



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:52 PM UTC

PDB ID : 4JRE / pdb_00004jre
Title : Crystal structure of nitrate/nitrite exchanger NarK with nitrite bound
Authors : Zheng, H.; Wisedchaisri, G.; Gonen, T.
Deposited on : 2013-03-21
Resolution : 2.80 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

<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

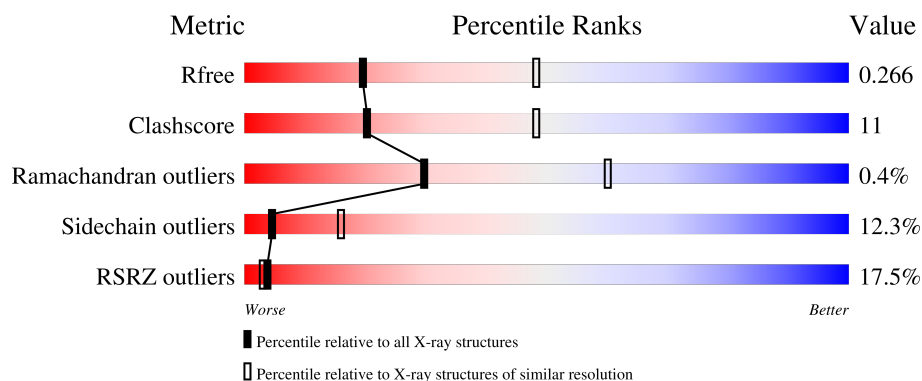
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	466	18% 67% 18% • 12%
1	D	466	31% 65% 18% • 14%
2	B	217	5% 67% 26% • •
2	H	217	6% 67% 28% • •
3	C	211	9% 71% 25% •

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Mol	Chain	Length	Quality of chain
3	L	211	10% 71% 27%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12589 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 Nitrite extrusion protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	0	0
			3088	2055	492	521	20			
1	D	402	Total	C	N	O	S	0	0	0
			3054	2040	484	510	20			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P10903
A	-1	SER	-	expression tag	UNP P10903
A	0	HIS	-	expression tag	UNP P10903
D	-2	GLY	-	expression tag	UNP P10903
D	-1	SER	-	expression tag	UNP P10903
D	0	HIS	-	expression tag	UNP P10903

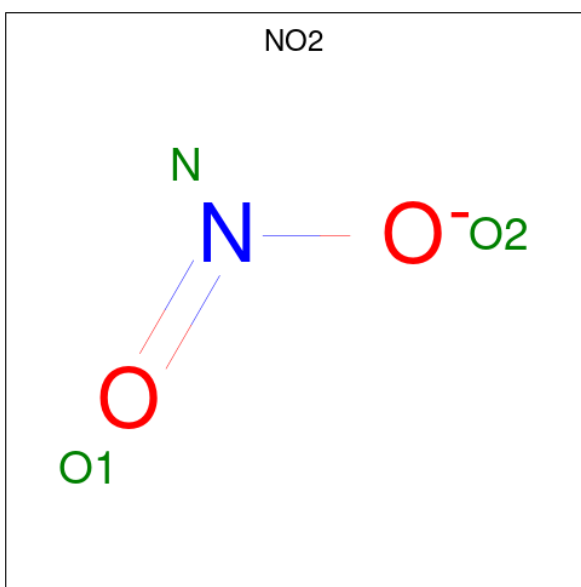
- Molecule 2 is a protein called Immunoglobulin Gamma-2a, Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	213	Total	C	N	O	S	0	0	0
			1594	1017	261	309	7			
2	H	213	Total	C	N	O	S	0	0	0
			1592	1016	261	308	7			

- Molecule 3 is a protein called Immunoglobulin Kappa, Light chain.

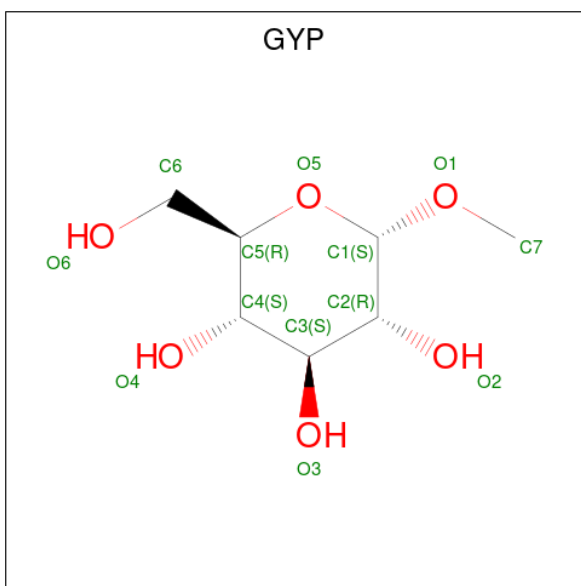
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	211	Total	C	N	O	S	0	0	0
			1597	1002	263	326	6			
3	L	211	Total	C	N	O	S	0	0	0
			1597	1002	262	327	6			

- Molecule 4 is NITRITE ION (CCD ID: NO2) (formula: NO₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	N	O	0	0
			3	1	2		
4	D	1	Total	N	O	0	0
			3	1	2		

- Molecule 5 is methyl alpha-D-glucopyranoside (CCD ID: GYP) (formula: C₇H₁₄O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			13	7	6		
5	D	1	Total	C	O	0	0
			13	7	6		

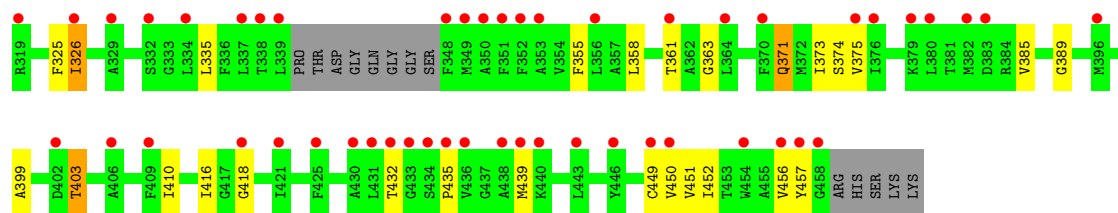
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total 1	O 1	0	0
6	B	9	Total 9	O 9	0	0
6	C	6	Total 6	O 6	0	0
6	D	1	Total 1	O 1	0	0
6	H	11	Total 11	O 11	0	0
6	L	7	Total 7	O 7	0	0

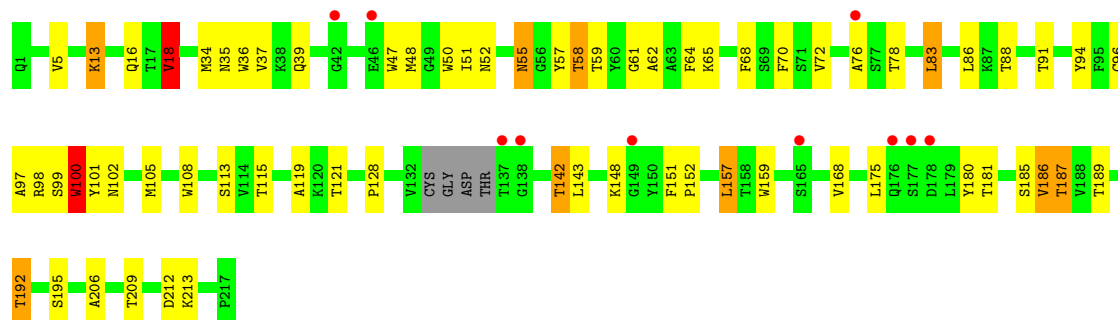
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- Molecule 1: Nitrite extrusion protein 1

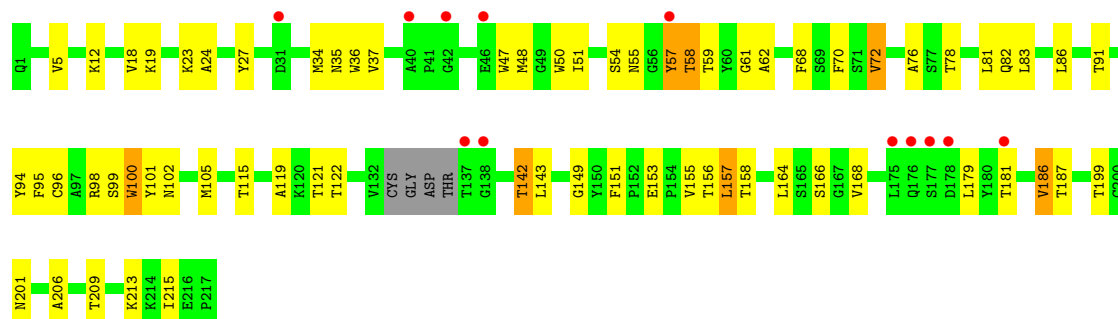




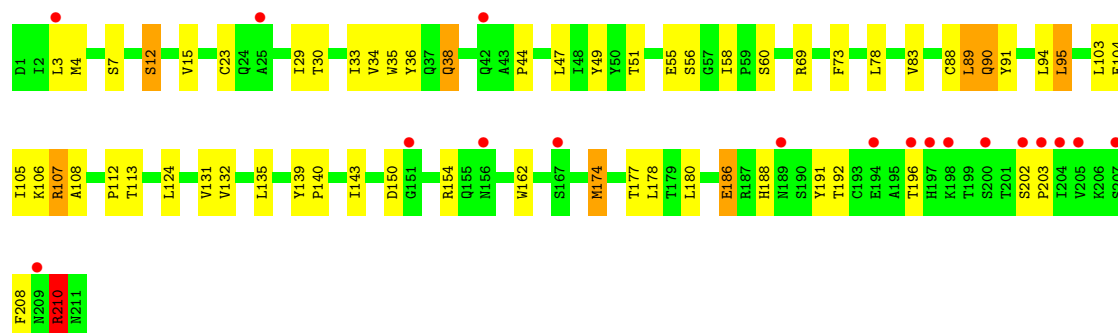
• Molecule 2: Immunoglobulin Gamma-2a, Heavy chain



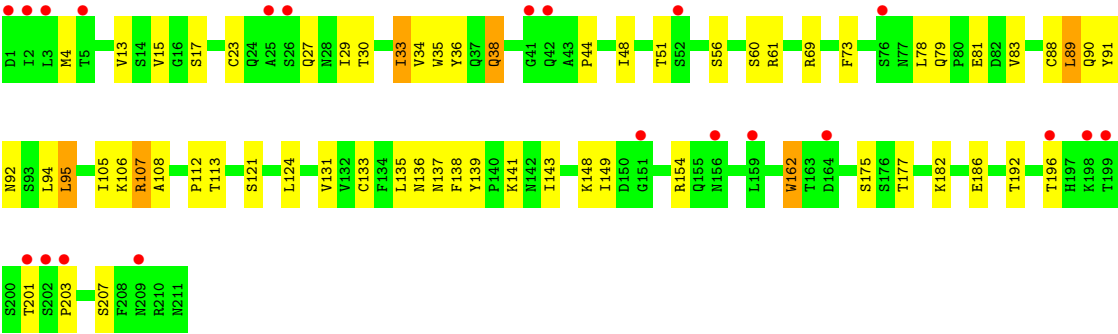
• Molecule 2: Immunoglobulin Gamma-2a, Heavy chain



• Molecule 3: Immunoglobulin Kappa, Light chain



• Molecule 3: Immunoglobulin Kappa, Light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	81.91Å 81.41Å 138.49Å 100.07° 96.38° 115.92°	Depositor
Resolution (Å)	50.00 – 2.80 50.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.5 (50.00-2.80) 94.5 (50.00-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.223 , 0.269 0.223 , 0.266	Depositor DCC
R_{free} test set	3827 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	50.7	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.001 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	12589	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% 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: NO2, GYP

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	0.56	0/3173	0.88	0/4312
1	D	0.57	0/3138	0.88	0/4263
2	B	0.75	0/1638	0.97	3/2237 (0.1%)
2	H	0.74	0/1636	0.93	1/2234 (0.0%)
3	C	0.66	0/1633	0.89	2/2230 (0.1%)
3	L	0.65	0/1633	0.86	1/2230 (0.0%)
All	All	0.64	0/12851	0.90	7/17506 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	101	TYR	N-CA-C	7.44	122.33	111.02
2	H	101	TYR	N-CA-C	6.81	121.46	112.13
3	C	202	SER	CA-C-N	5.77	125.72	119.78
3	C	202	SER	C-N-CA	5.77	125.72	119.78
2	B	18	VAL	CB-CA-C	-5.22	103.38	110.90

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	3088	0	3119	54	0
1	D	3054	0	3096	56	0
2	B	1594	0	1546	50	0
2	H	1592	0	1541	51	0
3	C	1597	0	1500	41	0
3	L	1597	0	1498	37	0
4	A	3	0	0	0	0
4	D	3	0	0	0	0
5	A	13	0	14	0	0
5	D	13	0	14	0	0
6	A	1	0	0	0	0
6	B	9	0	0	0	0
6	C	6	0	0	0	0
6	D	1	0	0	0	0
6	H	11	0	0	1	0
6	L	7	0	0	1	0
All	All	12589	0	12328	281	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 11.

The worst 5 of 281 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:B:100:TRP:HE3	2:B:100:TRP:O	1.39	1.05
2:H:18:VAL:HG23	2:H:86:LEU:HD11	1.43	1.01
1:A:37:ASN:HD21	1:A:235:ASN:HD22	1.04	0.99
2:H:37:VAL:CG2	2:H:105:MET:HE1	1.93	0.98
2:H:37:VAL:HG21	2:H:105:MET:HE1	1.47	0.96

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	403/466 (86%)	384 (95%)	18 (4%)	1 (0%)	43	72
1	D	394/466 (84%)	377 (96%)	17 (4%)	0	100	100
2	B	209/217 (96%)	197 (94%)	10 (5%)	2 (1%)	12	38
2	H	209/217 (96%)	200 (96%)	8 (4%)	1 (0%)	24	55
3	C	209/211 (99%)	193 (92%)	15 (7%)	1 (0%)	24	55
3	L	209/211 (99%)	197 (94%)	11 (5%)	1 (0%)	24	55
All	All	1633/1788 (91%)	1548 (95%)	79 (5%)	6 (0%)	30	60

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	99	SER
1	A	342	ASP
3	C	210	ARG
2	H	99	SER
3	L	92	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	314/364 (86%)	279 (89%)	35 (11%)	6	20
1	D	311/364 (85%)	279 (90%)	32 (10%)	7	23
2	B	175/182 (96%)	151 (86%)	24 (14%)	3	13
2	H	174/182 (96%)	151 (87%)	23 (13%)	4	14
3	C	178/190 (94%)	154 (86%)	24 (14%)	4	13
3	L	178/190 (94%)	152 (85%)	26 (15%)	3	11
All	All	1330/1472 (90%)	1166 (88%)	164 (12%)	4	16

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	5	VAL

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Mol	Chain	Res	Type
3	L	56	SER
2	H	72	VAL
2	H	164	LEU
3	L	89	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	175	ASN
1	D	289	GLN
3	L	197	HIS
1	D	235	ASN
1	D	324	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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
4	NO2	D	501	-	1,2,2	0.06	0	0,1,1	-	-
4	NO2	A	501	-	1,2,2	0.09	0	0,1,1	-	-
5	GYP	A	502	-	13,13,13	0.78	1 (7%)	18,18,18	1.47	2 (11%)
5	GYP	D	502	-	13,13,13	0.81	1 (7%)	18,18,18	1.47	2 (11%)

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
5	GYP	D	502	-	-	2/4/24/24	0/1/1/1
5	GYP	A	502	-	-	2/4/24/24	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	502	GYP	O1-C1	2.40	1.44	1.40
5	A	502	GYP	O1-C1	2.36	1.44	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	502	GYP	O1-C1-C2	4.99	113.89	108.14
5	D	502	GYP	O1-C1-C2	4.66	113.52	108.14
5	D	502	GYP	C1-O5-C5	2.62	118.84	113.72
5	A	502	GYP	C1-C2-C3	2.45	115.17	110.01

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	502	GYP	C2-C1-O1-C7
5	D	502	GYP	O5-C1-O1-C7
5	A	502	GYP	C2-C1-O1-C7
5	A	502	GYP	O5-C1-O1-C7

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	409/466 (87%)	1.28	83 (20%) 3 2	30, 73, 105, 139	0
1	D	402/466 (86%)	1.62	146 (36%) 1 0	30, 78, 105, 125	0
2	B	213/217 (98%)	0.26	10 (4%) 36 29	23, 36, 62, 112	0
2	H	213/217 (98%)	0.23	12 (5%) 30 23	24, 35, 63, 94	0
3	C	211/211 (100%)	0.48	18 (8%) 16 12	25, 41, 69, 84	0
3	L	211/211 (100%)	0.45	21 (9%) 12 9	23, 40, 70, 84	0
All	All	1659/1788 (92%)	0.89	290 (17%) 4 3	23, 53, 100, 139	0

The worst 5 of 290 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	314	ARG	11.0
1	A	314	ARG	7.8
1	D	313	ASP	7.6
1	D	315	LEU	7.4
1	D	236	ASP	6.8

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($\text{\AA}^2$)	Q<0.9
5	GYP	D	502	13/13	0.78	0.21	86,96,108,119	0
5	GYP	A	502	13/13	0.84	0.22	82,91,99,106	0
4	NO2	D	501	3/3	0.85	0.29	71,71,72,73	0
4	NO2	A	501	3/3	0.87	0.19	78,78,80,80	0

6.5 Other polymers [i](#)

There are no such residues in this entry.