wwPDB X-ray Structure Validation Summary Report (i)

Oct 11, 2021 – 12:57 PM EDT

PDB ID	:	2HTY
Title	:	N1 neuraminidase
Authors	:	Russell, R.J.; Haire, L.F.; Stevens, D.J.; Collins, P.J.; Lin, Y.P.; Blackburn, G.M.; Hay, A.J.; Gamblin, S.J.; Skehel, J.J.
Deposited on	:	2006-07-26
Resolution	:	2.50 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

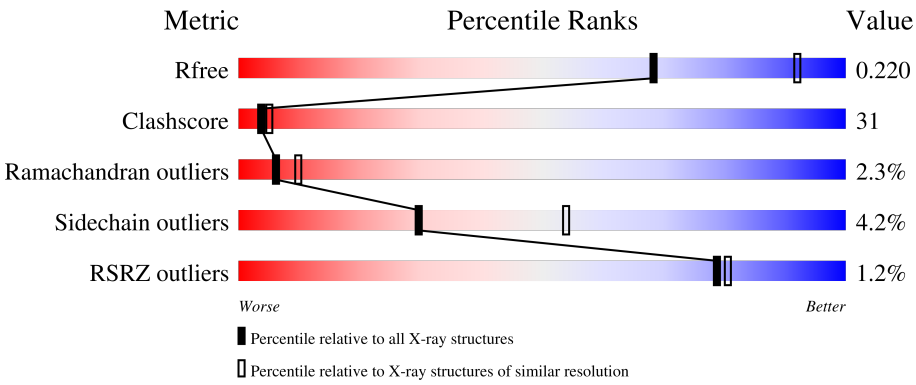
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 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))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 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	387	58% 37% • •
1	B	387	% 56% 37% 6% •
1	C	387	2% 57% 36% 6% •
1	D	387	% 59% 35% 5% •
1	E	387	2% 55% 40% • •

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Mol	Chain	Length	Quality of chain
1	F	387	% 57% 37% 5%
1	G	387	% 56% 37% 5%
1	H	387	3% 54% 41%

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	NDG	A	1146	-	-	-	X
2	NDG	B	1146	-	-	-	X
2	NDG	C	1146	-	-	-	X
2	NDG	D	1146	-	-	-	X
2	NDG	F	1146	-	-	-	X
2	NDG	G	1146	-	-	-	X
2	NDG	H	1146	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 24458 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.

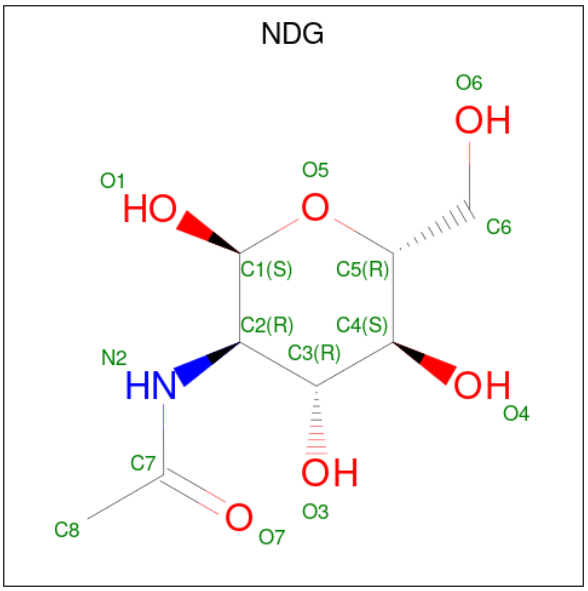
- Molecule 1 is a protein called Neuraminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	385	2962	1858	510	573	21	0	0	0
1	B	385	2962	1858	510	573	21	0	0	0
1	C	385	2962	1858	510	573	21	0	0	0
1	D	385	2962	1858	510	573	21	0	0	0
1	E	385	2962	1858	510	573	21	0	0	0
1	F	385	2962	1858	510	573	21	0	0	0
1	G	385	2962	1858	510	573	21	0	0	0
1	H	385	2962	1858	510	573	21	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169A	TYR	HIS	engineered mutation	UNP Q6DPL2
B	169A	TYR	HIS	engineered mutation	UNP Q6DPL2
C	169A	TYR	HIS	engineered mutation	UNP Q6DPL2
D	169A	TYR	HIS	engineered mutation	UNP Q6DPL2
E	169A	TYR	HIS	engineered mutation	UNP Q6DPL2
F	169A	TYR	HIS	engineered mutation	UNP Q6DPL2
G	169A	TYR	HIS	engineered mutation	UNP Q6DPL2
H	169A	TYR	HIS	engineered mutation	UNP Q6DPL2

- Molecule 2 is 2-acetamido-2-deoxy-alpha-D-glucopyranose (three-letter code: NDG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	15	8	1	6	0	0
2	B	1	15	8	1	6	0	0
2	C	1	15	8	1	6	0	0
2	D	1	15	8	1	6	0	0
2	F	1	15	8	1	6	0	0
2	G	1	15	8	1	6	0	0
2	H	1	15	8	1	6	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

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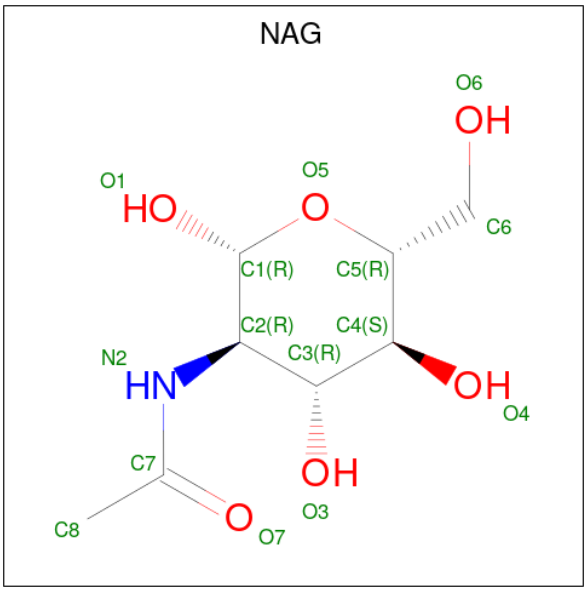
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	F	1	Total Ca 1 1	0	0
3	G	1	Total Ca 1 1	0	0
3	H	1	Total Ca 1 1	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total C N O 15 8 1 6	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	111	Total O 111 111	0	0
5	B	91	Total O 91 91	0	0
5	C	102	Total O 102 102	0	0
5	D	104	Total O 104 104	0	0
5	E	54	Total O 54 54	0	0

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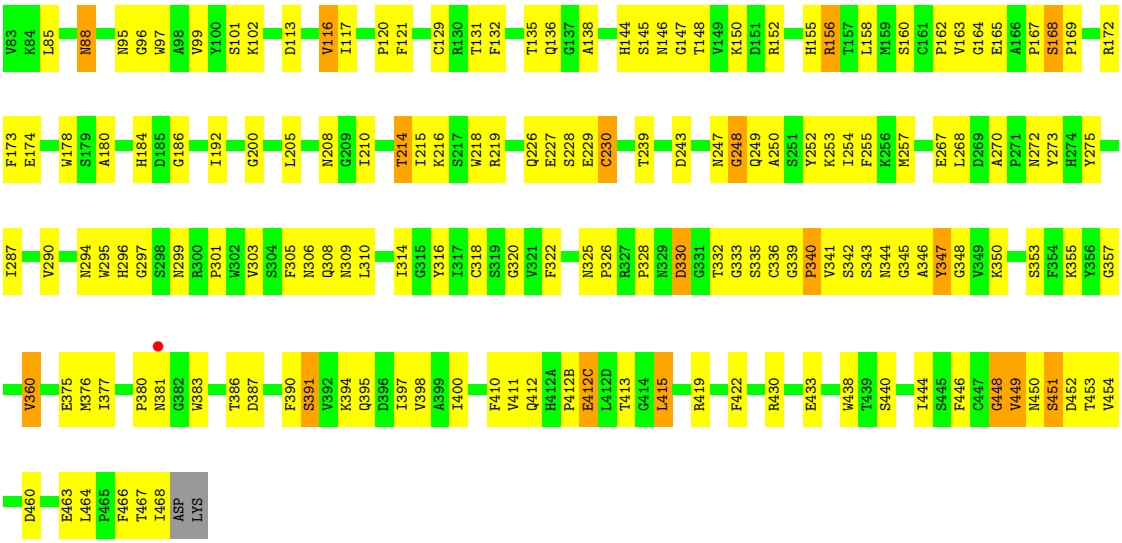
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	F	46	46	46	0	0
			Total	O		
5	G	86	86	86	0	0
			Total	O		
5	H	40	40	40	0	0

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.

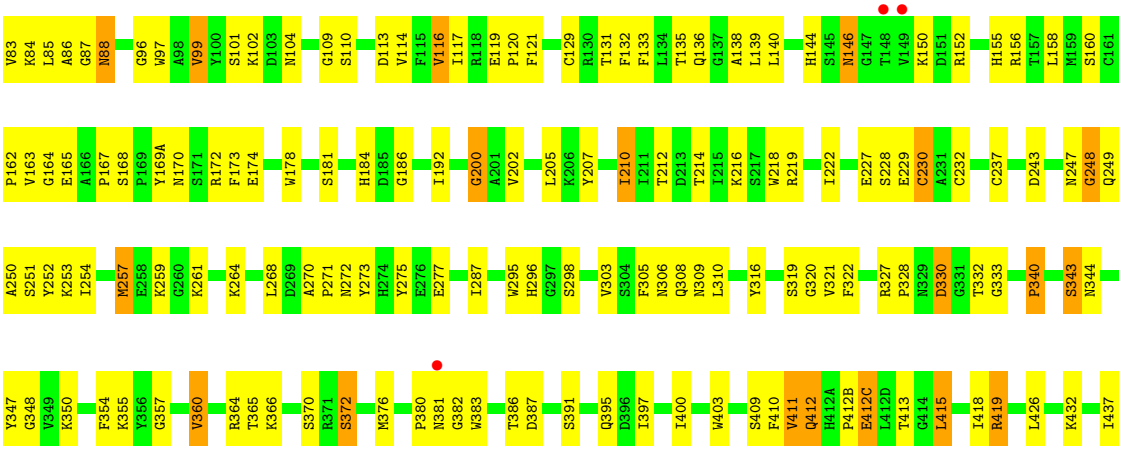
• Molecule 1: Neuraminidase

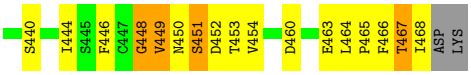
Chain A: 58% 37%



• Molecule 1: Neuraminidase

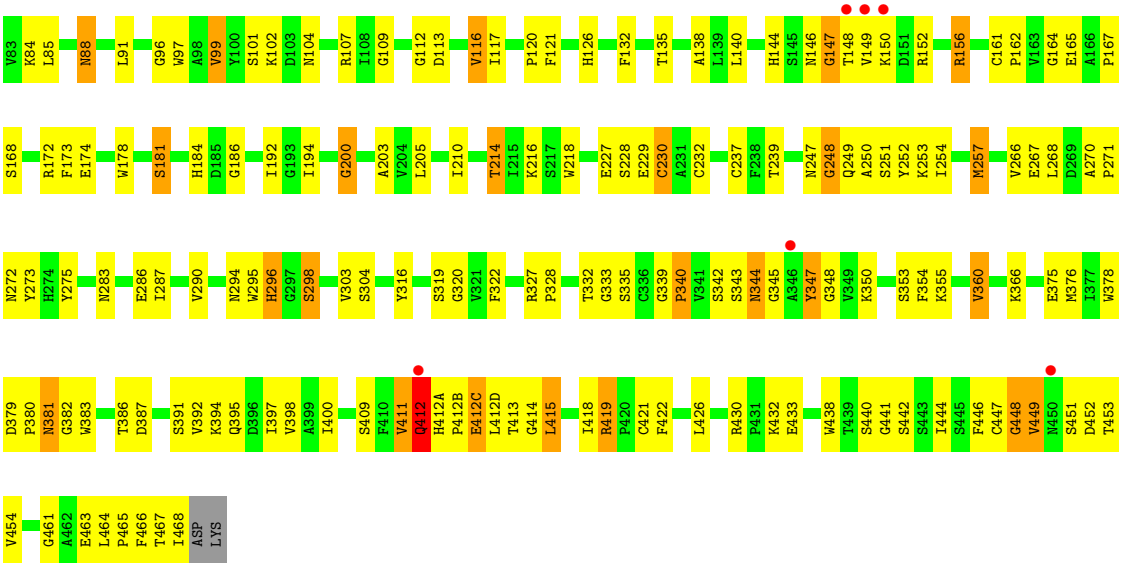
Chain B: % 56% 37% 6%





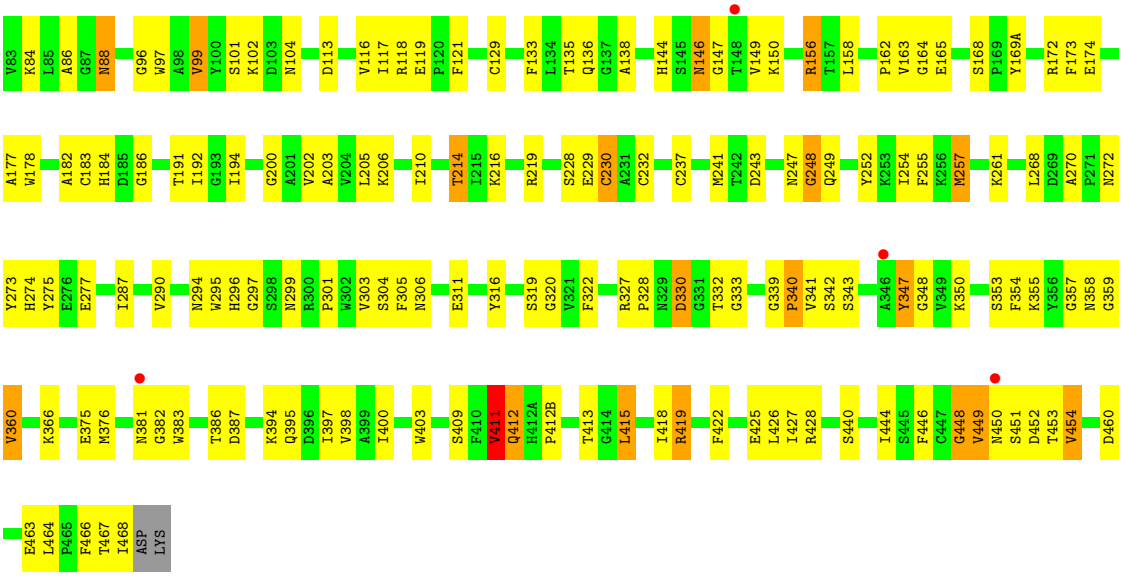
• Molecule 1: Neuraminidase

Chain C:



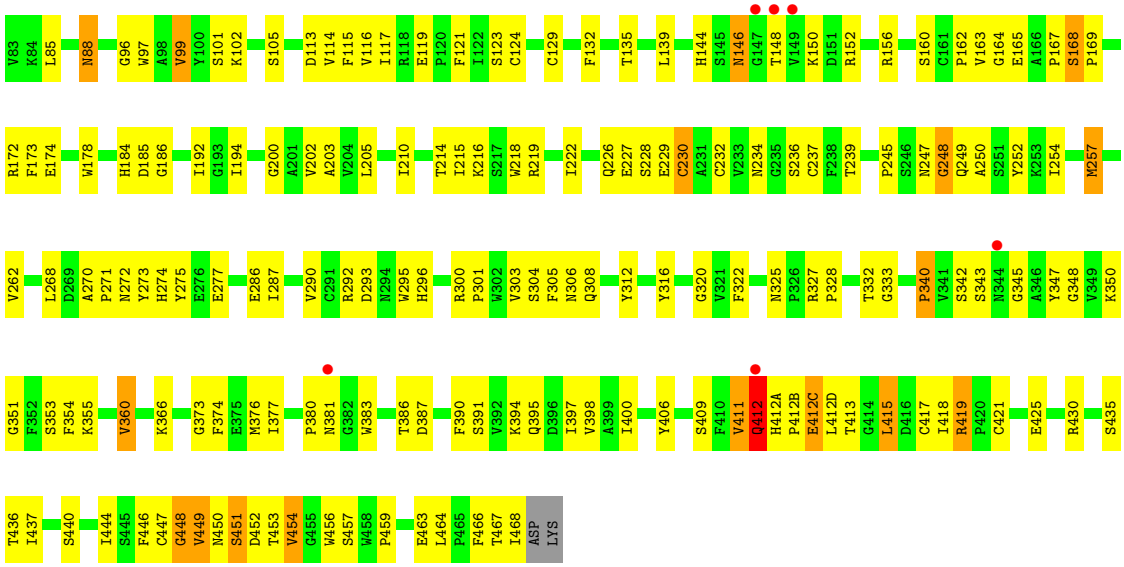
• Molecule 1: Neuraminidase

Chain D:



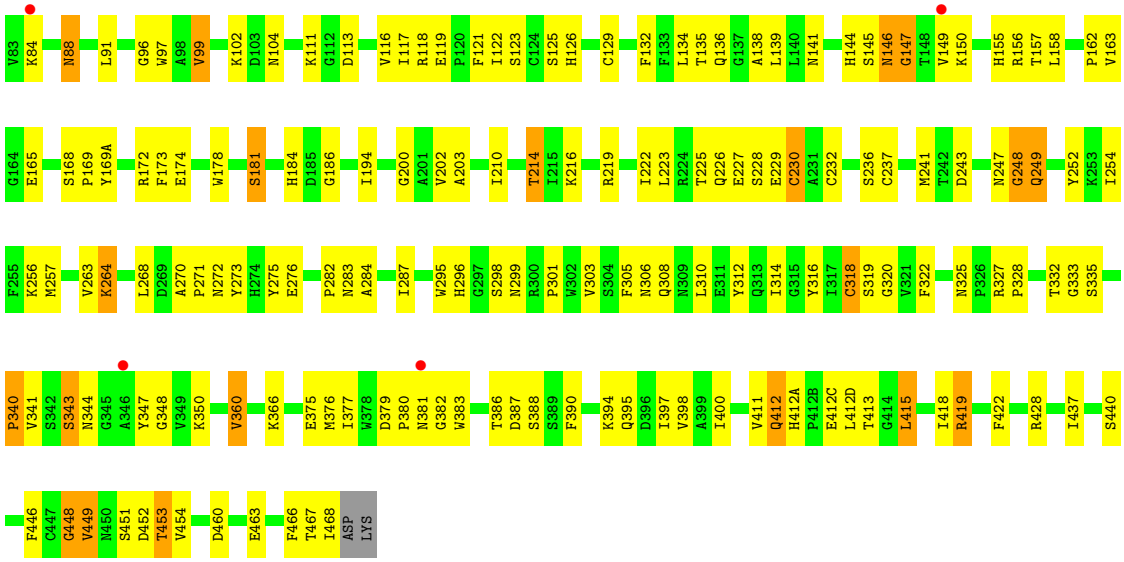
• Molecule 1: Neuraminidase

Chain E:



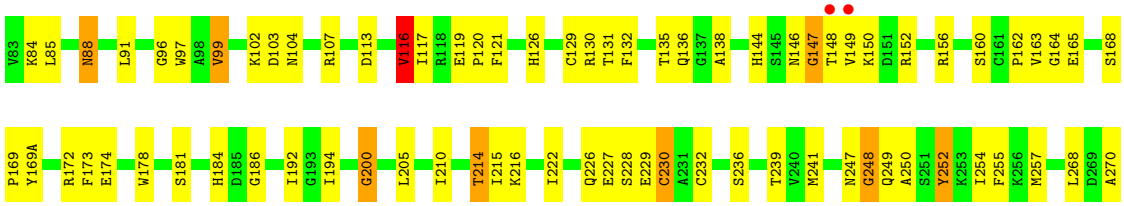
- Molecule 1: Neuraminidase

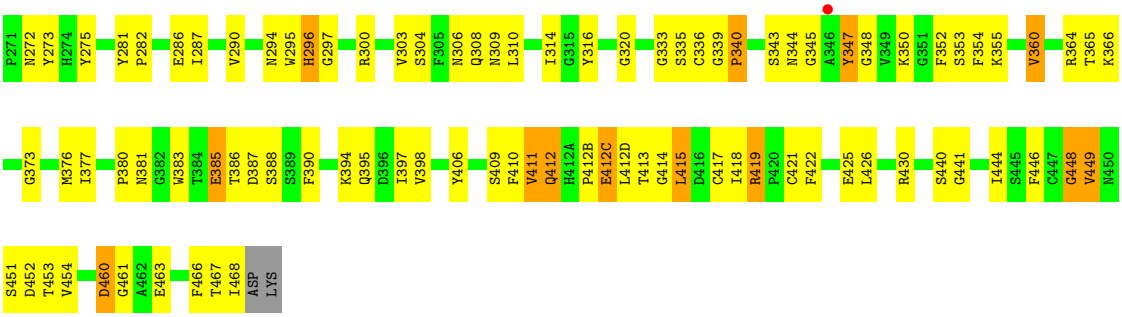
Chain F:



- Molecule 1: Neuraminidase

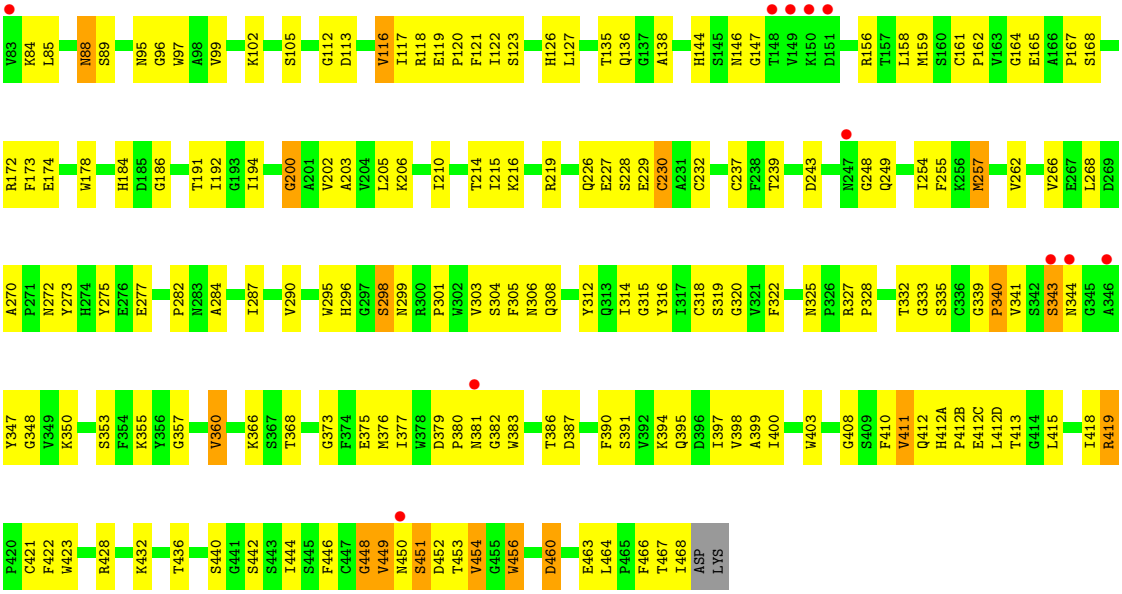
Chain G:





- Molecule 1: Neuraminidase

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	200.21Å 200.77Å 211.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.50 19.99 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.50) 98.0 (19.99-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	1.59 (at 2.50Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.232 , 0.262 0.220 , 0.220	Depositor DCC
R_{free} test set	7196 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	29.9	Xtriage
Anisotropy	0.341	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 4.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.054 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	24458	wwPDB-VP
Average B, all atoms (Å^2)	27.0	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 22.02 % 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 6.2128e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, CA, NDG

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	0.45	0/3045	0.74	0/4141
1	B	0.65	4/3045 (0.1%)	0.82	4/4141 (0.1%)
1	C	0.64	2/3045 (0.1%)	0.92	7/4141 (0.2%)
1	D	0.60	3/3045 (0.1%)	0.81	3/4141 (0.1%)
1	E	0.58	3/3045 (0.1%)	0.87	6/4141 (0.1%)
1	F	0.40	0/3045	0.71	0/4141
1	G	0.47	1/3045 (0.0%)	0.77	4/4141 (0.1%)
1	H	0.39	0/3045	0.71	1/4141 (0.0%)
All	All	0.53	13/24360 (0.1%)	0.80	25/33128 (0.1%)

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	C	0	2
1	D	0	1
1	E	0	2
1	F	0	1
All	All	0	6

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	411	VAL	CB-CG2	21.65	1.98	1.52
1	C	411	VAL	CB-CG2	20.64	1.96	1.52
1	B	411	VAL	CB-CG2	20.57	1.96	1.52
1	E	411	VAL	CB-CG2	19.57	1.94	1.52
1	B	411	VAL	CB-CG1	-14.30	1.22	1.52

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	412	GLN	O-C-N	-19.52	91.47	122.70
1	B	411	VAL	CA-CB-CG2	-17.61	84.48	110.90
1	E	411	VAL	CA-CB-CG2	-16.36	86.37	110.90
1	E	412	GLN	O-C-N	-16.21	96.76	122.70
1	D	411	VAL	CA-CB-CG2	-15.69	87.36	110.90

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	412	GLN	Mainchain,Peptide
1	D	411	VAL	Mainchain
1	E	412	GLN	Mainchain,Peptide
1	F	412	GLN	Mainchain

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	2962	0	2783	186	0
1	B	2962	0	2783	196	0
1	C	2962	0	2782	217	1
1	D	2962	0	2783	197	0
1	E	2962	0	2781	200	0
1	F	2962	0	2783	181	0
1	G	2962	0	2783	199	0
1	H	2962	0	2783	199	0
2	A	15	0	12	2	0
2	B	15	0	12	2	0
2	C	15	0	12	4	0
2	D	15	0	12	4	0
2	F	15	0	12	3	0
2	G	15	0	12	3	0
2	H	15	0	12	4	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	E	15	0	15	2	0
5	A	111	0	0	24	0
5	B	91	0	0	29	0
5	C	102	0	0	41	0
5	D	104	0	0	25	1
5	E	54	0	0	16	0
5	F	46	0	0	17	0
5	G	86	0	0	26	0
5	H	40	0	0	27	0
All	All	24458	0	22360	1443	1

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 31.

The worst 5 of 1443 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:G:412:GLN:CG	1:G:412:GLN:CB	1.79	1.51
1:C:411:VAL:CG2	1:C:411:VAL:CB	1.96	1.44
1:E:411:VAL:CG2	1:E:411:VAL:CB	1.94	1.43
1:B:411:VAL:CB	1:B:411:VAL:CG2	1.96	1.42
1:D:411:VAL:CB	1:D:411:VAL:CG2	1.98	1.42

All (1) 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:C:343:SER:OG	5:D:1242:HOH:O[8_456]	2.13	0.07

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	383/387 (99%)	342 (89%)	32 (8%)	9 (2%)	6	10
1	B	383/387 (99%)	341 (89%)	32 (8%)	10 (3%)	5	8
1	C	383/387 (99%)	338 (88%)	35 (9%)	10 (3%)	5	8
1	D	383/387 (99%)	344 (90%)	31 (8%)	8 (2%)	7	11
1	E	383/387 (99%)	342 (89%)	32 (8%)	9 (2%)	6	10
1	F	383/387 (99%)	335 (88%)	37 (10%)	11 (3%)	4	6
1	G	383/387 (99%)	346 (90%)	30 (8%)	7 (2%)	8	14
1	H	383/387 (99%)	344 (90%)	31 (8%)	8 (2%)	7	11
All	All	3064/3096 (99%)	2732 (89%)	260 (8%)	72 (2%)	6	10

5 of 72 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	343	SER
1	B	448	GLY
1	D	340	PRO
1	E	340	PRO
1	E	412(A)	HIS

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	329/331 (99%)	313 (95%)	16 (5%)	25	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	329/331 (99%)	314 (95%)	15 (5%)	27	50
1	C	329/331 (99%)	315 (96%)	14 (4%)	29	53
1	D	329/331 (99%)	318 (97%)	11 (3%)	38	64
1	E	329/331 (99%)	316 (96%)	13 (4%)	31	56
1	F	329/331 (99%)	315 (96%)	14 (4%)	29	53
1	G	329/331 (99%)	314 (95%)	15 (5%)	27	50
1	H	329/331 (99%)	316 (96%)	13 (4%)	31	56
All	All	2632/2648 (99%)	2521 (96%)	111 (4%)	30	54

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	99	VAL
1	H	460	ASP
1	F	141	ASN
1	H	456	TRP
1	H	99	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	313	GLN
1	F	412(A)	HIS
1	F	88	ASN
1	F	221	ASN
1	G	144	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
2	NDG	A	1146	-	15,15,15	0.74	0	21,21,21	0.74	0
2	NDG	F	1146	-	15,15,15	0.71	0	21,21,21	0.60	0
2	NDG	B	1146	-	15,15,15	0.69	0	21,21,21	0.74	0
2	NDG	H	1146	-	15,15,15	0.58	0	21,21,21	0.75	0
2	NDG	G	1146	-	15,15,15	0.82	1 (6%)	21,21,21	0.68	0
4	NAG	E	1146	-	15,15,15	0.90	1 (6%)	21,21,21	0.93	0
2	NDG	D	1146	-	15,15,15	0.62	0	21,21,21	0.88	1 (4%)
2	NDG	C	1146	-	15,15,15	0.68	0	21,21,21	0.77	0

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	NDG	A	1146	-	-	4/6/26/26	0/1/1/1
2	NDG	F	1146	-	-	2/6/26/26	0/1/1/1
2	NDG	B	1146	-	-	4/6/26/26	0/1/1/1
2	NDG	H	1146	-	-	4/6/26/26	0/1/1/1
2	NDG	G	1146	-	-	4/6/26/26	0/1/1/1
4	NAG	E	1146	-	-	2/6/26/26	0/1/1/1
2	NDG	D	1146	-	-	4/6/26/26	0/1/1/1
2	NDG	C	1146	-	-	4/6/26/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1146	NAG	C1-C2	2.68	1.56	1.52
2	G	1146	NDG	C1-C2	2.00	1.55	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1146	NDG	C1-C2-N2	-2.45	107.89	110.73

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1146	NDG	O5-C5-C6-O6
4	E	1146	NAG	O5-C5-C6-O6
2	C	1146	NDG	O5-C5-C6-O6
2	F	1146	NDG	O5-C5-C6-O6
2	B	1146	NDG	O5-C5-C6-O6

There are no ring outliers.

8 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1146	NDG	2	0
2	F	1146	NDG	3	0
2	B	1146	NDG	2	0
2	H	1146	NDG	4	0
2	G	1146	NDG	3	0
4	E	1146	NAG	2	0
2	D	1146	NDG	4	0
2	C	1146	NDG	4	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1
1	E	1
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	412:GLN	C	412(A):HIS	N	1.19
1	E	412:GLN	C	412(A):HIS	N	1.08
1	C	412:GLN	C	412(A):HIS	N	1.02

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	385/387 (99%)	-0.62	1 (0%)	94	94	9, 20, 36, 50	0
1	B	385/387 (99%)	-0.54	3 (0%)	86	87	8, 22, 36, 58	0
1	C	385/387 (99%)	-0.55	6 (1%)	72	74	10, 21, 35, 58	0
1	D	385/387 (99%)	-0.60	4 (1%)	82	84	8, 20, 33, 55	0
1	E	385/387 (99%)	-0.35	6 (1%)	72	74	17, 32, 44, 69	0
1	F	385/387 (99%)	-0.31	4 (1%)	82	84	22, 35, 50, 64	0
1	G	385/387 (99%)	-0.47	3 (0%)	86	87	14, 27, 41, 63	0
1	H	385/387 (99%)	-0.24	11 (2%)	51	55	23, 37, 51, 68	0
All	All	3080/3096 (99%)	-0.46	38 (1%)	79	80	8, 27, 45, 69	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	148	THR	5.6
1	D	381	ASN	4.4
1	F	381	ASN	4.2
1	C	148	THR	3.9
1	E	149	VAL	3.6

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 monosaccharides 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(Å^2)	Q<0.9
2	NDG	F	1146	15/15	0.28	0.63	74,77,79,80	0
2	NDG	C	1146	15/15	0.46	0.54	64,69,73,75	0
2	NDG	A	1146	15/15	0.46	0.56	66,69,73,74	0
2	NDG	G	1146	15/15	0.51	0.49	65,67,68,69	0
2	NDG	D	1146	15/15	0.55	0.43	60,64,65,66	0
2	NDG	B	1146	15/15	0.59	0.46	65,69,71,71	0
4	NAG	E	1146	15/15	0.63	0.39	57,62,65,65	0
2	NDG	H	1146	15/15	0.65	0.46	64,68,71,72	0
3	CA	H	998	1/1	0.94	0.09	40,40,40,40	0
3	CA	D	994	1/1	0.97	0.10	23,23,23,23	0
3	CA	G	997	1/1	0.97	0.11	29,29,29,29	0
3	CA	E	995	1/1	0.98	0.09	28,28,28,28	0
3	CA	F	996	1/1	0.98	0.10	46,46,46,46	0
3	CA	B	992	1/1	0.98	0.09	21,21,21,21	0
3	CA	C	993	1/1	0.98	0.10	22,22,22,22	0
3	CA	A	991	1/1	0.98	0.12	21,21,21,21	0

6.5 Other polymers (i)

There are no such residues in this entry.