.77	0.24	15.38	63,68,69,71	0
5	PEG	A	614	7/7	0.80	0.26	10.82	54,61,63,64	0
5	PEG	C	610	7/7	0.81	0.24	8.86	54,58,61,63	0
5	PEG	B	610	7/7	0.81	0.18	5.08	58,59,63,66	0
7	EDO	B	621	4/4	0.94	0.16	4.97	51,52,52,53	0
5	PEG	C	613	7/7	0.86	0.17	3.91	50,55,60,61	0
5	PEG	A	610	7/7	0.94	0.25	3.85	56,57,64,67	0
7	EDO	B	616	4/4	0.80	0.20	3.75	60,61,62,63	0
5	PEG	A	611	7/7	0.92	0.19	3.48	53,55,57,59	0
9	PG4	B	614	13/13	0.87	0.16	3.30	43,50,64,65	0
6	PGE	A	615	10/10	0.88	0.18	3.27	52,55,62,62	0
6	PGE	C	614	10/10	0.91	0.16	2.07	49,52,54,57	0
5	PEG	C	609	7/7	0.91	0.17	1.90	55,59,59,61	0
8	P6G	B	613	19/19	0.87	0.16	1.77	54,60,64,65	0
3	HEC	B	607	43/43	0.99	0.13	1.58	15,21,31,36	0
5	PEG	C	622	7/7	0.83	0.24	1.44	43,48,50,51	0
3	HEC	B	606	43/43	0.99	0.13	1.43	15,21,25,26	0
5	PEG	C	611	7/7	0.82	0.20	1.35	54,60,63,64	0
3	HEC	B	605	43/43	0.99	0.11	1.33	17,24,30,36	0
4	ISW	A	608	43/43	0.96	0.11	1.17	21,32,46,47	0
3	HEC	C	608	43/43	0.99	0.14	1.14	16,21,32,33	0
3	HEC	A	605	43/43	0.99	0.15	1.10	17,23,37,39	0
3	HEC	C	605	43/43	0.99	0.11	1.00	17,25,30,32	0
3	HEC	A	606	43/43	0.99	0.12	1.00	17,23,29,30	0
3	HEC	A	602	43/43	0.98	0.11	0.92	20,24,29,34	0
4	ISW	C	601	43/43	0.95	0.14	0.91	20,32,47,50	0
5	PEG	A	612	7/7	0.88	0.18	0.89	56,58,61,64	0
5	PEG	A	613	7/7	0.86	0.21	0.89	56,57,58,60	0
3	HEC	A	603	43/43	0.98	0.10	0.66	20,28,32,34	0
3	HEC	C	606	43/43	0.99	0.12	0.63	17,22,33,44	0
4	ISW	B	608	43/43	0.95	0.14	0.56	22,34,51,56	0
3	HEC	A	607	43/43	0.99	0.10	0.55	20,24,30,32	0
3	HEC	A	604	43/43	0.99	0.12	0.53	20,25,31,36	0
3	HEC	B	604	43/43	0.99	0.10	0.38	15,24,28,33	0
5	PEG	B	609	7/7	0.92	0.12	0.37	46,48,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	HEC	C	603	43/43	0.98	0.10	0.34	18,25,28,31	0
3	HEC	C	607	43/43	0.99	0.12	0.34	16,22,28,32	0
3	HEC	A	601	43/43	0.98	0.10	0.17	21,29,33,44	0
7	EDO	B	620	4/4	0.80	0.14	0.06	46,51,52,55	0
3	HEC	B	603	43/43	0.98	0.09	-0.06	23,29,33,35	0
3	HEC	C	604	43/43	0.98	0.10	-0.11	20,25,29,31	0
10	NO3	B	617	4/4	0.93	0.12	-0.29	51,53,54,56	0
7	EDO	B	619	4/4	0.95	0.10	-0.33	45,47,49,50	0
3	HEC	B	601	43/43	0.98	0.09	-0.57	26,34,43,48	0
3	HEC	C	602	43/43	0.98	0.09	-0.59	25,34,39,43	0
3	HEC	B	602	43/43	0.99	0.09	-0.68	21,26,31,33	0
7	EDO	C	617	4/4	0.93	0.09	-0.77	42,45,46,49	0
7	EDO	A	616	4/4	0.88	0.13	-1.30	44,46,46,50	0
7	EDO	C	621	4/4	0.92	0.16	-	41,42,44,45	0
5	PEG	B	611	7/7	0.91	0.12	-	60,61,61,62	0
10	NO3	F	101	4/4	0.80	0.28	-	70,71,71,71	0
7	EDO	A	618	4/4	0.93	0.10	-	42,46,46,52	0
10	NO3	C	619	4/4	0.83	0.24	-	72,72,72,72	0
7	EDO	A	619	4/4	0.95	0.19	-	44,45,48,49	0
7	EDO	C	615	4/4	0.91	0.12	-	50,51,52,55	0
7	EDO	A	617	4/4	0.74	0.25	-	63,63,63,65	0
7	EDO	B	615	4/4	0.83	0.17	-	50,51,51,55	0
7	EDO	C	618	4/4	0.84	0.17	-	51,52,53,55	0
5	PEG	C	612	7/7	0.85	0.14	-	54,56,58,60	0
7	EDO	C	620	4/4	0.87	0.14	-	48,48,49,51	0
7	EDO	C	616	4/4	0.92	0.14	-	40,45,46,50	0
5	PEG	F	102	7/7	0.88	0.24	-	50,51,54,56	0
10	NO3	B	618	4/4	0.78	0.25	-	67,68,68,69	0
5	PEG	A	609	7/7	0.93	0.13	-	44,45,51,51	0

6.5 Other polymers (i)

There are no such residues in this entry.