



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:01 PM GMT

PDB ID : 4GX2
Title : GsuK channel bound to NAD
Authors : Kong, C.; Zeng, W.; Ye, S.; Chen, L.; Sauer, D.B.; Lam, Y.; Derebe, M.G.; Jiang, Y.
Deposited on : 2012-09-03
Resolution : 3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

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

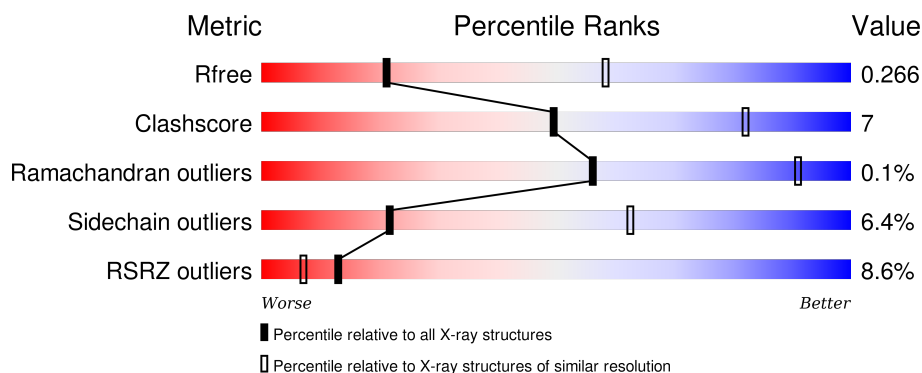
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	565	<div> <div>2%</div> <div>56%</div> <div>9%</div> <div>34%</div> </div>
1	B	565	<div> <div>15%</div> <div>74%</div> <div>21%</div> </div>
1	C	565	<div> <div>8%</div> <div>77%</div> <div>19%</div> </div>
1	D	565	<div> <div>3%</div> <div>55%</div> <div>11%</div> <div>33%</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
5	NAD	A	608	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14511 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 TrkA domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	375	Total	C	N	O	S	0	0	0
			2922	1880	506	525	11			
1	B	548	Total	C	N	O	S	0	0	0
			4208	2693	729	771	15			
1	C	547	Total	C	N	O	S	0	0	0
			4197	2687	725	770	15			
1	D	376	Total	C	N	O	S	0	0	0
			2928	1883	507	527	11			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	MET	-	EXPRESSION TAG	UNP Q74FS9
A	5	GLN	-	EXPRESSION TAG	UNP Q74FS9
A	6	ARG	-	EXPRESSION TAG	UNP Q74FS9
A	7	GLY	-	EXPRESSION TAG	UNP Q74FS9
A	8	SER	-	EXPRESSION TAG	UNP Q74FS9
A	52	ALA	GLU	ENGINEERED MUTATION	UNP Q74FS9
A	77	GLU	GLN	ENGINEERED MUTATION	UNP Q74FS9
A	97	ASP	LEU	ENGINEERED MUTATION	UNP Q74FS9
A	565	LEU	-	EXPRESSION TAG	UNP Q74FS9
A	566	VAL	-	EXPRESSION TAG	UNP Q74FS9
A	567	PRO	-	EXPRESSION TAG	UNP Q74FS9
A	568	ARG	-	EXPRESSION TAG	UNP Q74FS9
B	4	MET	-	EXPRESSION TAG	UNP Q74FS9
B	5	GLN	-	EXPRESSION TAG	UNP Q74FS9
B	6	ARG	-	EXPRESSION TAG	UNP Q74FS9
B	7	GLY	-	EXPRESSION TAG	UNP Q74FS9
B	8	SER	-	EXPRESSION TAG	UNP Q74FS9
B	52	ALA	GLU	ENGINEERED MUTATION	UNP Q74FS9
B	77	GLU	GLN	ENGINEERED MUTATION	UNP Q74FS9
B	97	ASP	LEU	ENGINEERED MUTATION	UNP Q74FS9
B	565	LEU	-	EXPRESSION TAG	UNP Q74FS9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	566	VAL	-	EXPRESSION TAG	UNP Q74FS9
B	567	PRO	-	EXPRESSION TAG	UNP Q74FS9
B	568	ARG	-	EXPRESSION TAG	UNP Q74FS9
C	4	MET	-	EXPRESSION TAG	UNP Q74FS9
C	5	GLN	-	EXPRESSION TAG	UNP Q74FS9
C	6	ARG	-	EXPRESSION TAG	UNP Q74FS9
C	7	GLY	-	EXPRESSION TAG	UNP Q74FS9
C	8	SER	-	EXPRESSION TAG	UNP Q74FS9
C	52	ALA	GLU	ENGINEERED MUTATION	UNP Q74FS9
C	77	GLU	GLN	ENGINEERED MUTATION	UNP Q74FS9
C	97	ASP	LEU	ENGINEERED MUTATION	UNP Q74FS9
C	565	LEU	-	EXPRESSION TAG	UNP Q74FS9
C	566	VAL	-	EXPRESSION TAG	UNP Q74FS9
C	567	PRO	-	EXPRESSION TAG	UNP Q74FS9
C	568	ARG	-	EXPRESSION TAG	UNP Q74FS9
D	4	MET	-	EXPRESSION TAG	UNP Q74FS9
D	5	GLN	-	EXPRESSION TAG	UNP Q74FS9
D	6	ARG	-	EXPRESSION TAG	UNP Q74FS9
D	7	GLY	-	EXPRESSION TAG	UNP Q74FS9
D	8	SER	-	EXPRESSION TAG	UNP Q74FS9
D	52	ALA	GLU	ENGINEERED MUTATION	UNP Q74FS9
D	77	GLU	GLN	ENGINEERED MUTATION	UNP Q74FS9
D	97	ASP	LEU	ENGINEERED MUTATION	UNP Q74FS9
D	565	LEU	-	EXPRESSION TAG	UNP Q74FS9
D	566	VAL	-	EXPRESSION TAG	UNP Q74FS9
D	567	PRO	-	EXPRESSION TAG	UNP Q74FS9
D	568	ARG	-	EXPRESSION TAG	UNP Q74FS9

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

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

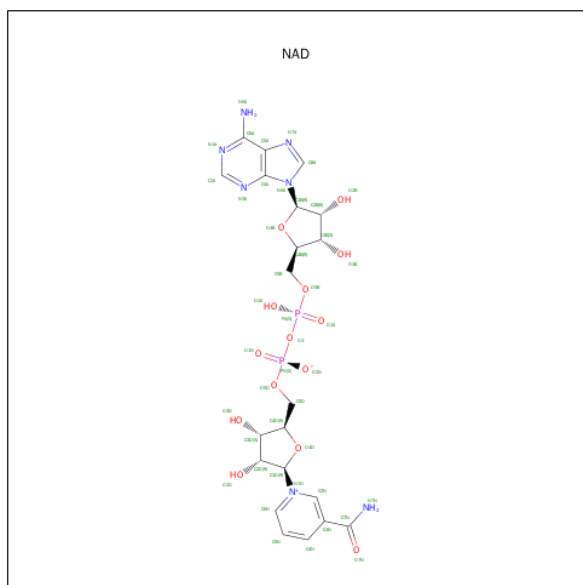
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 5 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



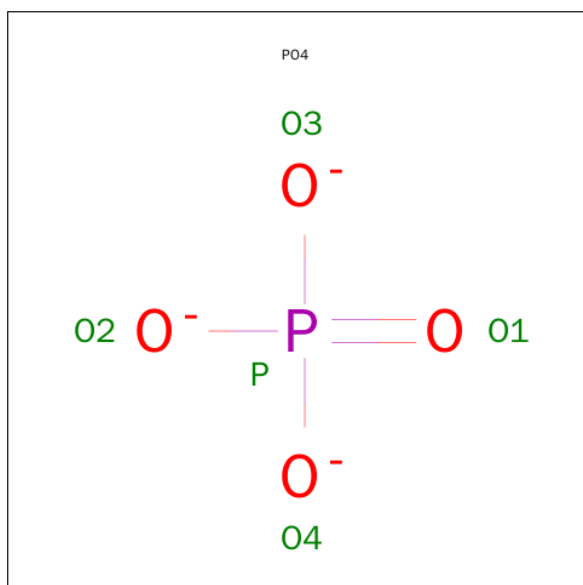
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 44	C 21	N 7	O 14	P 2	0	0
5	B	1	Total 44	C 21	N 7	O 14	P 2	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
5	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	P	0	0
			5	4	1		
6	C	1	Total	O	P	0	0
			5	4	1		

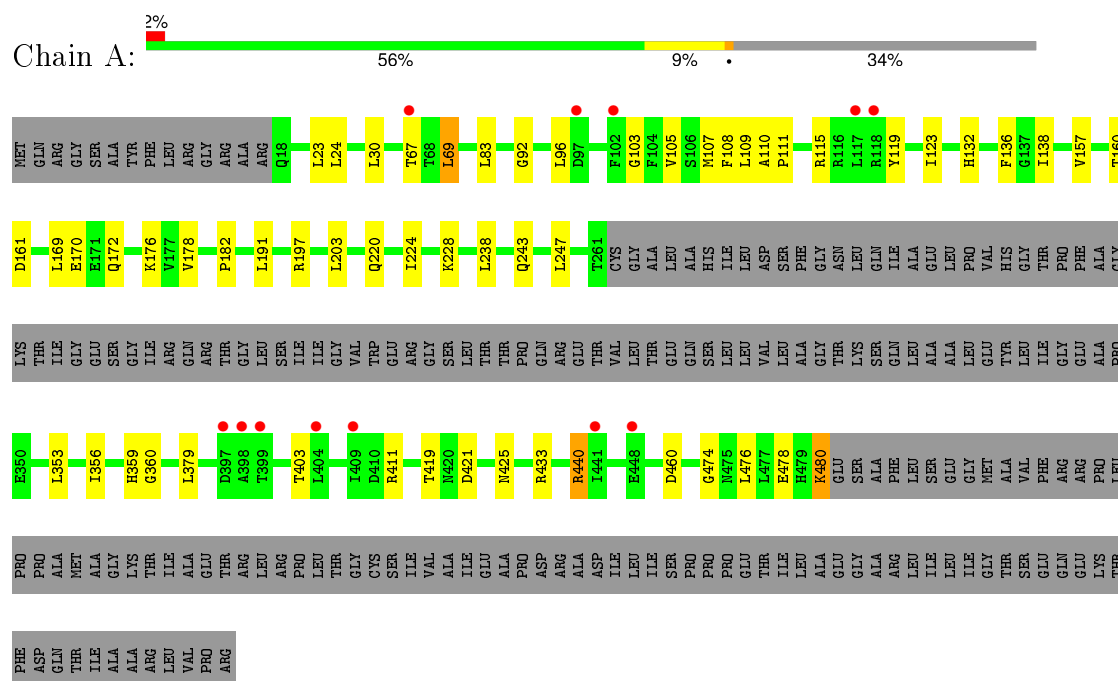
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	17	Total	O	0	0
			17	17		
7	B	9	Total	O	0	0
			9	9		
7	C	18	Total	O	0	0
			18	18		
7	D	6	Total	O	0	0
			6	6		

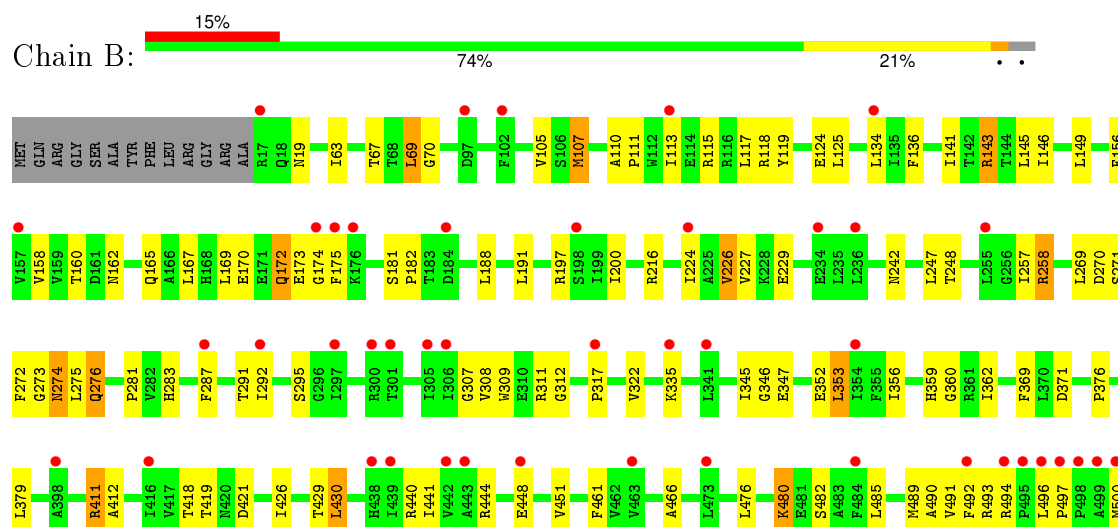
3 Residue-property plots

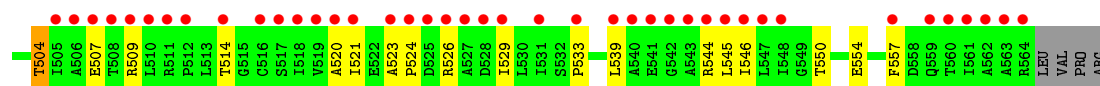
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

• Molecule 1: TrkA domain protein

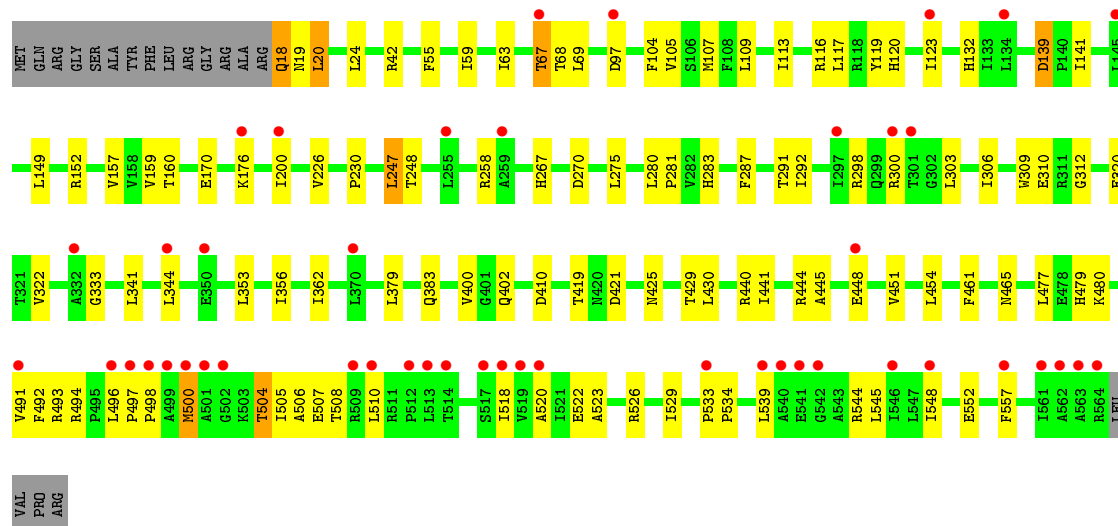
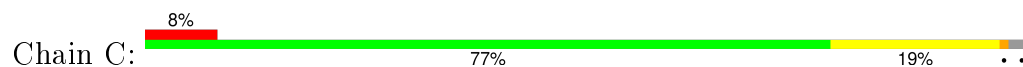


• Molecule 1: TrkA domain protein

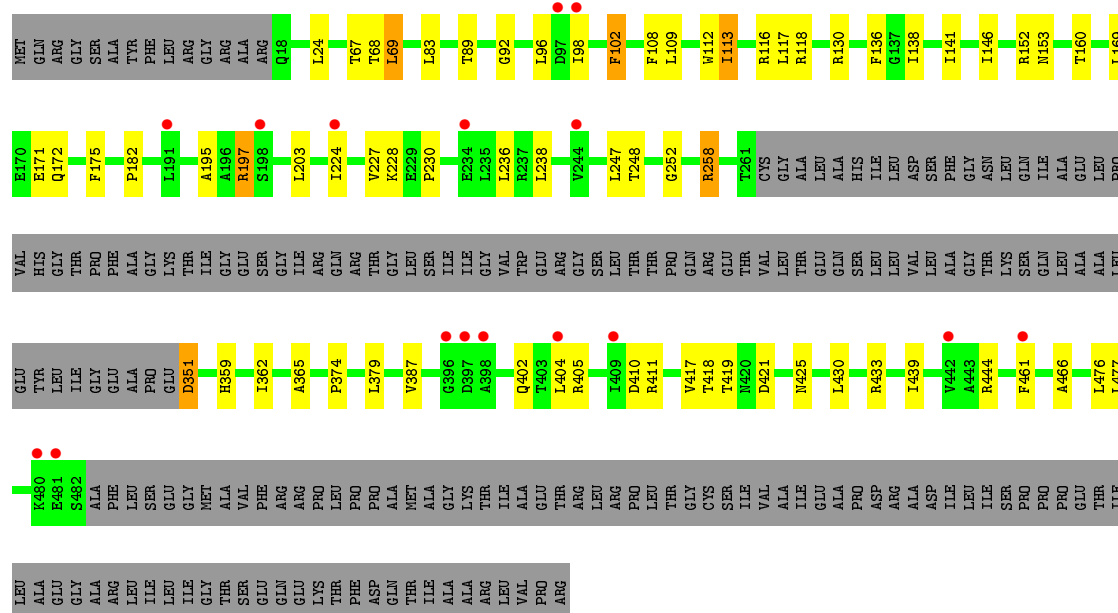




• Molecule 1: TrkA domain protein



• Molecule 1: TrkA domain protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	232.55Å 111.10Å 164.56Å 90.00° 134.78° 90.00°	Depositor
Resolution (Å)	41.14 – 3.20 49.31 – 3.20	Depositor EDS
% Data completeness (in resolution range)	95.5 (41.14-3.20) 94.1 (49.31-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 3.19Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.230 , 0.270 0.228 , 0.266	Depositor DCC
R_{free} test set	2384 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	88.7	Xtriage
Anisotropy	0.415	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.206 for h+2*l,k,-h-l 0.023 for h,-k,-h-l 0.028 for -h-2*l,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 47121 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14511	wwPDB-VP
Average B, all atoms (Å ²)	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.45 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to $4.2821e-04$. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: K, ZN, CA, PO4, NAD

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	0.22	0/2982	0.42	0/4060
1	B	0.22	0/4291	0.41	0/5843
1	C	0.23	0/4280	0.42	0/5829
1	D	0.23	0/2988	0.43	0/4068
All	All	0.22	0/14541	0.42	0/19800

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	2922	0	2957	33	0
1	B	4208	0	4282	77	0
1	C	4197	0	4269	64	0
1	D	2928	0	2962	40	0
2	A	5	0	0	0	0
2	B	1	0	0	0	0
2	C	5	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	2	0	0	0	0
5	A	44	0	26	6	0
5	B	44	0	26	4	0
5	C	44	0	26	6	0
5	D	44	0	26	6	0
6	B	5	0	0	0	0
6	C	5	0	0	0	0
7	A	17	0	0	0	0
7	B	9	0	0	0	0
7	C	18	0	0	0	0
7	D	6	0	0	0	0
All	All	14511	0	14574	206	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 7.

The worst 5 of 206 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:C:69:LEU:HD23	1:D:68:THR:HA	1.59	0.84
1:A:247:LEU:H	5:A:608:NAD:H4N	1.45	0.82
1:C:226:VAL:HG12	5:C:610:NAD:H5N	1.62	0.80
1:A:69:LEU:HD22	1:B:70:GLY:HA3	1.62	0.80
1:A:69:LEU:CD2	1:B:70:GLY:HA3	2.13	0.79

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	371/565 (66%)	348 (94%)	23 (6%)	0	100	100
1	B	546/565 (97%)	517 (95%)	28 (5%)	1 (0%)	52	88
1	C	545/565 (96%)	525 (96%)	20 (4%)	0	100	100
1	D	372/565 (66%)	358 (96%)	13 (4%)	1 (0%)	46	85
All	All	1834/2260 (81%)	1748 (95%)	84 (5%)	2 (0%)	56	91

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	374	PRO
1	B	524	PRO

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	313/463 (68%)	293 (94%)	20 (6%)	22	62
1	B	449/463 (97%)	423 (94%)	26 (6%)	25	66
1	C	448/463 (97%)	417 (93%)	31 (7%)	19	59
1	D	314/463 (68%)	293 (93%)	21 (7%)	20	60
All	All	1524/1852 (82%)	1426 (94%)	98 (6%)	22	62

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	504	THR
1	C	120	HIS
1	D	238	LEU
1	B	509	ARG
1	C	67	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	402	GLN
1	B	172	GLN
1	C	276	GLN
1	C	425	ASN
1	C	465	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 26 ligands modelled in this entry, 20 are monoatomic - leaving 6 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	$\# Z > 2$
5	NAD	A	608	-	38,48,48	1.65	6 (15%)	47,73,73	2.20	10 (21%)
6	PO4	B	604	-	4,4,4	0.47	0	6,6,6	0.27	0
5	NAD	B	605	-	38,48,48	1.64	5 (13%)	47,73,73	2.13	12 (25%)
6	PO4	C	609	-	4,4,4	0.47	0	6,6,6	0.28	0
5	NAD	C	610	-	38,48,48	1.64	5 (13%)	47,73,73	2.18	12 (25%)
5	NAD	D	603	-	38,48,48	1.65	6 (15%)	47,73,73	2.26	10 (21%)

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	NAD	A	608	-	-	0/22/62/62	0/5/5/5
6	PO4	B	604	-	-	0/0/0/0	0/0/0/0
5	NAD	B	605	-	-	0/22/62/62	0/5/5/5
6	PO4	C	609	-	-	0/0/0/0	0/0/0/0
5	NAD	C	610	-	-	0/22/62/62	0/5/5/5
5	NAD	D	603	-	-	0/22/62/62	0/5/5/5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	605	NAD	C2D-C3D	-4.03	1.42	1.53
5	A	608	NAD	C2D-C3D	-4.03	1.42	1.53
5	C	610	NAD	C2D-C3D	-4.01	1.42	1.53
5	D	603	NAD	C2D-C3D	-4.01	1.42	1.53
5	C	610	NAD	C2B-C3B	-3.29	1.44	1.53

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	610	NAD	N3A-C2A-N1A	-10.48	120.87	128.89
5	D	603	NAD	N3A-C2A-N1A	-10.39	120.94	128.89
5	B	605	NAD	N3A-C2A-N1A	-10.38	120.95	128.89
5	A	608	NAD	N3A-C2A-N1A	-10.24	121.05	128.89
5	D	603	NAD	PN-O3-PA	-4.66	119.66	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	608	NAD	6	0
5	B	605	NAD	4	0
5	C	610	NAD	6	0
5	D	603	NAD	6	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	375/565 (66%)	0.32	12 (3%) 51 36	64, 90, 166, 214	0
1	B	548/565 (96%)	0.93	85 (15%) 3 2	67, 115, 249, 357	0
1	C	547/565 (96%)	0.62	46 (8%) 14 7	66, 111, 192, 261	0
1	D	376/565 (66%)	0.30	16 (4%) 39 25	60, 89, 168, 234	0
All	All	1846/2260 (81%)	0.59	159 (8%) 13 7	60, 100, 212, 357	0

The worst 5 of 159 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	496	LEU	12.1
1	B	543	ALA	12.1
1	B	516	CYS	9.9
1	B	542	GLY	9.6
1	C	561	ILE	8.9

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 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, 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
5	NAD	A	608	44/44	0.76	0.41	0.79	67,221,245,282	0
4	CA	C	608	1/1	0.90	0.23	0.18	90,90,90,90	0
5	NAD	C	610	44/44	0.82	0.27	-0.04	78,179,210,212	0
4	CA	B	603	1/1	0.99	0.23	-0.07	89,89,89,89	0
5	NAD	D	603	44/44	0.81	0.27	-0.19	83,197,221,223	0
6	PO4	B	604	5/5	0.83	0.27	-0.38	131,134,136,137	0
4	CA	C	607	1/1	0.95	0.23	-0.52	87,87,87,87	0
6	PO4	C	609	5/5	0.93	0.22	-0.78	139,139,142,142	0
5	NAD	B	605	44/44	0.88	0.19	-1.01	57,151,214,216	0
2	K	C	603	1/1	0.99	0.15	-1.29	68,68,68,68	1
2	K	A	602	1/1	0.91	0.24	-1.29	87,87,87,87	1
2	K	A	601	1/1	0.99	0.16	-1.50	88,88,88,88	1
2	K	C	602	1/1	0.96	0.21	-1.52	64,64,64,64	1
4	CA	A	607	1/1	0.97	0.16	-1.74	89,89,89,89	0
2	K	A	603	1/1	0.87	0.16	-1.81	71,71,71,71	1
2	K	C	601	1/1	0.91	0.14	-2.04	73,73,73,73	1
2	K	A	605	1/1	0.64	0.26	-	136,136,136,136	1
3	ZN	A	606	1/1	0.98	0.31	-	91,91,91,91	0
2	K	C	604	1/1	0.94	0.28	-	100,100,100,100	1
3	ZN	C	606	1/1	0.97	0.29	-	87,87,87,87	0
2	K	A	604	1/1	0.98	0.31	-	109,109,109,109	1
2	K	B	601	1/1	0.54	0.62	-	222,222,222,222	1
3	ZN	B	602	1/1	0.98	0.29	-	92,92,92,92	0
2	K	D	601	1/1	0.96	0.22	-	136,136,136,136	1
2	K	C	605	1/1	0.78	0.50	-	207,207,207,207	1
3	ZN	D	602	1/1	0.99	0.28	-	81,81,81,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.