



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:43 PM UTC

PDB ID : 2Y3Y / pdb_00002y3y
Title : Holo-Ni(II) HpNikR is a symmetric tetramer containing four canonic square-planar Ni(II) ions at physiological pH
Authors : Benini, S.; Cianci, M.; Ciurli, S.
Deposited on : 2011-01-04
Resolution : 2.39 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

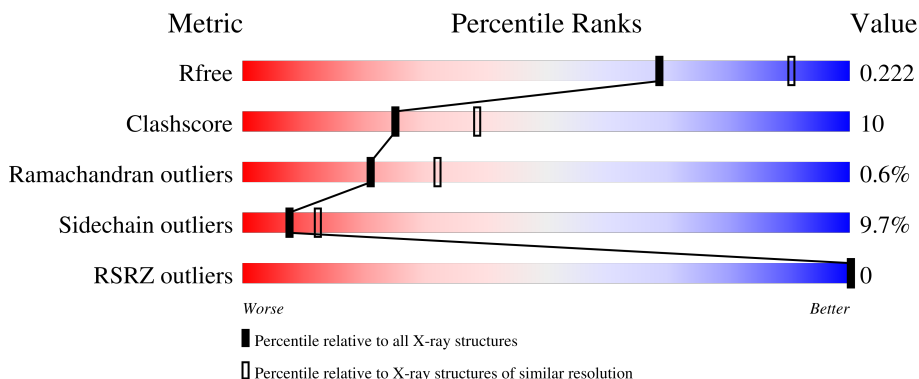
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	91	
1	B	91	
1	C	91	
1	D	91	
2	Q	11	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 2807 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PUTATIVE NICKEL-RESPONSIVE REGULATOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	83	Total	C	N	O	S	0	0	0
			661	412	123	122	4			
1	B	83	Total	C	N	O	S	0	0	0
			662	412	123	123	4			
1	C	81	Total	C	N	O	S	0	0	0
			648	405	120	119	4			
1	D	83	Total	C	N	O	S	0	0	0
			662	412	123	123	4			

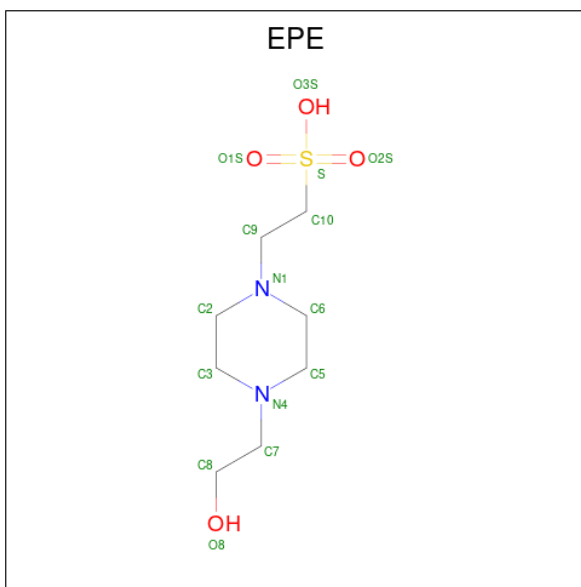
- Molecule 2 is a protein called UNDECAPEPTIDE-GSSSGSASGAG.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	Q	11	Total	C	N	O	0	0	1
			53	28	10	15			

- Molecule 3 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

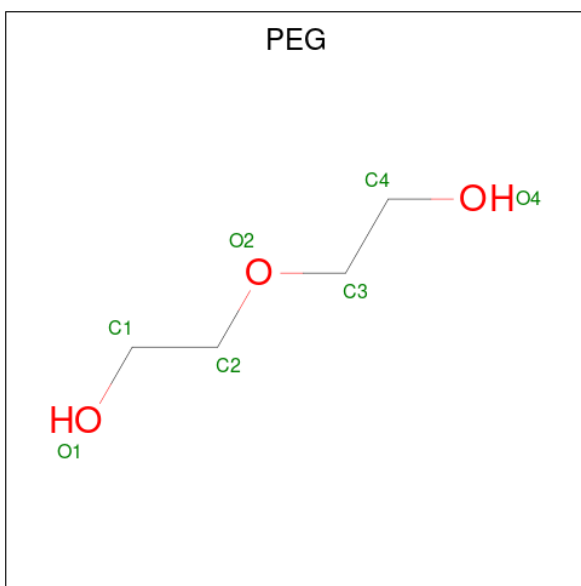
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ni	0	0
			1	1		
3	B	1	Total	Ni	0	0
			1	1		
3	C	1	Total	Ni	0	0
			1	1		
3	D	1	Total	Ni	0	0
			1	1		

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	18	Total	O	0	0
			18	18		
6	B	17	Total	O	0	0
			17	17		
6	C	17	Total	O	0	0
			17	17		
6	D	13	Total	O	0	0
			13	13		
6	Q	1	Total	O	0	0
			1	1		

3 Residue-property plots [i](#)

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

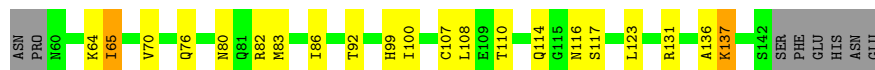
• Molecule 1: PUTATIVE NICKEL-RESPONSIVE REGULATOR

Chain A: 



• Molecule 1: PUTATIVE NICKEL-RESPONSIVE REGULATOR

Chain B: 



• Molecule 1: PUTATIVE NICKEL-RESPONSIVE REGULATOR

Chain C: 



• Molecule 1: PUTATIVE NICKEL-RESPONSIVE REGULATOR

Chain D: 



• Molecule 2: UNDECAPEPTIDE-GSSSGSASGAG

Chain Q: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	72.97 Å 72.97 Å 116.73 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.98 – 2.39 72.97 – 2.39	Depositor EDS
% Data completeness (in resolution range)	94.8 (72.98-2.39) 94.8 (72.97-2.39)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.67 (at 2.38 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.229 , 0.279 (Not available) , 0.222	Depositor DCC
R_{free} test set	1177 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	42.7	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 14.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.489 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2807	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NI, EPE, PEG

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	1.40	1/670 (0.1%)	1.25	3/902 (0.3%)
1	B	1.55	3/671 (0.4%)	1.35	1/903 (0.1%)
1	C	1.43	3/657 (0.5%)	1.36	4/884 (0.5%)
1	D	1.47	2/671 (0.3%)	1.39	4/903 (0.4%)
2	Q	0.87	0/52	1.49	0/68
All	All	1.45	9/2721 (0.3%)	1.34	12/3660 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	100	ILE	CA-CB	6.25	1.61	1.54
1	C	72	TYR	N-CA	-5.90	1.38	1.46
1	C	80	ASN	CA-C	-5.73	1.45	1.52
1	D	100	ILE	CA-CB	5.55	1.61	1.54
1	B	70	VAL	CA-CB	5.47	1.61	1.54
1	D	127	ILE	CA-CB	5.42	1.60	1.54
1	C	66	ALA	CA-CB	5.24	1.63	1.53
1	A	86	ILE	CA-CB	-5.17	1.48	1.54
1	B	136	ALA	CA-CB	-5.02	1.45	1.53

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	93	HIS	N-CA-C	6.14	118.78	111.71
1	D	75	HIS	N-CA-C	5.90	119.58	112.38
1	D	118	PHE	N-CA-C	-5.62	105.23	111.36
1	C	114	GLN	N-CA-C	-5.52	98.55	108.48
1	C	124	GLN	N-CA-C	5.51	116.96	111.07
1	C	88	HIS	N-CA-C	5.35	117.11	111.28
1	D	62	GLU	N-CA-C	5.29	115.54	108.23
1	A	82	ARG	N-CA-C	5.22	116.65	111.07
1	A	93	HIS	N-CA-C	5.22	118.43	111.75
1	A	63	SER	N-CA-C	5.14	117.15	109.59
1	D	86	ILE	N-CA-C	-5.09	105.02	110.36
1	B	137	LYS	N-CA-C	5.04	117.83	109.46

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	60	ASN	Peptide

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	661	0	660	18	0
1	B	662	0	663	19	0
1	C	648	0	652	10	0
1	D	662	0	663	16	0
2	Q	53	0	42	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	B	15	0	17	0	0
4	C	15	0	17	0	0
5	C	21	0	30	0	0
6	A	18	0	0	2	0
6	B	17	0	0	1	0
6	C	17	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	13	0	0	1	0
6	Q	1	0	0	0	0
All	All	2807	0	2744	53	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 10.

All (53) 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:A:60:ASN:HB3	1:A:62:GLU:OE1	1.72	0.90
1:A:116:ASN:ND2	1:A:118:PHE:H	1.70	0.88
1:A:116:ASN:HD22	1:A:118:PHE:H	1.21	0.86
1:B:110:THR:HG21	1:C:110:THR:HG21	1.57	0.86
1:D:92:THR:HG21	1:D:113:LEU:HD22	1.66	0.78
1:B:65:ILE:HG13	1:C:102:MET:HE3	1.66	0.74
1:B:86:ILE:HG22	1:B:123:LEU:CD1	2.22	0.70
1:B:110:THR:HG21	1:C:110:THR:CG2	2.24	0.67
1:C:61:ASP:N	6:C:2001:HOH:O	2.31	0.64
1:A:116:ASN:ND2	1:A:118:PHE:N	2.45	0.64
1:A:116:ASN:HD22	1:A:116:ASN:C	2.05	0.64
1:D:86:ILE:HG22	1:D:123:LEU:HD11	1.80	0.62
1:C:110:THR:O	1:C:110:THR:HG22	2.01	0.61
1:A:116:ASN:HD22	1:A:118:PHE:N	1.96	0.59
1:B:86:ILE:HG22	1:B:123:LEU:HD11	1.84	0.58
1:B:76:GLN:NE2	1:B:131:ARG:HD2	2.19	0.57
1:B:131:ARG:HG3	6:B:2015:HOH:O	2.05	0.56
1:A:116:ASN:ND2	1:A:116:ASN:C	2.63	0.56
1:A:122:ARG:CZ	6:A:2015:HOH:O	2.54	0.56
1:C:99:HIS:CD2	1:C:101:HIS:CE1	2.96	0.55
1:D:65:ILE:H	1:D:142:SER:HB2	1.74	0.53
1:B:82:ARG:O	1:B:86:ILE:HG12	2.08	0.52
1:A:116:ASN:HD22	1:A:117:SER:N	2.08	0.51
1:D:82:ARG:HD2	6:D:2003:HOH:O	2.11	0.50
1:D:77:ARG:O	1:D:78:GLU:HB3	2.10	0.50
1:C:101:HIS:HE2	1:D:87:GLN:NE2	2.10	0.50
1:A:60:ASN:HB2	1:A:116:ASN:HB2	1.94	0.49
1:B:82:ARG:HH12	1:B:86:ILE:CD1	2.26	0.49
1:C:80:ASN:HB3	1:D:80:ASN:HD22	1.78	0.48
1:D:99:HIS:CE1	1:D:107:CYS:HB3	2.48	0.48
1:A:141:ALA:HB1	1:D:71:ILE:CD1	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:64:LYS:O	1:B:114:GLN:HA	2.13	0.47
1:B:65:ILE:HD13	1:B:65:ILE:N	2.29	0.47
1:B:76:GLN:HE22	1:B:131:ARG:HD2	1.78	0.47
1:C:110:THR:CG2	1:C:110:THR:O	2.63	0.47
1:A:141:ALA:HB1	1:D:71:ILE:HD11	1.97	0.47
1:D:123:LEU:HD12	1:D:123:LEU:HA	1.83	0.46
1:D:141:ALA:O	1:D:142:SER:HB3	2.15	0.46
1:B:82:ARG:HH12	1:B:86:ILE:HD11	1.81	0.46
1:D:106:ASN:HD21	1:D:134:LYS:NZ	2.14	0.45
1:B:83:MET:HE2	1:B:83:MET:HB3	1.86	0.45
1:A:122:ARG:NH1	6:A:2015:HOH:O	2.52	0.43
1:D:78:GLU:O	1:D:78:GLU:HG2	2.19	0.43
1:D:99:HIS:HA	1:D:108:LEU:O	2.19	0.43
1:A:80:ASN:HB3	1:B:80:ASN:HD22	1.84	0.42
1:A:97:THR:OG1	1:B:99:HIS:HB3	2.20	0.42
1:C:82:ARG:HG3	6:C:2006:HOH:O	2.21	0.41
1:A:99:HIS:CD2	1:A:101:HIS:CE1	3.09	0.41
1:B:64:LYS:C	1:B:65:ILE:HD13	2.46	0.41
1:A:86:ILE:HD13	1:A:126:GLU:HB3	2.02	0.41
1:A:88:HIS:CE1	1:B:107:CYS:SG	3.14	0.41
1:B:116:ASN:OD1	1:B:116:ASN:C	2.63	0.41
1:D:64:LYS:O	1:D:114:GLN:HA	2.20	0.40

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	81/91 (89%)	77 (95%)	4 (5%)	0	100	100
1	B	81/91 (89%)	76 (94%)	5 (6%)	0	100	100
1	C	79/91 (87%)	77 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	81/91 (89%)	74 (91%)	5 (6%)	2 (2%)	4	5
2	Q	9/11 (82%)	9 (100%)	0	0	100	100
All	All	331/375 (88%)	313 (95%)	16 (5%)	2 (1%)	21	32

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	61	ASP
1	D	135	PHE

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	73/82 (89%)	67 (92%)	6 (8%)	10	18
1	B	74/82 (90%)	69 (93%)	5 (7%)	14	25
1	C	72/82 (88%)	64 (89%)	8 (11%)	6	9
1	D	74/82 (90%)	66 (89%)	8 (11%)	6	9
2	Q	5/5 (100%)	3 (60%)	2 (40%)	0	0
All	All	298/333 (90%)	269 (90%)	29 (10%)	8	12

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	84	ILE
1	A	116	ASN
1	A	122	ARG
1	A	123	LEU
1	A	131	ARG
1	A	140	LYS
1	B	65	ILE
1	B	92	THR
1	B	108	LEU

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Mol	Chain	Res	Type
1	B	117	SER
1	B	137	LYS
1	C	70	VAL
1	C	82	ARG
1	C	84	ILE
1	C	108	LEU
1	C	110	THR
1	C	122	ARG
1	C	123	LEU
1	C	125	LEU
1	D	62	GLU
1	D	63	SER
1	D	65	ILE
1	D	78	GLU
1	D	81	GLN
1	D	120	ILE
1	D	127	ILE
1	D	131	ARG
2	Q	2	SER
2	Q	6	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	106	ASN
1	A	114	GLN
1	A	116	ASN
1	B	74	HIS
1	B	76	GLN
1	B	80	ASN
1	B	114	GLN
1	D	75	HIS
1	D	80	ASN
1	D	81	GLN
1	D	87	GLN
1	D	106	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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	$\# Z > 2$
4	EPE	B	1144	-	15,15,15	0.77	1 (6%)	19,20,20	1.90	4 (21%)
4	EPE	C	1143	-	15,15,15	0.84	1 (6%)	19,20,20	1.81	5 (26%)
5	PEG	C	1145	-	6,6,6	0.62	0	5,5,5	0.37	0
5	PEG	C	1146	-	6,6,6	0.68	0	5,5,5	0.31	0
5	PEG	C	1144	-	6,6,6	0.74	0	5,5,5	0.54	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	EPE	B	1144	-	-	7/9/19/19	0/1/1/1
4	EPE	C	1143	-	-	5/9/19/19	0/1/1/1
5	PEG	C	1145	-	-	2/4/4/4	-
5	PEG	C	1146	-	-	4/4/4/4	-
5	PEG	C	1144	-	-	3/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1143	EPE	C10-S	2.65	1.81	1.77
4	B	1144	EPE	C10-S	2.57	1.81	1.77

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1144	EPE	C5-N4-C3	5.60	120.91	108.84
4	C	1143	EPE	C5-N4-C3	4.04	117.54	108.84
4	C	1143	EPE	C7-N4-C5	3.23	119.83	111.24
4	B	1144	EPE	C7-N4-C5	3.11	119.53	111.24
4	B	1144	EPE	C7-N4-C3	3.00	119.22	111.24
4	C	1143	EPE	O2S-S-C10	2.90	111.11	106.73
4	C	1143	EPE	C7-N4-C3	2.89	118.94	111.24
4	B	1144	EPE	O3S-S-C10	2.48	110.86	106.00
4	C	1143	EPE	C6-N1-C2	2.46	114.14	108.84

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1144	EPE	C10-C9-N1-C6
4	B	1144	EPE	C8-C7-N4-C5
4	B	1144	EPE	C9-C10-S-O2S
4	B	1144	EPE	C9-C10-S-O3S
4	C	1143	EPE	S-C10-C9-N1
5	C	1146	PEG	C1-C2-O2-C3
4	C	1143	EPE	C8-C7-N4-C3
4	B	1144	EPE	N4-C7-C8-O8
5	C	1145	PEG	O1-C1-C2-O2
4	B	1144	EPE	S-C10-C9-N1
4	C	1143	EPE	C9-C10-S-O3S
5	C	1146	PEG	O1-C1-C2-O2
4	B	1144	EPE	C9-C10-S-O1S
5	C	1145	PEG	C1-C2-O2-C3
5	C	1144	PEG	O2-C3-C4-O4
5	C	1144	PEG	O1-C1-C2-O2
5	C	1144	PEG	C4-C3-O2-C2
5	C	1146	PEG	O2-C3-C4-O4
5	C	1146	PEG	C4-C3-O2-C2
4	C	1143	EPE	C9-C10-S-O1S
4	C	1143	EPE	C9-C10-S-O2S

There are no ring outliers.

No monomer is involved in short contacts.

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	83/91 (91%)	-1.22	0 100 100	24, 40, 65, 83	0
1	B	83/91 (91%)	-1.15	0 100 100	23, 39, 59, 94	0
1	C	81/91 (89%)	-1.27	0 100 100	23, 40, 57, 71	0
1	D	83/91 (91%)	-1.13	0 100 100	22, 40, 64, 94	0
2	Q	11/11 (100%)	-0.74	0 100 100	79, 80, 83, 83	0
All	All	341/375 (90%)	-1.18	0 100 100	22, 41, 79, 94	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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. 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	B-factors(Å ²)	Q<0.9
5	PEG	C	1146	7/7	0.91	0.16	35,43,50,51	7
5	PEG	C	1145	7/7	0.92	0.15	44,50,53,54	7
4	EPE	C	1143	15/15	0.93	0.07	52,59,69,70	15

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	PEG	C	1144	7/7	0.94	0.16	45,47,50,50	7
4	EPE	B	1144	15/15	0.96	0.06	73,80,84,84	15
3	NI	B	1143	1/1	1.00	0.01	29,29,29,29	0
3	NI	C	1142	1/1	1.00	0.01	39,39,39,39	0
3	NI	D	1143	1/1	1.00	0.01	31,31,31,31	0
3	NI	A	1143	1/1	1.00	0.01	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.