Full wwPDB X-ray Structure Validation Report ⓘ

Sep 10, 2023 – 08:56 PM EDT

PDB ID	:	4J6S
Title	:	14-3-3gamma complexed with the N-terminal sequence of tyrosine hydroxylase (residues 1-43)
Authors	:	Mileni, M.; Martinez, A.; Stevens, R.C.
Deposited on	:	2013-02-11
Resolution	:	3.08 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:

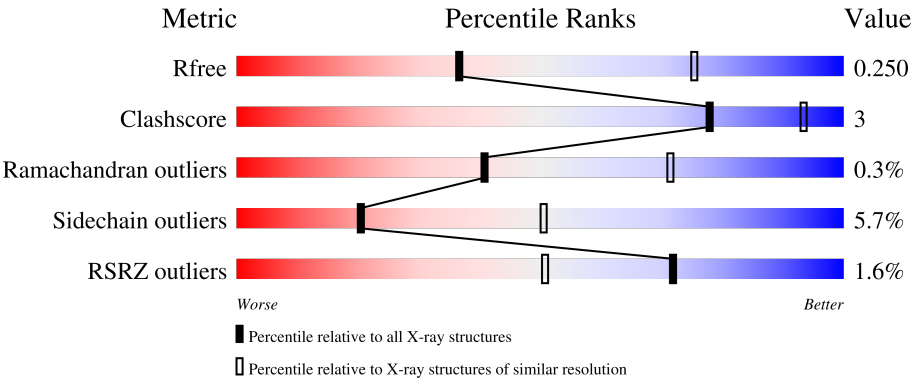
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.08 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}	130704	1447 (3.10-3.06)
Clashscore	141614	1546 (3.10-3.06)
Ramachandran outliers	138981	1487 (3.10-3.06)
Sidechain outliers	138945	1486 (3.10-3.06)
RSRZ outliers	127900	1416 (3.10-3.06)

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 <=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	255	81% 11% • 7%
1	B	255	83% 12% 5%
1	C	255	83% 9% 7%
1	D	255	82% 12% 6%
2	E	43	12% 5% 84%

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Mol	Chain	Length	Quality of chain
2	F	43	
2	G	43	
2	H	43	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7970 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 14-3-3 protein gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	0	0	0
			1909	1191	325	384	9			
1	B	243	Total	C	N	O	S	0	0	0
			1953	1216	333	395	9			
1	C	236	Total	C	N	O	S	0	0	0
			1901	1187	324	381	9			
1	D	240	Total	C	N	O	S	0	0	0
			1927	1202	328	388	9			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	SER	-	expression tag	UNP P61981
A	-5	ARG	-	expression tag	UNP P61981
A	-4	ARG	-	expression tag	UNP P61981
A	-3	ALA	-	expression tag	UNP P61981
A	-2	SER	-	expression tag	UNP P61981
A	-1	VAL	-	expression tag	UNP P61981
A	0	GLY	-	expression tag	UNP P61981
A	1	LEU	-	expression tag	UNP P61981
B	-6	SER	-	expression tag	UNP P61981
B	-5	ARG	-	expression tag	UNP P61981
B	-4	ARG	-	expression tag	UNP P61981
B	-3	ALA	-	expression tag	UNP P61981
B	-2	SER	-	expression tag	UNP P61981
B	-1	VAL	-	expression tag	UNP P61981
B	0	GLY	-	expression tag	UNP P61981
B	1	LEU	-	expression tag	UNP P61981
C	-6	SER	-	expression tag	UNP P61981
C	-5	ARG	-	expression tag	UNP P61981
C	-4	ARG	-	expression tag	UNP P61981
C	-3	ALA	-	expression tag	UNP P61981
C	-2	SER	-	expression tag	UNP P61981

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	VAL	-	expression tag	UNP P61981
C	0	GLY	-	expression tag	UNP P61981
C	1	LEU	-	expression tag	UNP P61981
D	-6	SER	-	expression tag	UNP P61981
D	-5	ARG	-	expression tag	UNP P61981
D	-4	ARG	-	expression tag	UNP P61981
D	-3	ALA	-	expression tag	UNP P61981
D	-2	SER	-	expression tag	UNP P61981
D	-1	VAL	-	expression tag	UNP P61981
D	0	GLY	-	expression tag	UNP P61981
D	1	LEU	-	expression tag	UNP P61981

- Molecule 2 is a protein called N-terminal motif of tyrosine hydroxylase.

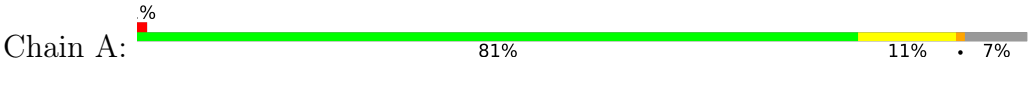
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	7	Total	C	N	O	P	0	0	0
			58	32	10	15	1			
2	F	9	Total	C	N	O	P	0	0	0
			74	41	15	17	1			
2	G	9	Total	C	N	O	P	0	0	0
			74	41	15	17	1			
2	H	9	Total	C	N	O	P	0	0	0
			74	41	15	17	1			

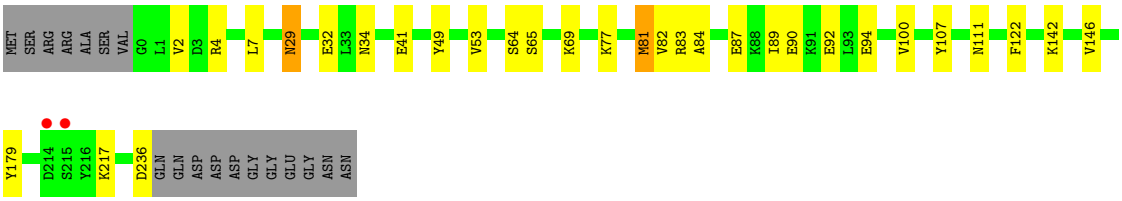
3 Residue-property plots (i)

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: 14-3-3 protein gamma

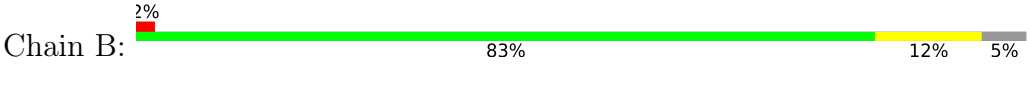
Chain A:

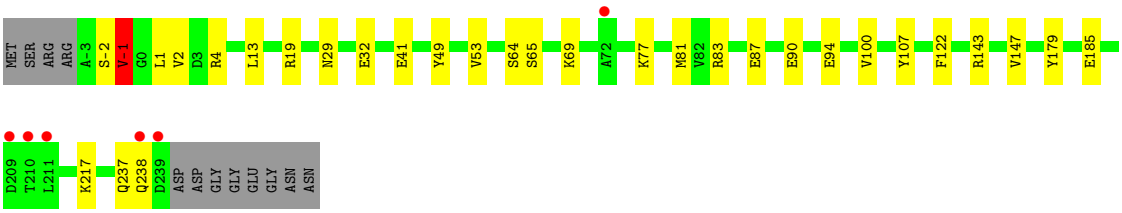




• Molecule 1: 14-3-3 protein gamma

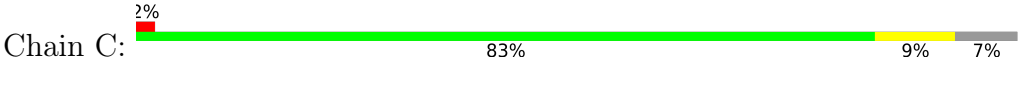
Chain B:

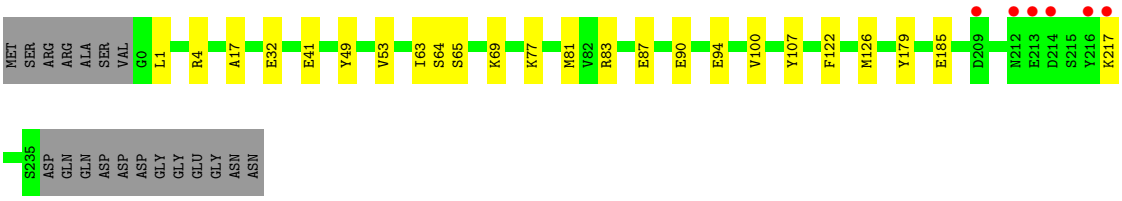




• Molecule 1: 14-3-3 protein gamma

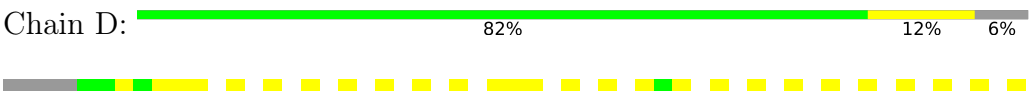
Chain C:

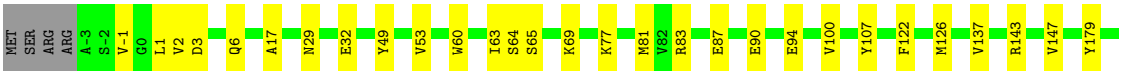


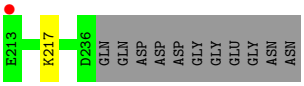


• Molecule 1: 14-3-3 protein gamma

Chain D:

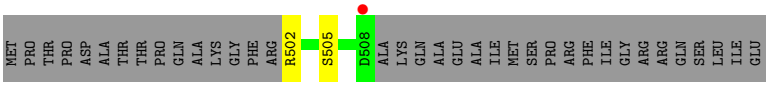






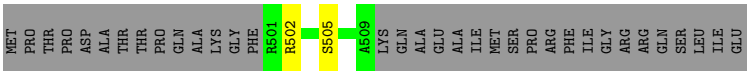
• Molecule 2: N-terminal motif of tyrosine hydroxylase

Chain E:



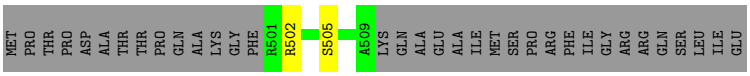
• Molecule 2: N-terminal motif of tyrosine hydroxylase

Chain F:



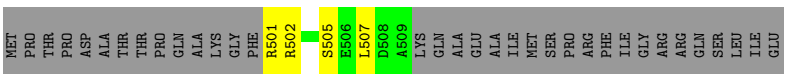
• Molecule 2: N-terminal motif of tyrosine hydroxylase

Chain G:



• Molecule 2: N-terminal motif of tyrosine hydroxylase

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	84.19Å 115.12Å 136.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.90 – 3.08 29.88 – 3.08	Depositor EDS
% Data completeness (in resolution range)	87.0 (29.90-3.08) 87.2 (29.88-3.08)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.38 (at 3.06Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.210 , 0.254 0.212 , 0.250	Depositor DCC
R_{free} test set	1100 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	60.1	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 28.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7970	wwPDB-VP
Average B, all atoms (Å^2)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: SEP

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	0.49	0/1937	0.63	0/2614
1	B	0.46	0/1981	0.61	0/2674
1	C	0.46	0/1929	0.63	0/2603
1	D	0.46	0/1955	0.62	0/2639
2	E	0.68	0/46	0.89	0/59
2	F	0.56	0/62	0.72	0/80
2	G	0.49	0/62	0.79	0/80
2	H	0.47	0/62	0.82	0/80
All	All	0.47	0/8034	0.63	0/10829

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

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	1909	0	1880	20	0
1	B	1953	0	1919	15	0
1	C	1901	0	1876	13	0
1	D	1927	0	1899	10	0
2	E	58	0	50	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	74	0	68	1	0
2	G	74	0	68	1	0
2	H	74	0	68	1	0
All	All	7970	0	7828	46	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 3.

All (46) 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:142:LYS:HD3	1:C:1:LEU:HD22	1.78	0.64
1:A:142:LYS:CD	1:C:1:LEU:HD22	2.30	0.61
1:A:81:MET:HA	1:B:1:LEU:CD1	2.33	0.58
1:C:185:GLU:OE2	2:G:502:ARG:HD2	2.04	0.57
1:B:185:GLU:OE2	2:F:502:ARG:HD2	2.05	0.57
1:C:63:ILE:HD11	1:D:17:ALA:HB2	1.87	0.55
1:D:1:LEU:HD23	1:D:6:GLN:NE2	2.22	0.54
1:B:83:ARG:NH1	1:B:87:GLU:OE2	2.42	0.52
1:C:32:GLU:HA	1:C:107:TYR:CE2	2.44	0.52
1:A:146:VAL:HG11	1:C:1:LEU:HD21	1.91	0.52
1:A:32:GLU:HA	1:A:107:TYR:CE2	2.47	0.50
1:A:82:VAL:HG22	1:B:13:LEU:HD11	1.93	0.50
1:A:89:ILE:HG13	1:B:19:ARG:NH1	2.27	0.49
1:C:83:ARG:NH1	1:C:87:GLU:OE2	2.45	0.49
1:D:83:ARG:NH1	1:D:87:GLU:OE2	2.45	0.49
1:A:83:ARG:NH1	1:A:87:GLU:OE2	2.46	0.48
1:B:2:VAL:O	1:B:2:VAL:HG12	2.15	0.46
1:B:32:GLU:HA	1:B:107:TYR:CE2	2.50	0.46
1:D:32:GLU:HA	1:D:107:TYR:CE2	2.52	0.45
1:C:49:TYR:CG	1:C:100:VAL:HG22	2.52	0.45
1:A:146:VAL:CG1	1:C:1:LEU:HD21	2.47	0.45
1:A:90:GLU:O	1:A:94:GLU:HG3	2.16	0.45
1:A:4:ARG:NH2	1:A:41:GLU:OE1	2.50	0.45
1:A:89:ILE:HG13	1:B:19:ARG:HH11	1.82	0.45
1:B:4:ARG:NH2	1:B:41:GLU:OE1	2.50	0.44
1:A:34:ASN:OD1	1:A:111:ASN:ND2	2.47	0.44
1:A:49:TYR:CD1	1:A:100:VAL:HG23	2.53	0.44
1:A:84:ALA:HB1	1:B:-1:VAL:HG22	1.99	0.44
1:C:17:ALA:HB2	1:D:63:ILE:HD11	2.00	0.44
2:H:501:ARG:O	2:H:502:ARG:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:TYR:CG	1:A:100:VAL:CG2	3.01	0.43
1:C:90:GLU:O	1:C:94:GLU:HG3	2.19	0.43
1:B:49:TYR:CG	1:B:100:VAL:HG22	2.54	0.43
1:D:2:VAL:HG22	1:D:2:VAL:O	2.19	0.42
1:B:90:GLU:O	1:B:94:GLU:HG3	2.19	0.42
1:D:49:TYR:CG	1:D:100:VAL:HG22	2.54	0.42
1:A:81:MET:HA	1:B:1:LEU:HD13	2.00	0.41
1:C:49:TYR:CD1	1:C:100:VAL:CG2	3.04	0.41
1:D:90:GLU:O	1:D:94:GLU:HG3	2.20	0.41
1:A:7:LEU:HD13	1:A:29:ASN:HB3	2.01	0.41
1:C:4:ARG:NH2	1:C:41:GLU:OE1	2.54	0.41
1:A:49:TYR:CD1	1:A:100:VAL:CG2	3.04	0.41
1:D:143:ARG:O	1:D:147:VAL:HG23	2.21	0.41
1:A:92:GLU:CD	1:B:19:ARG:HH22	2.25	0.40
1:D:60:TRP:CE2	1:D:137:VAL:HG12	2.57	0.40
1:B:143:ARG:O	1:B:147:VAL:HG23	2.22	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	235/255 (92%)	230 (98%)	5 (2%)	0	100 100
1	B	241/255 (94%)	233 (97%)	5 (2%)	3 (1%)	13 42
1	C	234/255 (92%)	228 (97%)	6 (3%)	0	100 100
1	D	238/255 (93%)	232 (98%)	6 (2%)	0	100 100
2	E	4/43 (9%)	3 (75%)	1 (25%)	0	100 100
2	F	6/43 (14%)	5 (83%)	1 (17%)	0	100 100
2	G	6/43 (14%)	5 (83%)	1 (17%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	H	6/43 (14%)	2 (33%)	4 (67%)	0	100 100
All	All	970/1192 (81%)	938 (97%)	29 (3%)	3 (0%)	41 71

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	-2	SER
1	B	238	GLN
1	B	-1	VAL

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	208/222 (94%)	196 (94%)	12 (6%)	20 50
1	B	213/222 (96%)	201 (94%)	12 (6%)	21 51
1	C	207/222 (93%)	197 (95%)	10 (5%)	25 57
1	D	210/222 (95%)	197 (94%)	13 (6%)	18 48
2	E	5/34 (15%)	4 (80%)	1 (20%)	1 5
2	F	6/34 (18%)	6 (100%)	0	100 100
2	G	6/34 (18%)	6 (100%)	0	100 100
2	H	6/34 (18%)	5 (83%)	1 (17%)	2 9
All	All	861/1024 (84%)	812 (94%)	49 (6%)	20 50

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	VAL
1	A	29	ASN
1	A	53	VAL
1	A	64	SER
1	A	65	SER

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Mol	Chain	Res	Type
1	A	69	LYS
1	A	77	LYS
1	A	81	MET
1	A	122	PHE
1	A	179	TYR
1	A	217	LYS
1	A	236	ASP
1	B	-1	VAL
1	B	29	ASN
1	B	53	VAL
1	B	64	SER
1	B	65	SER
1	B	69	LYS
1	B	77	LYS
1	B	81	MET
1	B	122	PHE
1	B	179	TYR
1	B	217	LYS
1	B	237	GLN
1	C	53	VAL
1	C	64	SER
1	C	65	SER
1	C	69	LYS
1	C	77	LYS
1	C	81	MET
1	C	122	PHE
1	C	126	MET
1	C	179	TYR
1	C	217	LYS
1	D	-1	VAL
1	D	3	ASP
1	D	29	ASN
1	D	53	VAL
1	D	64	SER
1	D	65	SER
1	D	69	LYS
1	D	77	LYS
1	D	81	MET
1	D	122	PHE
1	D	126	MET
1	D	179	TYR
1	D	217	LYS

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Mol	Chain	Res	Type
2	E	502	ARG
2	H	507	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	164	HIS
1	C	164	HIS
1	D	16	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)

4 non-standard protein/DNA/RNA residues 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	SEP	E	505	2	8,9,10	0.71	0	8,12,14	1.65	2 (25%)
2	SEP	F	505	2	8,9,10	0.77	0	8,12,14	1.71	3 (37%)
2	SEP	G	505	2	8,9,10	0.68	0	8,12,14	1.55	1 (12%)
2	SEP	H	505	2	8,9,10	0.73	0	8,12,14	1.47	2 (25%)

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	SEP	E	505	2	-	0/5/8/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SEP	F	505	2	-	0/5/8/10	-
2	SEP	G	505	2	-	1/5/8/10	-
2	SEP	H	505	2	-	1/5/8/10	-

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	505	SEP	OG-CB-CA	3.75	111.80	108.14
2	G	505	SEP	OG-CB-CA	3.25	111.30	108.14
2	F	505	SEP	OG-CB-CA	2.89	110.95	108.14
2	H	505	SEP	OG-P-O1P	-2.72	98.83	106.47
2	H	505	SEP	O2P-P-O1P	2.49	120.44	110.68
2	F	505	SEP	O2P-P-O1P	2.31	119.74	110.68
2	F	505	SEP	OG-P-O1P	-2.30	100.02	106.47
2	E	505	SEP	O3P-P-O2P	2.08	115.58	107.64

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	505	SEP	CB-OG-P-O1P
2	H	505	SEP	CB-OG-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides 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

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, 95^{th} 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	237/255 (92%)	-0.38	2 (0%) 86 71	30, 56, 105, 141	0
1	B	243/255 (95%)	-0.29	6 (2%) 57 33	32, 63, 132, 179	0
1	C	236/255 (92%)	-0.26	6 (2%) 57 33	38, 65, 131, 223	0
1	D	240/255 (94%)	-0.41	1 (0%) 92 84	39, 62, 117, 146	0
2	E	6/43 (13%)	0.48	1 (16%) 1 0	59, 81, 101, 111	0
2	F	8/43 (18%)	0.36	0 100 100	61, 91, 113, 114	0
2	G	8/43 (18%)	0.03	0 100 100	64, 88, 105, 120	0
2	H	8/43 (18%)	0.26	0 100 100	61, 82, 112, 120	0
All	All	986/1192 (82%)	-0.32	16 (1%) 72 51	30, 62, 120, 223	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	209	ASP	5.5
1	C	213	GLU	4.7
1	C	216	TYR	3.4
1	B	239	ASP	3.3
1	C	217	LYS	3.2
1	C	214	ASP	2.8
1	A	214	ASP	2.4
1	B	209	ASP	2.4
1	A	215	SER	2.4
1	B	238	GLN	2.3
1	B	72	ALA	2.3
1	B	210	THR	2.3
1	C	212	ASN	2.3
1	D	213	GLU	2.2
1	B	211	LEU	2.1
2	E	508	ASP	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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
2	SEP	G	505	10/11	0.97	0.20	47,53,63,70	0
2	SEP	H	505	10/11	0.97	0.13	40,44,51,51	0
2	SEP	E	505	10/11	0.98	0.13	30,37,49,51	0
2	SEP	F	505	10/11	0.98	0.17	40,48,55,59	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.