



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:47 PM GMT

PDB ID : 1QMA  
Title : NUCLEAR TRANSPORT FACTOR 2 (NTF2) W7A MUTANT  
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Stewart, M.J.  
Deposited on : 1999-09-23  
Resolution : 2.50 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](mailto: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.

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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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

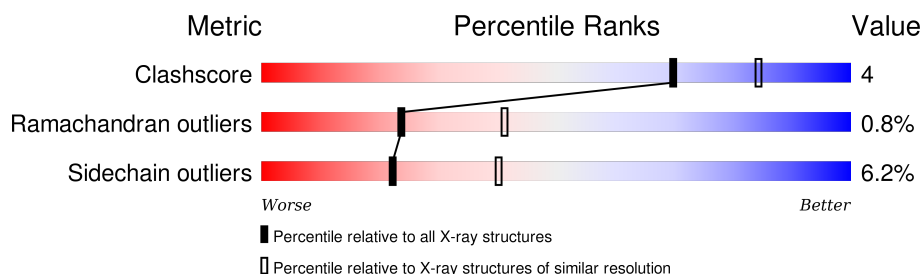
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)

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  $\geq 3$ , 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	126	
1	B	126	
1	C	126	
1	D	126	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4054 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 NUCLEAR TRANSPORT FACTOR 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	126	Total	C	N	O	S	66	0	0
			997	636	167	187	7			
1	B	124	Total	C	N	O	S	39	0	0
			988	631	166	184	7			
1	C	126	Total	C	N	O	S	63	0	0
			997	636	167	187	7			
1	D	124	Total	C	N	O	S	38	0	0
			988	631	166	184	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	ALA	TRP	ENGINEERED	UNP P13662
B	7	ALA	TRP	ENGINEERED	UNP P13662
C	7	ALA	TRP	ENGINEERED	UNP P13662
D	7	ALA	TRP	ENGINEERED	UNP P13662

- Molecule 2 is water.

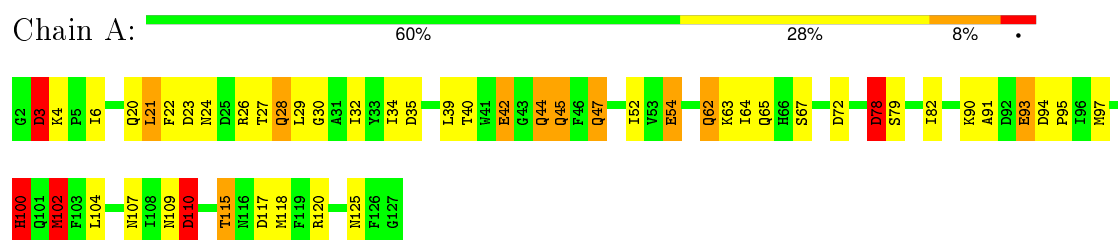
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	24	Total	O	0	0
			24	24		
2	B	21	Total	O	0	0
			21	21		
2	C	19	Total	O	0	0
			19	19		
2	D	20	Total	O	0	0
			20	20		

### 3 Residue-property plots [i](#)

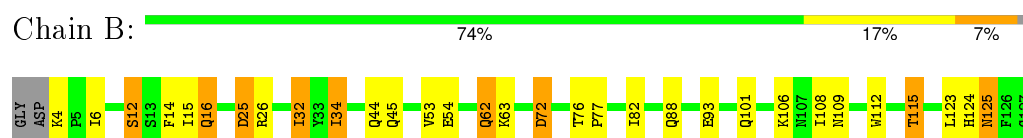
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

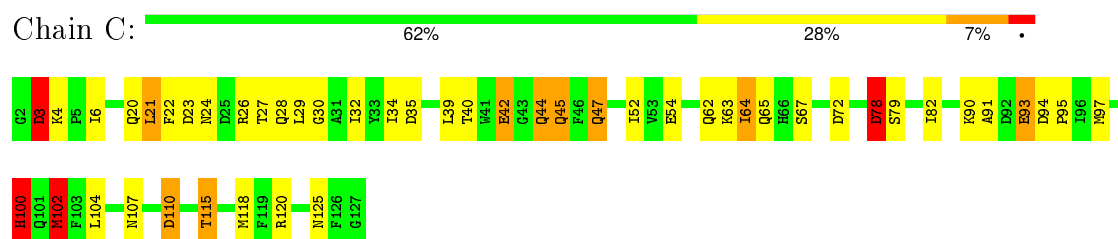
#### • Molecule 1: NUCLEAR TRANSPORT FACTOR 2



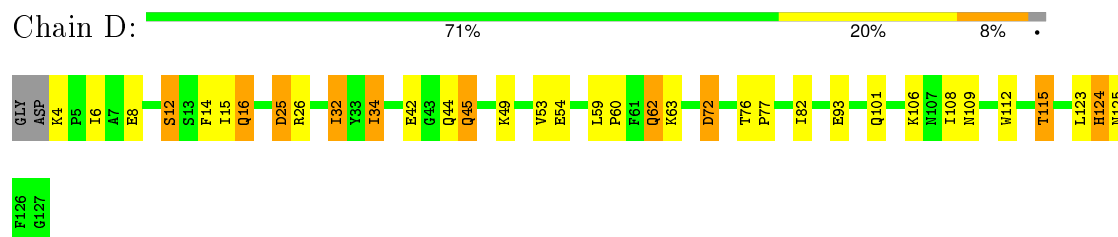
#### • Molecule 1: NUCLEAR TRANSPORT FACTOR 2



#### • Molecule 1: NUCLEAR TRANSPORT FACTOR 2



#### • Molecule 1: NUCLEAR TRANSPORT FACTOR 2



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.65Å 75.41Å 64.54Å 90.00° 115.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.50	Depositor
% Data completeness (in resolution range)	100.0 (6.00-2.50)	Depositor
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.208 , 0.240	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4054	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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	3.34	17/1021 (1.7%)	2.50	36/1382 (2.6%)
1	B	1.49	8/1012 (0.8%)	1.82	19/1370 (1.4%)
1	C	3.57	20/1021 (2.0%)	2.56	37/1382 (2.7%)
1	D	2.21	12/1012 (1.2%)	1.80	20/1370 (1.5%)
All	All	2.79	57/4066 (1.4%)	2.20	112/5504 (2.0%)

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	13
1	B	0	11
1	C	0	12
1	D	0	10
All	All	0	46

All (57) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	93	GLU	CD-OE1	72.32	2.05	1.25
1	C	93	GLU	CD-OE1	68.48	2.00	1.25
1	C	125	ASN	CB-CG	61.30	2.92	1.51
1	D	63	LYS	CE-NZ	54.04	2.84	1.49
1	A	125	ASN	CB-CG	41.98	2.47	1.51
1	C	28	GLN	CG-CD	26.70	2.12	1.51
1	A	62	GLN	CG-CD	26.25	2.11	1.51
1	A	93	GLU	CD-OE2	-25.93	0.97	1.25
1	A	65	GLN	CG-CD	-25.23	0.93	1.51
1	C	90	LYS	CG-CD	-24.75	0.68	1.52
1	C	65	GLN	CG-CD	-24.17	0.95	1.51
1	B	12	SER	CB-OG	-24.06	1.10	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	62	GLN	CG-CD	23.96	2.06	1.51
1	A	90	LYS	CG-CD	-22.85	0.74	1.52
1	B	63	LYS	CE-NZ	21.96	2.04	1.49
1	A	78	ASP	CG-OD2	21.16	1.74	1.25
1	C	78	ASP	CG-OD2	21.04	1.73	1.25
1	D	12	SER	CB-OG	-20.13	1.16	1.42
1	D	16	GLN	CD-OE1	17.63	1.62	1.24
1	B	16	GLN	CD-OE1	15.85	1.58	1.24
1	C	93	GLU	CD-OE2	-15.78	1.08	1.25
1	D	25	ASP	CB-CG	-14.90	1.20	1.51
1	B	93	GLU	CG-CD	-14.11	1.30	1.51
1	D	54	GLU	CG-CD	-13.77	1.31	1.51
1	D	93	GLU	CG-CD	-13.70	1.31	1.51
1	C	23	ASP	CG-OD1	-13.52	0.94	1.25
1	C	54	GLU	CD-OE2	13.40	1.40	1.25
1	A	20	GLN	CG-CD	13.36	1.81	1.51
1	B	25	ASP	CB-CG	-13.23	1.24	1.51
1	A	4	LYS	C-N	12.32	1.57	1.34
1	A	28	GLN	CG-CD	11.64	1.77	1.51
1	A	23	ASP	CG-OD1	-11.16	0.99	1.25
1	C	20	GLN	CG-CD	8.89	1.71	1.51
1	C	4	LYS	C-N	8.62	1.50	1.34
1	A	63	LYS	CG-CD	8.49	1.81	1.52
1	C	63	LYS	CG-CD	8.29	1.80	1.52
1	A	47	GLN	CD-OE1	8.16	1.42	1.24
1	C	54	GLU	CB-CG	-7.96	1.37	1.52
1	C	110	ASP	CB-CG	7.73	1.68	1.51
1	A	109	ASN	CB-CG	7.68	1.68	1.51
1	C	47	GLN	CD-OE1	7.48	1.40	1.24
1	B	62	GLN	CB-CG	-7.15	1.33	1.52
1	D	124	HIS	CB-CG	-6.94	1.37	1.50
1	D	49	LYS	CE-NZ	6.72	1.65	1.49
1	D	4	LYS	CG-CD	-6.62	1.29	1.52
1	D	44	GLN	CG-CD	6.55	1.66	1.51
1	A	54	GLU	CB-CG	-6.38	1.40	1.52
1	C	3	ASP	C-N	6.17	1.48	1.34
1	D	62	GLN	CB-CG	-6.16	1.35	1.52
1	A	3	ASP	C-N	6.13	1.48	1.34
1	C	44	GLN	CD-NE2	-6.01	1.17	1.32
1	A	44	GLN	CD-NE2	-5.87	1.18	1.32
1	B	4	LYS	CG-CD	-5.74	1.32	1.52
1	B	88	GLN	CD-NE2	-5.74	1.18	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	24	ASN	CG-OD1	-5.45	1.11	1.24
1	C	35	ASP	CB-CG	5.40	1.63	1.51
1	D	125	ASN	CB-CG	5.31	1.63	1.51

All (112) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	78	ASP	OD1-CG-OD2	-37.33	52.37	123.30
1	A	78	ASP	OD1-CG-OD2	-36.75	53.47	123.30
1	C	93	GLU	OE1-CD-OE2	-29.96	87.35	123.30
1	A	93	GLU	OE1-CD-OE2	-29.42	88.00	123.30
1	A	78	ASP	CB-CG-OD2	-27.86	93.23	118.30
1	C	78	ASP	CB-CG-OD2	-23.88	96.81	118.30
1	C	23	ASP	CB-CG-OD1	21.71	137.84	118.30
1	A	23	ASP	CB-CG-OD1	19.14	135.53	118.30
1	A	93	GLU	CG-CD-OE2	19.00	156.31	118.30
1	C	93	GLU	CG-CD-OE2	18.93	156.15	118.30
1	C	65	GLN	CB-CG-CD	16.84	155.39	111.60
1	C	110	ASP	CB-CG-OD1	16.69	133.32	118.30
1	B	25	ASP	CB-CG-OD2	16.57	133.21	118.30
1	C	125	ASN	CA-CB-CG	-16.33	77.47	113.40
1	D	25	ASP	CB-CG-OD2	16.09	132.78	118.30
1	A	65	GLN	CB-CG-CD	15.84	152.79	111.60
1	D	25	ASP	CB-CG-OD1	-15.36	104.48	118.30
1	B	25	ASP	CB-CG-OD1	-15.20	104.62	118.30
1	A	110	ASP	CB-CG-OD1	14.23	131.10	118.30
1	D	25	ASP	CA-CB-CG	14.04	144.28	113.40
1	C	35	ASP	CB-CG-OD2	13.77	130.70	118.30
1	B	25	ASP	CA-CB-CG	13.62	143.37	113.40
1	A	35	ASP	CB-CG-OD2	13.55	130.49	118.30
1	C	110	ASP	CB-CG-OD2	-13.06	106.54	118.30
1	B	125	ASN	CB-CG-OD1	-12.51	96.58	121.60
1	D	16	GLN	OE1-CD-NE2	-12.43	93.32	121.90
1	A	125	ASN	CA-CB-CG	-12.32	86.30	113.40
1	B	16	GLN	OE1-CD-NE2	-11.91	94.50	121.90
1	C	65	GLN	CG-CD-OE1	-11.80	98.00	121.60
1	C	102	MET	CA-CB-CG	11.49	132.83	113.30
1	B	63	LYS	CD-CE-NZ	-11.43	85.41	111.70
1	A	102	MET	CA-CB-CG	11.41	132.70	113.30
1	A	44	GLN	CG-CD-NE2	-11.18	89.87	116.70
1	D	4	LYS	CB-CG-CD	10.81	139.71	111.60
1	A	110	ASP	CB-CG-OD2	-10.64	108.73	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	65	GLN	CG-CD-OE1	-10.39	100.81	121.60
1	C	35	ASP	CB-CG-OD1	-10.18	109.14	118.30
1	C	65	GLN	CG-CD-NE2	10.11	140.97	116.70
1	C	44	GLN	CG-CD-NE2	-9.99	92.72	116.70
1	A	35	ASP	CB-CG-OD1	-9.96	109.33	118.30
1	B	125	ASN	CB-CG-ND2	9.85	140.33	116.70
1	A	23	ASP	CB-CG-OD2	-9.82	109.46	118.30
1	C	28	GLN	CG-CD-OE1	-9.67	102.26	121.60
1	C	23	ASP	CB-CG-OD2	-9.18	110.04	118.30
1	A	47	GLN	OE1-CD-NE2	-9.13	100.89	121.90
1	C	28	GLN	CG-CD-NE2	8.86	137.95	116.70
1	A	65	GLN	CG-CD-NE2	8.77	137.74	116.70
1	C	47	GLN	OE1-CD-NE2	-8.67	101.96	121.90
1	A	93	GLU	CG-CD-OE1	-8.50	101.31	118.30
1	B	4	LYS	CB-CG-CD	8.49	133.68	111.60
1	C	28	GLN	CB-CG-CD	-8.39	89.78	111.60
1	C	110	ASP	CA-CB-CG	-8.05	95.69	113.40
1	D	109	ASN	CA-CB-CG	7.93	130.85	113.40
1	D	4	LYS	CG-CD-CE	7.88	135.54	111.90
1	D	54	GLU	CG-CD-OE1	7.75	133.80	118.30
1	A	110	ASP	CA-CB-CG	-7.56	96.77	113.40
1	C	93	GLU	CG-CD-OE1	-7.32	103.66	118.30
1	C	62	GLN	CB-CG-CD	-7.29	92.64	111.60
1	B	26	ARG	C-N-CA	7.26	139.84	121.70
1	D	26	ARG	C-N-CA	7.24	139.79	121.70
1	C	3	ASP	CA-C-N	-7.12	101.53	117.20
1	A	3	ASP	CA-C-N	-7.12	101.54	117.20
1	C	23	ASP	OD1-CG-OD2	-6.91	110.18	123.30
1	B	54	GLU	CG-CD-OE1	6.87	132.04	118.30
1	C	3	ASP	C-N-CA	-6.83	104.62	121.70
1	C	3	ASP	CB-CG-OD2	6.82	124.44	118.30
1	A	3	ASP	C-N-CA	-6.82	104.66	121.70
1	A	3	ASP	CB-CG-OD2	6.80	124.42	118.30
1	D	12	SER	CA-CB-OG	6.80	129.55	111.20
1	A	62	GLN	CB-CG-CD	-6.78	93.97	111.60
1	A	109	ASN	CA-CB-CG	-6.69	98.69	113.40
1	D	124	HIS	CA-CB-CG	6.66	124.93	113.60
1	B	72	ASP	CB-CG-OD1	-6.54	112.42	118.30
1	C	44	GLN	OE1-CD-NE2	-6.50	106.95	121.90
1	A	3	ASP	CB-CG-OD1	-6.48	112.47	118.30
1	C	3	ASP	CB-CG-OD1	-6.48	112.47	118.30
1	D	54	GLU	CB-CG-CD	-6.45	96.78	114.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	26	ARG	NE-CZ-NH2	-6.34	117.13	120.30
1	D	72	ASP	CB-CG-OD1	-6.34	112.59	118.30
1	B	4	LYS	CG-CD-CE	6.33	130.88	111.90
1	B	54	GLU	CB-CG-CD	-6.27	97.27	114.20
1	D	45	GLN	CB-CG-CD	-6.24	95.37	111.60
1	A	26	ARG	NE-CZ-NH2	-6.23	117.19	120.30
1	D	54	GLU	CG-CD-OE2	-6.11	106.09	118.30
1	B	77	PRO	O-C-N	-6.00	113.10	122.70
1	D	44	GLN	OE1-CD-NE2	6.00	135.69	121.90
1	B	109	ASN	CA-CB-CG	5.96	126.52	113.40
1	A	23	ASP	OD1-CG-OD2	-5.95	112.00	123.30
1	D	77	PRO	O-C-N	-5.85	113.33	122.70
1	D	42	GLU	OE1-CD-OE2	-5.81	116.32	123.30
1	C	100	HIS	CA-CB-CG	5.81	123.48	113.60
1	A	115	THR	O-C-N	-5.78	113.45	122.70
1	A	100	HIS	CA-CB-CG	5.76	123.39	113.60
1	B	93	GLU	CB-CG-CD	5.76	129.74	114.20
1	B	12	SER	CA-CB-OG	5.74	126.69	111.20
1	C	47	GLN	CG-CD-OE1	-5.72	110.16	121.60
1	D	16	GLN	CG-CD-NE2	5.72	130.42	116.70
1	C	45	GLN	O-C-N	-5.70	113.57	122.70
1	B	54	GLU	CG-CD-OE2	-5.52	107.26	118.30
1	D	8	GLU	OE1-CD-OE2	5.51	129.91	123.30
1	C	115	THR	O-C-N	-5.49	113.91	122.70
1	C	26	ARG	C-N-CA	5.49	135.42	121.70
1	A	45	GLN	O-C-N	-5.47	113.94	122.70
1	A	26	ARG	C-N-CA	5.41	135.22	121.70
1	A	24	ASN	CB-CG-OD1	-5.38	110.84	121.60
1	A	117	ASP	CB-CG-OD1	5.30	123.07	118.30
1	A	20	GLN	CB-CG-CD	-5.28	97.88	111.60
1	C	21	LEU	O-C-N	-5.23	114.33	122.70
1	A	21	LEU	O-C-N	-5.19	114.39	122.70
1	B	16	GLN	CG-CD-NE2	5.13	129.01	116.70
1	C	42	GLU	O-C-N	-5.09	114.55	123.20
1	A	42	GLU	O-C-N	-5.03	114.66	123.20

There are no chirality outliers.

All (46) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	115	THR	Mainchain
1	A	27	THR	Mainchain

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Mol	Chain	Res	Type	Group
1	A	28	GLN	Sidechain
1	A	3	ASP	Mainchain
1	A	30	GLY	Mainchain
1	A	34	ILE	Mainchain
1	A	42	GLU	Mainchain
1	A	44	GLN	Sidechain
1	A	45	GLN	Mainchain
1	A	47	GLN	Sidechain
1	A	72	ASP	Mainchain
1	A	78	ASP	Sidechain
1	A	93	GLU	Sidechain
1	B	101	GLN	Mainchain
1	B	112	TRP	Mainchain
1	B	115	THR	Mainchain
1	B	15	ILE	Mainchain
1	B	16	GLN	Sidechain
1	B	34	ILE	Mainchain
1	B	44	GLN	Sidechain
1	B	45	GLN	Sidechain
1	B	53	VAL	Mainchain
1	B	72	ASP	Mainchain
1	B	76	THR	Mainchain
1	C	115	THR	Mainchain
1	C	27	THR	Mainchain
1	C	3	ASP	Mainchain
1	C	30	GLY	Mainchain
1	C	34	ILE	Mainchain
1	C	42	GLU	Mainchain
1	C	44	GLN	Sidechain
1	C	45	GLN	Mainchain
1	C	47	GLN	Sidechain
1	C	72	ASP	Mainchain
1	C	78	ASP	Sidechain
1	C	93	GLU	Sidechain
1	D	101	GLN	Mainchain
1	D	112	TRP	Mainchain
1	D	115	THR	Mainchain
1	D	15	ILE	Mainchain
1	D	16	GLN	Sidechain
1	D	34	ILE	Mainchain
1	D	45	GLN	Sidechain
1	D	53	VAL	Mainchain

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Mol	Chain	Res	Type	Group
1	D	72	ASP	Mainchain
1	D	76	THR	Mainchain

## 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	997	0	959	12	0
1	B	988	0	956	6	0
1	C	997	0	959	12	0
1	D	988	0	956	7	0
2	A	24	0	0	0	0
2	B	21	0	0	0	0
2	C	19	0	0	0	0
2	D	20	0	0	0	0
All	All	4054	0	3830	33	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (33) 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:107:ASN:HD21	1:A:110:ASP:HA	1.67	0.60
1:C:107:ASN:HD21	1:C:110:ASP:HA	1.66	0.59
1:A:94:ASP:HB3	1:A:95:PRO:HD2	1.86	0.58
1:A:102:MET:HE1	1:B:82:ILE:HD13	1.86	0.57
1:C:94:ASP:HB3	1:C:95:PRO:HD2	1.85	0.57
1:C:78:ASP:O	1:C:79:SER:HB2	2.08	0.54
1:A:78:ASP:O	1:A:79:SER:HB2	2.08	0.54
1:C:64:ILE:HD12	1:C:91:ALA:HB2	1.90	0.53
1:D:34:ILE:HD11	1:D:115:THR:HG22	1.93	0.50
1:A:64:ILE:HD12	1:A:91:ALA:HB2	1.93	0.50
1:C:102:MET:HE1	1:D:82:ILE:HD13	1.94	0.50
1:C:104:LEU:HD22	1:D:82:ILE:HD11	1.94	0.49
1:A:104:LEU:HD22	1:B:82:ILE:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:106:LYS:HD3	1:B:108:ILE:HD11	1.95	0.48
1:C:82:ILE:HD12	1:C:104:LEU:HD13	1.96	0.48
1:B:14:PHE:HZ	1:B:32:ILE:HD13	1.79	0.47
1:B:34:ILE:HD11	1:B:115:THR:HG22	1.97	0.47
1:C:39:LEU:HD22	1:C:52:ILE:HG23	1.98	0.46
1:D:14:PHE:HZ	1:D:32:ILE:HD13	1.81	0.45
1:A:100:HIS:CD2	1:A:120:ARG:HB3	2.51	0.45
1:C:100:HIS:CD2	1:C:120:ARG:HB3	2.51	0.45
1:D:106:LYS:HD3	1:D:108:ILE:HD11	1.99	0.45
1:A:82:ILE:HD12	1:A:104:LEU:HD13	1.98	0.44
1:A:39:LEU:HD22	1:A:52:ILE:HG23	2.00	0.44
1:A:40:THR:HB	1:A:118:MET:HG2	2.00	0.44
1:C:40:THR:HB	1:C:118:MET:HG2	2.01	0.43
1:C:29:LEU:O	1:C:32:ILE:HG12	2.19	0.43
1:A:29:LEU:O	1:A:32:ILE:HG12	2.19	0.43
1:D:59:LEU:HA	1:D:60:PRO:HD3	1.87	0.42
1:B:106:LYS:HG2	1:B:108:ILE:HG13	2.02	0.42
1:A:21:LEU:O	1:A:22:PHE:C	2.59	0.41
1:C:21:LEU:O	1:C:22:PHE:C	2.59	0.41
1:D:106:LYS:HG2	1:D:108:ILE:HG13	2.02	0.41

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	124/126 (98%)	116 (94%)	7 (6%)	1 (1%)	24	41
1	B	122/126 (97%)	114 (93%)	7 (6%)	1 (1%)	24	41
1	C	124/126 (98%)	116 (94%)	7 (6%)	1 (1%)	24	41
1	D	122/126 (97%)	114 (93%)	7 (6%)	1 (1%)	24	41
All	All	492/504 (98%)	460 (94%)	28 (6%)	4 (1%)	24	41

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	ASP
1	C	3	ASP
1	B	124	HIS
1	D	124	HIS

### 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	108/109 (99%)	100 (93%)	8 (7%)	17	31
1	B	108/109 (99%)	101 (94%)	7 (6%)	21	39
1	C	108/109 (99%)	102 (94%)	6 (6%)	26	47
1	D	108/109 (99%)	102 (94%)	6 (6%)	26	47
All	All	432/436 (99%)	405 (94%)	27 (6%)	22	40

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ILE
1	A	54	GLU
1	A	62	GLN
1	A	67	SER
1	A	97	MET
1	A	100	HIS
1	A	102	MET
1	A	110	ASP
1	B	6	ILE
1	B	12	SER
1	B	25	ASP
1	B	32	ILE
1	B	62	GLN
1	B	123	LEU
1	B	125	ASN
1	C	6	ILE

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Mol	Chain	Res	Type
1	C	64	ILE
1	C	67	SER
1	C	97	MET
1	C	100	HIS
1	C	102	MET
1	D	6	ILE
1	D	12	SER
1	D	25	ASP
1	D	32	ILE
1	D	62	GLN
1	D	123	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	HIS
1	A	107	ASN
1	A	116	ASN
1	B	44	GLN
1	B	71	GLN
1	B	73	HIS
1	B	100	HIS
1	B	116	ASN
1	C	100	HIS
1	C	107	ASN
1	C	116	ASN
1	D	44	GLN
1	D	71	GLN
1	D	73	HIS
1	D	100	HIS
1	D	116	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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.