



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:38 AM UTC

PDB ID : 4AB7 / pdb_00004ab7
Title : Crystal structure of a tetrameric acetylglutamate kinase from *Saccharomyces cerevisiae* complexed with its substrate N- acetylglutamate
Authors : de Cima, S.; Gil-Ortiz, F.; Crabeel, M.; Fita, I.; Rubio, V.
Deposited on : 2011-12-07
Resolution : 3.25 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

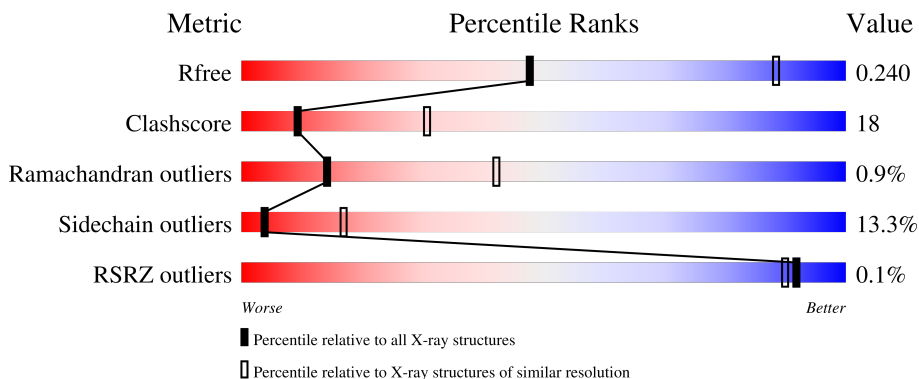
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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	1605 (3.30-3.22)
Clashscore	190562	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)
RSRZ outliers	180081	1605 (3.30-3.22)

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	464	59% 22% 5% • 13%
1	B	464	58% 31% 5% 6%
1	C	464	58% 30% 5% • 6%
1	D	464	60% 21% 6% • 13%
1	E	464	59% 22% 6% 13%

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Mol	Chain	Length	Quality of chain
1	F	464	
1	G	464	
1	H	464	

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
2	NLG	D	1503	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 26320 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 PROTEIN ARG5,6, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	405	Total 3140	C 2002	N 525	O 604	S 9	0	0	0
1	B	436	Total 3400	C 2164	N 572	O 655	S 9	0	0	0
1	C	436	Total 3394	C 2161	N 569	O 655	S 9	0	0	0
1	D	405	Total 3140	C 2002	N 525	O 604	S 9	0	0	0
1	E	405	Total 3142	C 2002	N 527	O 604	S 9	0	0	0
1	F	436	Total 3402	C 2167	N 571	O 655	S 9	0	0	0
1	G	436	Total 3396	C 2161	N 571	O 655	S 9	0	0	0
1	H	422	Total 3280	C 2093	N 547	O 631	S 9	0	0	0

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	MET	-	expression tag	UNP Q01217
A	51	GLY	-	expression tag	UNP Q01217
A	52	HIS	-	expression tag	UNP Q01217
A	53	HIS	-	expression tag	UNP Q01217
A	54	HIS	-	expression tag	UNP Q01217
A	55	HIS	-	expression tag	UNP Q01217
A	56	HIS	-	expression tag	UNP Q01217
A	57	HIS	-	expression tag	UNP Q01217
B	50	MET	-	expression tag	UNP Q01217
B	51	GLY	-	expression tag	UNP Q01217
B	52	HIS	-	expression tag	UNP Q01217
B	53	HIS	-	expression tag	UNP Q01217
B	54	HIS	-	expression tag	UNP Q01217

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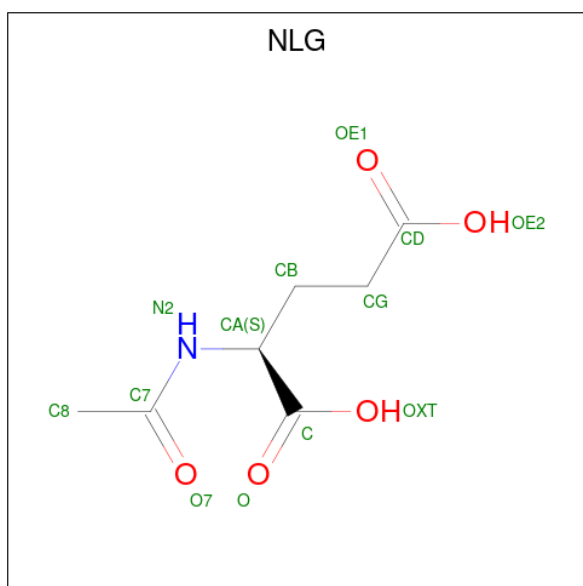
Chain	Residue	Modelled	Actual	Comment	Reference
B	55	HIS	-	expression tag	UNP Q01217
B	56	HIS	-	expression tag	UNP Q01217
B	57	HIS	-	expression tag	UNP Q01217
C	50	MET	-	expression tag	UNP Q01217
C	51	GLY	-	expression tag	UNP Q01217
C	52	HIS	-	expression tag	UNP Q01217
C	53	HIS	-	expression tag	UNP Q01217
C	54	HIS	-	expression tag	UNP Q01217
C	55	HIS	-	expression tag	UNP Q01217
C	56	HIS	-	expression tag	UNP Q01217
C	57	HIS	-	expression tag	UNP Q01217
D	50	MET	-	expression tag	UNP Q01217
D	51	GLY	-	expression tag	UNP Q01217
D	52	HIS	-	expression tag	UNP Q01217
D	53	HIS	-	expression tag	UNP Q01217
D	54	HIS	-	expression tag	UNP Q01217
D	55	HIS	-	expression tag	UNP Q01217
D	56	HIS	-	expression tag	UNP Q01217
D	57	HIS	-	expression tag	UNP Q01217
E	50	MET	-	expression tag	UNP Q01217
E	51	GLY	-	expression tag	UNP Q01217
E	52	HIS	-	expression tag	UNP Q01217
E	53	HIS	-	expression tag	UNP Q01217
E	54	HIS	-	expression tag	UNP Q01217
E	55	HIS	-	expression tag	UNP Q01217
E	56	HIS	-	expression tag	UNP Q01217
E	57	HIS	-	expression tag	UNP Q01217
F	50	MET	-	expression tag	UNP Q01217
F	51	GLY	-	expression tag	UNP Q01217
F	52	HIS	-	expression tag	UNP Q01217
F	53	HIS	-	expression tag	UNP Q01217
F	54	HIS	-	expression tag	UNP Q01217
F	55	HIS	-	expression tag	UNP Q01217
F	56	HIS	-	expression tag	UNP Q01217
F	57	HIS	-	expression tag	UNP Q01217
G	50	MET	-	expression tag	UNP Q01217
G	51	GLY	-	expression tag	UNP Q01217
G	52	HIS	-	expression tag	UNP Q01217
G	53	HIS	-	expression tag	UNP Q01217
G	54	HIS	-	expression tag	UNP Q01217
G	55	HIS	-	expression tag	UNP Q01217
G	56	HIS	-	expression tag	UNP Q01217

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Chain	Residue	Modelled	Actual	Comment	Reference
G	57	HIS	-	expression tag	UNP Q01217
H	50	MET	-	expression tag	UNP Q01217
H	51	GLY	-	expression tag	UNP Q01217
H	52	HIS	-	expression tag	UNP Q01217
H	53	HIS	-	expression tag	UNP Q01217
H	54	HIS	-	expression tag	UNP Q01217
H	55	HIS	-	expression tag	UNP Q01217
H	56	HIS	-	expression tag	UNP Q01217
H	57	HIS	-	expression tag	UNP Q01217

- Molecule 2 is N-ACETYL-L-GLUTAMATE (CCD ID: NLG) (formula: C₇H₁₁NO₅).



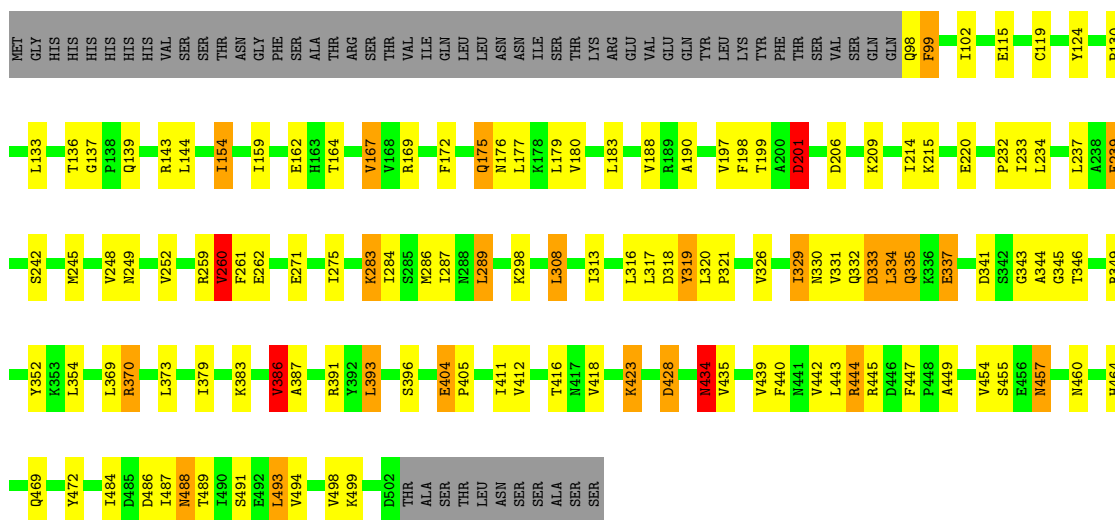
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
2	D	1	Total	C	N	O	0	0
			13	7	1	5		
2	H	1	Total	C	N	O	0	0
			13	7	1	5		

3 Residue-property plots

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.

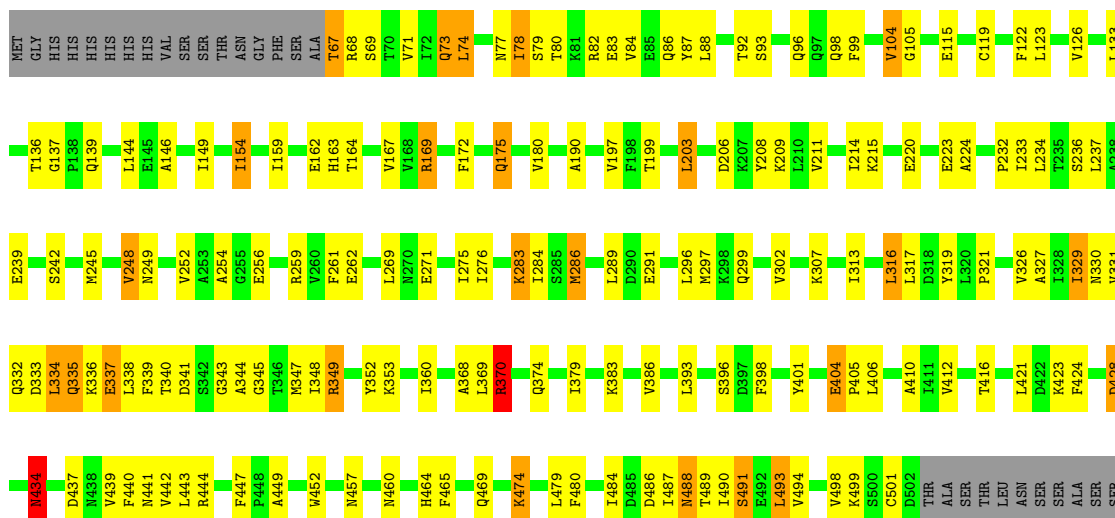
• Molecule 1: PROTEIN ARG5,6, MITOCHONDRIAL

Chain A: 

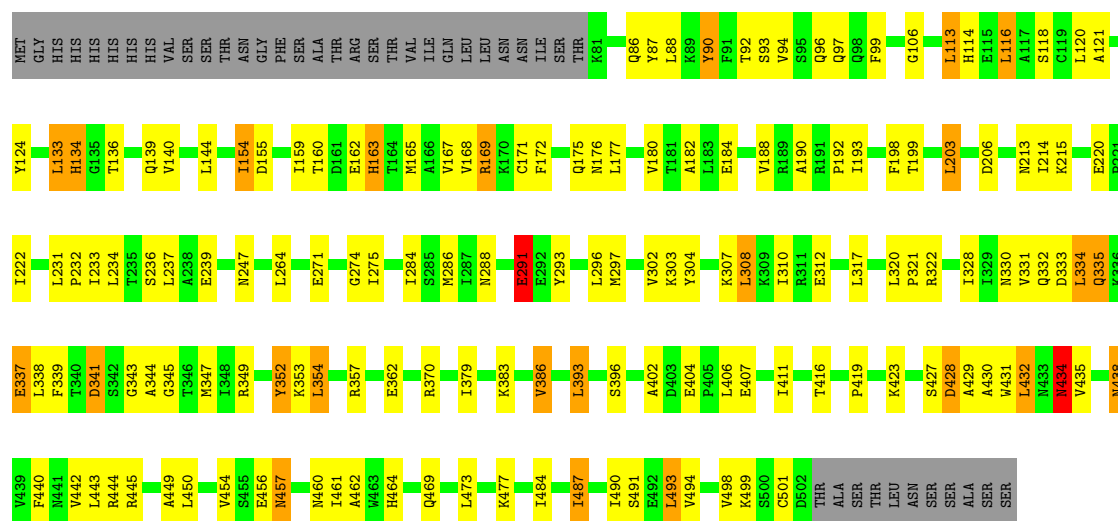


• Molecule 1: PROTEIN ARG5,6, MITOCHONDRIAL

Chain B: 



Chain H: 58% 28% 5% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	92.88Å 103.27Å 111.31Å 77.31° 89.27° 70.43°	Depositor
Resolution (Å)	108.36 – 3.25 108.36 – 3.25	Depositor EDS
% Data completeness (in resolution range)	96.2 (108.36-3.25) 95.6 (108.36-3.25)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 3.25Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.193 , 0.238 0.196 , 0.240	Depositor DCC
R_{free} test set	2874 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	81.9	Xtrriage
Anisotropy	0.066	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 89.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	26320	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section:
NLG

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	1.00	2/3195 (0.1%)	1.07	11/4329 (0.3%)
1	B	1.04	4/3458 (0.1%)	1.12	9/4685 (0.2%)
1	C	1.05	5/3452 (0.1%)	1.13	14/4678 (0.3%)
1	D	0.99	3/3195 (0.1%)	1.09	8/4329 (0.2%)
1	E	0.94	2/3197 (0.1%)	1.04	8/4332 (0.2%)
1	F	1.01	2/3460 (0.1%)	1.10	12/4686 (0.3%)
1	G	0.98	2/3454 (0.1%)	1.12	13/4681 (0.3%)
1	H	1.00	6/3338 (0.2%)	1.07	9/4522 (0.2%)
All	All	1.00	26/26749 (0.1%)	1.09	84/36242 (0.2%)

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	B	0	2
1	C	0	1
1	F	0	2
1	G	0	1
All	All	0	6

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	95	SER	CA-C	7.18	1.62	1.52
1	E	114	HIS	CG-CD2	6.82	1.43	1.35
1	B	163	HIS	CG-CD2	6.10	1.42	1.35
1	F	134	HIS	CG-ND1	-6.04	1.31	1.38
1	D	134	HIS	CG-ND1	-5.89	1.31	1.38

The worst 5 of 84 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	375	ARG	NE-CZ-NH2	-10.84	109.45	119.20
1	D	344	ALA	N-CA-C	9.67	124.20	107.28
1	A	423	LYS	CB-CG-CD	8.39	130.59	111.30
1	C	319	TYR	CA-CB-CG	-8.21	99.13	113.90
1	H	96	GLN	N-CA-C	8.13	121.06	111.71

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	92	THR	Peptide
1	B	96	GLN	Peptide
1	C	95	SER	Peptide
1	F	95	SER	Peptide
1	F	96	GLN	Peptide

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	3140	0	3153	103	1
1	B	3400	0	3418	143	0
1	C	3394	0	3407	132	1
1	D	3140	0	3153	120	0
1	E	3142	0	3153	117	1
1	F	3402	0	3429	156	1
1	G	3396	0	3407	157	1
1	H	3280	0	3286	106	1
2	D	13	0	9	10	0
2	H	13	0	9	2	0
All	All	26320	0	26424	956	3

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 18.

The worst 5 of 956 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:B:474:LYS:HE2	1:B:501:CYS:SG	1.27	1.67
1:B:474:LYS:CE	1:B:501:CYS:SG	2.09	1.38
1:F:72:ILE:O	1:G:89:LYS:NZ	1.65	1.29
1:B:379:ILE:HD11	1:B:423:LYS:NZ	1.52	1.23
1:B:379:ILE:HG21	1:B:386:VAL:CG2	1.72	1.20

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:488:ASN:OD1	1:H:362:GLU:OE2[1_554]	1.75	0.45
1:E:207:LYS:NZ	1:G:282:GLU:OE2[1_545]	2.14	0.06
1:C:146:ALA:O	1:F:433:ASN:ND2[1_655]	2.19	0.01

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	403/464 (87%)	371 (92%)	29 (7%)	3 (1%)	18	48
1	B	434/464 (94%)	397 (92%)	32 (7%)	5 (1%)	10	36
1	C	434/464 (94%)	397 (92%)	33 (8%)	4 (1%)	14	42
1	D	403/464 (87%)	370 (92%)	31 (8%)	2 (0%)	24	55
1	E	403/464 (87%)	369 (92%)	31 (8%)	3 (1%)	18	48
1	F	434/464 (94%)	395 (91%)	36 (8%)	3 (1%)	18	48
1	G	434/464 (94%)	392 (90%)	36 (8%)	6 (1%)	9	33
1	H	420/464 (90%)	386 (92%)	30 (7%)	4 (1%)	12	40
All	All	3365/3712 (91%)	3077 (91%)	258 (8%)	30 (1%)	14	42

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	416	THR
1	A	487	ILE
1	B	416	THR
1	C	93	SER
1	C	416	THR

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	340/397 (86%)	293 (86%)	47 (14%)	3	15
1	B	371/397 (94%)	321 (86%)	50 (14%)	4	16
1	C	370/397 (93%)	324 (88%)	46 (12%)	4	19
1	D	340/397 (86%)	297 (87%)	43 (13%)	4	19
1	E	340/397 (86%)	298 (88%)	42 (12%)	4	19
1	F	372/397 (94%)	323 (87%)	49 (13%)	4	17
1	G	370/397 (93%)	318 (86%)	52 (14%)	3	15
1	H	355/397 (89%)	305 (86%)	50 (14%)	3	15
All	All	2858/3176 (90%)	2479 (87%)	379 (13%)	4	17

5 of 379 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	77	ASN
1	G	143	ARG
1	F	154	ILE
1	F	374	GLN
1	G	289	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	335	GLN

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Mol	Chain	Res	Type
1	H	112	ASN
1	F	433	ASN
1	G	374	GLN
1	H	335	GLN

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](#)

2 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	$\# Z > 2$
2	NLG	H	1503	-	12,12,12	2.06	3 (25%)	15,15,15	1.53	3 (20%)
2	NLG	D	1503	-	12,12,12	2.28	2 (16%)	15,15,15	2.13	7 (46%)

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
2	NLG	H	1503	-	-	0/13/13/13	-
2	NLG	D	1503	-	-	6/13/13/13	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1503	NLG	C8-C7	-5.93	1.38	1.50
2	H	1503	NLG	C8-C7	-4.74	1.40	1.50
2	H	1503	NLG	CA-C	3.23	1.60	1.52
2	D	1503	NLG	CG-CD	2.97	1.57	1.50
2	H	1503	NLG	CG-CD	2.65	1.56	1.50

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1503	NLG	CB-CA-N2	4.75	120.31	110.91
2	D	1503	NLG	C8-C7-N2	3.18	121.39	116.12
2	H	1503	NLG	C-CA-N2	3.15	117.89	110.57
2	H	1503	NLG	O7-C7-C8	-3.00	116.72	122.05
2	D	1503	NLG	CA-N2-C7	2.61	128.90	121.58

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1503	NLG	CB-CA-N2-C7
2	D	1503	NLG	C8-C7-N2-CA
2	D	1503	NLG	O7-C7-N2-CA
2	D	1503	NLG	OXT-C-CA-N2
2	D	1503	NLG	O-C-CA-N2

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	1503	NLG	2	0
2	D	1503	NLG	10	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

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	405/464 (87%)	-0.52	0 100 100	46, 81, 135, 187	0
1	B	436/464 (93%)	-0.53	0 100 100	37, 73, 149, 245	0
1	C	436/464 (93%)	-0.56	0 100 100	35, 73, 151, 219	0
1	D	405/464 (87%)	-0.56	0 100 100	45, 80, 142, 205	0
1	E	405/464 (87%)	-0.30	1 (0%) 91 85	55, 102, 230, 344	0
1	F	436/464 (93%)	-0.51	1 (0%) 91 85	45, 83, 151, 217	0
1	G	436/464 (93%)	-0.39	1 (0%) 91 85	53, 96, 184, 263	0
1	H	422/464 (90%)	-0.51	0 100 100	50, 86, 170, 237	0
All	All	3381/3712 (91%)	-0.48	3 (0%) 92 90	35, 84, 166, 344	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	415	ASP	2.7
1	E	147	GLN	2.2
1	G	85	GLU	2.1

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(\AA^2)	Q<0.9
2	NLG	H	1503	13/13	0.93	0.08	64,81,101,106	0
2	NLG	D	1503	13/13	0.94	0.08	48,59,72,79	0

6.5 Other polymers [i](#)

There are no such residues in this entry.