



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:46 AM UTC

PDB ID : 6HR6 / pdb_00006hr6
Title : Nitrocefin reacted with catalytic serine (Ser294) of penicillin-binding protein 3 from *Pseudomonas aeruginosa*
Authors : Bellini, D.; Dowson, C.G.
Deposited on : 2018-09-26
Resolution : 2.53 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

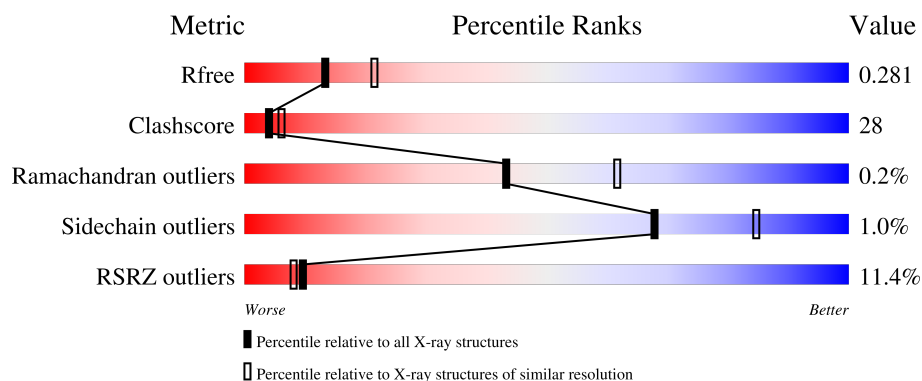
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.53 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	7383 (2.54-2.50)
Clashscore	190562	8079 (2.54-2.50)
Ramachandran outliers	187476	7944 (2.54-2.50)
Sidechain outliers	187428	7946 (2.54-2.50)
RSRZ outliers	180081	7387 (2.54-2.50)

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 $\leq 5\%$. 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	535	10% 64% 26% 8%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3819 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.

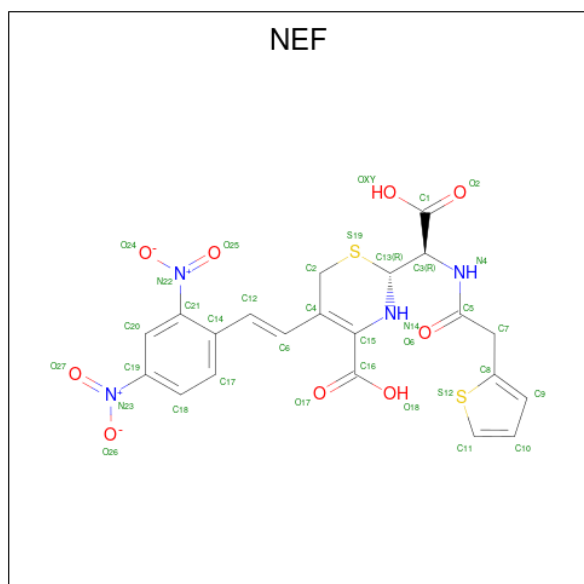
- Molecule 1 is a protein called Peptidoglycan D,D-transpeptidase FtsI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	492	3764	2373	684	695	12	0	1	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	45	GLY	-	expression tag	UNP G3XD46
A	46	TYR	-	expression tag	UNP G3XD46
A	47	GLN	-	expression tag	UNP G3XD46
A	48	ASP	-	expression tag	UNP G3XD46
A	49	PRO	-	expression tag	UNP G3XD46

- Molecule 2 is Nitrocefin - open form (CCD ID: NEF) (formula: $C_{21}H_{18}N_4O_9S_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			35	21	4	8	2		

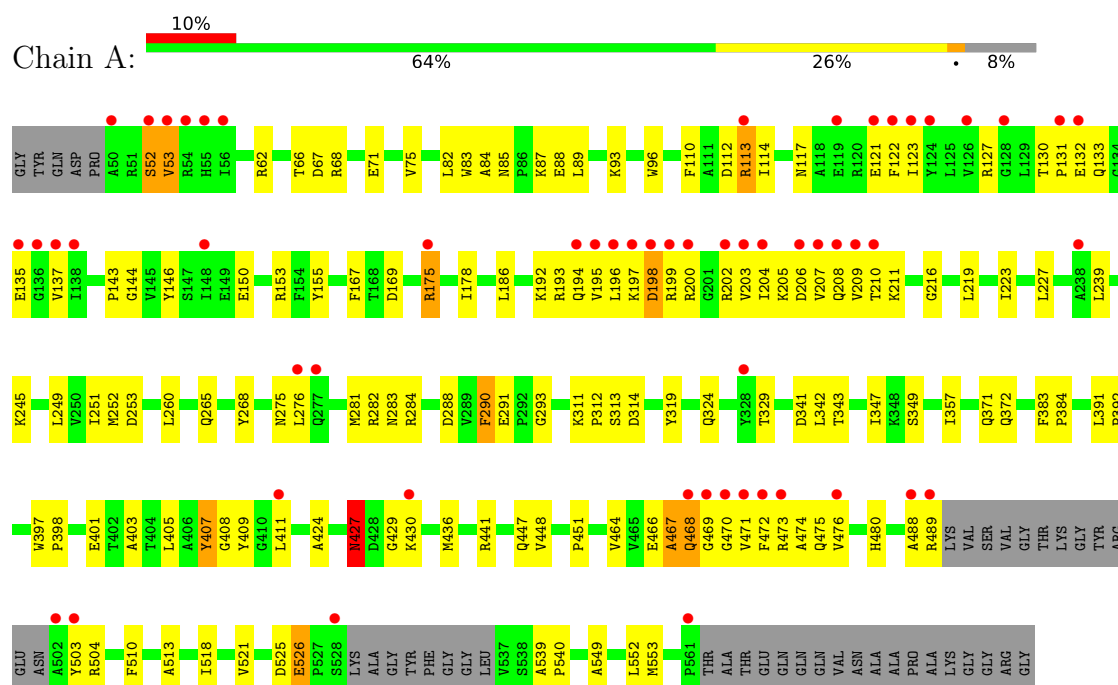
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	20	Total	O	0	0
			20	20		

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: Peptidoglycan D,D-transpeptidase FtsI



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.68Å 83.27Å 89.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.54 – 2.53 45.54 – 2.53	Depositor EDS
% Data completeness (in resolution range)	97.8 (45.54-2.53) 98.2 (45.54-2.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.54Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.228 , 0.286 0.247 , 0.281	Depositor DCC
R_{free} test set	818 reflections (4.63%)	wwPDB-VP
Wilson B-factor (Å ²)	45.0	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3819	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.68% 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

5.1 Standard geometry

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

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	1.02	11/3836 (0.3%)	1.28	38/5205 (0.7%)

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	4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	476	VAL	C-N	16.18	1.50	1.33
1	A	397	TRP	C-N	13.26	1.49	1.33
1	A	427	ASN	C-O	-10.31	1.11	1.23
1	A	424	ALA	C-O	-9.12	1.13	1.24
1	A	392	PRO	C-O	-8.20	1.14	1.23
1	A	319	TYR	C-N	7.74	1.49	1.34
1	A	113	ARG	CZ-NH1	7.27	1.43	1.32
1	A	526	GLU	C-O	-6.08	1.21	1.23
1	A	464	VAL	C-O	-5.78	1.17	1.24
1	A	113	ARG	CG-CD	5.46	1.68	1.52
1	A	451	PRO	C-O	-5.10	1.17	1.24

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	469	GLY	CA-C-N	14.09	135.86	121.35
1	A	469	GLY	C-N-CA	14.09	135.86	121.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	397	TRP	CA-C-N	12.95	132.85	120.03
1	A	397	TRP	C-N-CA	12.95	132.85	120.03
1	A	113	ARG	CB-CG-CD	-10.84	86.36	111.30
1	A	476	VAL	CA-C-N	9.59	132.02	120.23
1	A	476	VAL	C-N-CA	9.59	132.02	120.23
1	A	275	ASN	CB-CA-C	8.38	123.93	110.19
1	A	427	ASN	CA-C-O	-8.00	112.39	121.19
1	A	198	ASP	CA-CB-CG	7.78	120.38	112.60
1	A	427	ASN	N-CA-C	-7.37	99.54	110.23
1	A	113	ARG	CA-CB-CG	7.31	128.72	114.10
1	A	199	ARG	CA-C-N	-7.24	109.44	123.13
1	A	199	ARG	C-N-CA	-7.24	109.44	123.13
1	A	466	GLU	CB-CG-CD	6.68	123.95	112.60
1	A	276	LEU	CA-C-O	-6.50	114.00	120.82
1	A	198	ASP	CB-CA-C	6.45	125.06	110.67
1	A	470	GLY	CA-C-N	6.13	133.00	121.97
1	A	470	GLY	C-N-CA	6.13	133.00	121.97
1	A	525	ASP	CB-CA-C	-6.11	98.18	109.37
1	A	112	ASP	CA-C-N	6.04	128.87	120.29
1	A	112	ASP	C-N-CA	6.04	128.87	120.29
1	A	290	PHE	CA-C-O	-5.84	114.80	121.40
1	A	407	TYR	CB-CA-C	5.83	120.40	111.02
1	A	319	TYR	CB-CA-C	5.77	119.19	109.67
1	A	113	ARG	N-CA-C	-5.61	105.24	111.36
1	A	384	PRO	CB-CA-C	-5.50	104.70	111.64
1	A	476	VAL	O-C-N	-5.49	117.65	121.55
1	A	175	ARG	CA-CB-CG	5.45	125.00	114.10
1	A	476	VAL	N-CA-C	-5.42	102.62	107.56
1	A	113	ARG	CD-NE-CZ	5.37	131.92	124.40
1	A	199	ARG	CA-C-O	-5.30	112.92	120.51
1	A	52	SER	CA-C-N	-5.26	115.95	123.10
1	A	52	SER	C-N-CA	-5.26	115.95	123.10
1	A	113	ARG	CA-C-N	5.24	128.93	120.55
1	A	113	ARG	C-N-CA	5.24	128.93	120.55
1	A	472	PHE	N-CA-C	-5.07	107.22	113.41
1	A	467	ALA	N-CA-C	5.07	116.61	111.14

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	132	GLU	Mainchain

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Mol	Chain	Res	Type	Group
1	A	349[A]	SER	Mainchain
1	A	427	ASN	Mainchain
1	A	468	GLN	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	3764	0	3815	210	0
2	A	35	0	0	1	0
3	A	20	0	0	1	0
All	All	3819	0	3815	211	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 28.

All (211) 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:473:ARG:HD2	1:A:540:PRO:CG	1.16	1.62
1:A:52:SER:OG	1:A:197:LYS:CB	1.65	1.43
1:A:52:SER:OG	1:A:197:LYS:CD	1.72	1.35
1:A:473:ARG:CD	1:A:540:PRO:CG	2.04	1.34
1:A:85:ASN:ND2	1:A:200:ARG:O	1.58	1.33
1:A:169:ASP:HB3	1:A:175:ARG:CD	1.56	1.32
1:A:169:ASP:HB2	1:A:175:ARG:CZ	1.60	1.28
1:A:169:ASP:CB	1:A:175:ARG:NE	1.96	1.27
1:A:473:ARG:HD2	1:A:540:PRO:CD	1.64	1.27
1:A:110:PHE:O	1:A:113:ARG:HG2	1.37	1.23
1:A:195:VAL:CG1	1:A:203:VAL:HG13	1.67	1.22
1:A:473:ARG:CD	1:A:540:PRO:HG3	1.63	1.21
1:A:169:ASP:CB	1:A:175:ARG:CZ	2.20	1.19
1:A:195:VAL:CG2	1:A:206:ASP:OD1	1.90	1.19
1:A:52:SER:OG	1:A:197:LYS:CG	1.94	1.16
1:A:195:VAL:HG22	1:A:206:ASP:OD1	0.98	1.16
1:A:196:LEU:HD11	1:A:205:LYS:HE2	1.29	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:ASP:OD1	1:A:204:ILE:HD11	1.43	1.15
1:A:391:LEU:HD12	1:A:411:LEU:CD2	1.77	1.15
1:A:88:GLU:OE1	1:A:144:GLY:HA2	1.44	1.14
1:A:169:ASP:OD2	1:A:175:ARG:NE	1.81	1.13
1:A:239:LEU:HD11	1:A:265:GLN:CB	1.78	1.13
1:A:239:LEU:CD1	1:A:265:GLN:HG3	1.78	1.13
1:A:391:LEU:HD12	1:A:411:LEU:HD22	1.32	1.12
1:A:52:SER:OG	1:A:197:LYS:HB2	1.41	1.12
1:A:405:LEU:CD1	1:A:411:LEU:HD11	1.82	1.10
1:A:473:ARG:HD2	1:A:540:PRO:HG2	1.34	1.08
1:A:52:SER:OG	1:A:197:LYS:HD2	1.55	1.07
1:A:169:ASP:HB3	1:A:175:ARG:HD2	1.16	1.06
1:A:169:ASP:HB3	1:A:175:ARG:NE	1.62	1.06
1:A:195:VAL:HG11	1:A:203:VAL:CG1	1.86	1.06
1:A:391:LEU:HA	1:A:411:LEU:HD22	1.11	1.06
1:A:239:LEU:HD11	1:A:265:GLN:HB2	1.34	1.05
1:A:87:LYS:HB3	1:A:200:ARG:HD3	1.33	1.04
1:A:391:LEU:CD1	1:A:411:LEU:HD13	1.88	1.04
1:A:405:LEU:CD1	1:A:411:LEU:CD1	2.36	1.03
1:A:473:ARG:HD2	1:A:540:PRO:HG3	1.08	1.03
1:A:169:ASP:CG	1:A:175:ARG:NE	2.17	1.02
1:A:474:ALA:HB2	1:A:539:ALA:HB1	1.42	1.02
1:A:195:VAL:HG11	1:A:203:VAL:HG13	1.05	1.02
1:A:473:ARG:CG	1:A:540:PRO:HG3	1.89	1.01
1:A:239:LEU:HD12	1:A:265:GLN:HG3	1.38	1.01
1:A:239:LEU:CD1	1:A:265:GLN:CB	2.39	1.00
1:A:488:ALA:O	1:A:504:ARG:N	1.93	0.99
1:A:239:LEU:HD11	1:A:265:GLN:CG	1.93	0.97
1:A:239:LEU:CD1	1:A:265:GLN:CG	2.43	0.97
1:A:52:SER:OG	1:A:197:LYS:HB3	1.66	0.94
1:A:110:PHE:C	1:A:113:ARG:HG2	1.92	0.94
1:A:196:LEU:CD1	1:A:205:LYS:HE2	1.98	0.93
1:A:110:PHE:O	1:A:113:ARG:CG	2.17	0.92
1:A:169:ASP:HB2	1:A:175:ARG:NH1	1.84	0.92
1:A:196:LEU:HD11	1:A:205:LYS:CE	2.01	0.91
1:A:194:GLN:HG3	1:A:210:THR:CG2	2.00	0.91
1:A:169:ASP:CB	1:A:175:ARG:CD	2.45	0.90
1:A:52:SER:OG	1:A:197:LYS:HD3	1.70	0.90
1:A:391:LEU:CD1	1:A:411:LEU:CD1	2.51	0.89
1:A:245:LYS:HD2	1:A:526:GLU:OE1	1.74	0.87
1:A:391:LEU:CA	1:A:411:LEU:HD22	2.02	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:GLN:HG3	1:A:210:THR:HG23	1.56	0.86
1:A:52:SER:CB	1:A:197:LYS:HD3	2.05	0.86
1:A:405:LEU:HD13	1:A:411:LEU:HD11	1.57	0.85
1:A:117:ASN:ND2	1:A:123:ILE:HD13	1.91	0.85
1:A:239:LEU:HD11	1:A:265:GLN:HG3	1.54	0.85
1:A:405:LEU:HD11	1:A:411:LEU:HD11	1.58	0.84
1:A:52:SER:CB	1:A:197:LYS:CD	2.55	0.83
1:A:473:ARG:CD	1:A:540:PRO:HG2	1.96	0.83
1:A:198:ASP:CG	1:A:204:ILE:HD11	2.05	0.81
1:A:391:LEU:HA	1:A:411:LEU:CD2	1.98	0.81
1:A:473:ARG:HD2	1:A:540:PRO:HD3	1.60	0.81
1:A:198:ASP:OD1	1:A:204:ILE:CD1	2.28	0.79
1:A:87:LYS:HB3	1:A:200:ARG:CD	2.10	0.79
1:A:87:LYS:CB	1:A:200:ARG:HB3	2.14	0.78
1:A:195:VAL:HG12	1:A:196:LEU:N	1.96	0.77
1:A:391:LEU:CD1	1:A:411:LEU:HD22	2.12	0.77
1:A:405:LEU:CD1	1:A:411:LEU:HD12	2.15	0.77
1:A:110:PHE:CA	1:A:113:ARG:HG2	2.15	0.77
1:A:110:PHE:HA	1:A:113:ARG:HG2	1.68	0.76
1:A:195:VAL:HG12	1:A:196:LEU:H	1.50	0.76
1:A:117:ASN:HB3	1:A:123:ILE:HD11	1.68	0.75
1:A:391:LEU:HD13	1:A:411:LEU:HD13	1.68	0.75
1:A:195:VAL:CG1	1:A:203:VAL:CG1	2.56	0.75
1:A:117:ASN:HD22	1:A:123:ILE:HD13	1.52	0.74
1:A:195:VAL:HG13	1:A:205:LYS:O	1.87	0.74
1:A:52:SER:HB3	1:A:197:LYS:HD3	1.69	0.72
1:A:473:ARG:CD	1:A:540:PRO:CD	2.53	0.72
1:A:198:ASP:HB2	1:A:202:ARG:HB2	1.71	0.72
1:A:117:ASN:CB	1:A:123:ILE:HD11	2.22	0.70
1:A:405:LEU:HD12	1:A:411:LEU:HD12	1.72	0.70
1:A:473:ARG:HG2	1:A:540:PRO:HG3	1.73	0.70
1:A:239:LEU:CD1	1:A:265:GLN:HB2	2.13	0.70
1:A:473:ARG:CD	1:A:540:PRO:HD3	2.22	0.69
1:A:87:LYS:HB2	1:A:200:ARG:HB3	1.73	0.69
1:A:430:LYS:CG	1:A:447:GLN:OE1	2.42	0.68
1:A:391:LEU:HD12	1:A:411:LEU:CD1	2.24	0.68
1:A:117:ASN:ND2	1:A:123:ILE:CD1	2.56	0.68
1:A:441:ARG:HH11	1:A:441:ARG:HB3	1.59	0.67
1:A:195:VAL:CG1	1:A:196:LEU:H	2.07	0.66
1:A:405:LEU:HD11	1:A:411:LEU:CD1	2.16	0.66
1:A:489:ARG:C	1:A:503:TYR:HA	2.20	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:LYS:HB3	1:A:200:ARG:HB3	1.77	0.66
1:A:85:ASN:ND2	1:A:88:GLU:HG3	2.11	0.65
1:A:342:LEU:HD22	1:A:357:ILE:HD11	1.78	0.65
1:A:194:GLN:HG3	1:A:210:THR:HG21	1.76	0.65
1:A:110:PHE:HA	1:A:113:ARG:CG	2.27	0.65
1:A:195:VAL:CG1	1:A:196:LEU:N	2.61	0.63
1:A:239:LEU:CD1	1:A:265:GLN:HB3	2.28	0.63
1:A:207:VAL:O	1:A:208:GLN:HG3	1.98	0.63
1:A:430:LYS:HG2	1:A:447:GLN:OE1	1.99	0.62
1:A:194:GLN:O	1:A:206:ASP:HA	1.99	0.62
1:A:284:ARG:HG2	1:A:284:ARG:HH11	1.65	0.62
1:A:391:LEU:HD12	1:A:411:LEU:HD21	1.74	0.61
1:A:196:LEU:HB2	1:A:204:ILE:HB	1.83	0.61
1:A:53:VAL:HG12	1:A:53:VAL:O	2.01	0.61
1:A:131:PRO:O	1:A:135:GLU:HG3	2.00	0.61
1:A:343:THR:HG22	1:A:347:ILE:HD12	1.83	0.60
1:A:391:LEU:HD11	1:A:411:LEU:HD13	1.81	0.60
1:A:441:ARG:HB3	1:A:441:ARG:NH1	2.17	0.59
1:A:239:LEU:HD12	1:A:265:GLN:CG	2.19	0.59
1:A:155:TYR:OH	1:A:167:PHE:HA	2.03	0.59
1:A:405:LEU:HD12	1:A:411:LEU:CD1	2.27	0.58
1:A:227:LEU:HD23	1:A:552:LEU:HD12	1.85	0.58
1:A:268:TYR:CE1	1:A:281:MET:HA	2.39	0.57
1:A:391:LEU:HD11	1:A:411:LEU:CD1	2.32	0.57
1:A:197:LYS:O	1:A:198:ASP:OD1	2.24	0.56
1:A:117:ASN:CB	1:A:123:ILE:CD1	2.84	0.56
1:A:89:LEU:HD23	1:A:143:PRO:O	2.06	0.56
1:A:284:ARG:HG2	1:A:288:ASP:OD2	2.05	0.56
1:A:67:ASP:HB2	1:A:223:ILE:O	2.06	0.55
1:A:82:LEU:HD13	1:A:137:VAL:HG11	1.88	0.55
1:A:291:GLU:OE1	1:A:409:TYR:HD1	1.89	0.55
1:A:52:SER:CB	1:A:197:LYS:HD2	2.28	0.55
1:A:186:LEU:O	1:A:216:GLY:HA3	2.07	0.54
1:A:117:ASN:CG	1:A:123:ILE:HD11	2.32	0.54
1:A:403:ALA:O	1:A:407:TYR:CD2	2.61	0.53
1:A:85:ASN:HD22	1:A:88:GLU:HG3	1.71	0.53
1:A:473:ARG:HD3	1:A:540:PRO:HG2	1.84	0.53
1:A:282:ARG:HD2	1:A:284:ARG:CZ	2.38	0.53
1:A:489:ARG:HA	1:A:503:TYR:HA	1.91	0.53
2:A:1101:NEF:C2	2:A:1101:NEF:N4	2.72	0.52
1:A:196:LEU:HD12	1:A:205:LYS:CG	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:LYS:HG2	1:A:198:ASP:N	2.24	0.52
1:A:68:ARG:HG3	1:A:223:ILE:O	2.10	0.52
1:A:83:TRP:CE2	1:A:146:TYR:HB2	2.45	0.52
1:A:169:ASP:CG	1:A:175:ARG:CZ	2.74	0.51
1:A:430:LYS:CE	1:A:447:GLN:OE1	2.58	0.51
1:A:398:PRO:HD2	1:A:401:GLU:HB2	1.91	0.51
1:A:253:ASP:HB2	1:A:260:LEU:HD11	1.92	0.51
1:A:239:LEU:HD13	1:A:265:GLN:HB3	1.93	0.50
1:A:343:THR:HG22	1:A:347:ILE:CD1	2.41	0.50
1:A:467:ALA:O	1:A:468:GLN:HG3	2.11	0.50
1:A:87:LYS:HD3	1:A:200:ARG:HG2	1.93	0.50
1:A:83:TRP:NE1	1:A:146:TYR:HB2	2.27	0.50
1:A:227:LEU:HD12	1:A:260:LEU:HB3	1.94	0.50
1:A:178:ILE:HD11	1:A:436:MET:HG2	1.94	0.49
1:A:193:ARG:HD3	1:A:206:ASP:OD2	2.13	0.49
1:A:489:ARG:CA	1:A:503:TYR:HA	2.43	0.49
1:A:169:ASP:CB	1:A:175:ARG:NH1	2.60	0.49
1:A:518:ILE:HD11	1:A:553:MET:SD	2.52	0.49
1:A:192:LYS:H	1:A:211:LYS:HB2	1.78	0.48
1:A:194:GLN:CG	1:A:210:THR:HG21	2.41	0.48
1:A:284:ARG:HG2	1:A:284:ARG:NH1	2.26	0.48
1:A:122:PHE:O	1:A:123:ILE:HG13	2.14	0.48
1:A:324:GLN:HG2	1:A:329:THR:OG1	2.14	0.47
1:A:75:VAL:N	1:A:153:ARG:HD2	2.30	0.47
1:A:87:LYS:HB3	1:A:200:ARG:CB	2.42	0.47
1:A:430:LYS:HG3	1:A:447:GLN:OE1	2.14	0.47
1:A:473:ARG:NE	1:A:540:PRO:HD3	2.29	0.47
1:A:196:LEU:HD12	1:A:205:LYS:HG2	1.97	0.47
1:A:311:LYS:HE2	1:A:313:SER:OG	2.15	0.47
1:A:314:ASP:O	1:A:341:ASP:HA	2.15	0.46
1:A:169:ASP:OD2	1:A:175:ARG:CZ	2.58	0.46
1:A:207:VAL:C	1:A:208:GLN:HG3	2.40	0.46
1:A:209:VAL:HG12	1:A:209:VAL:O	2.15	0.46
1:A:290:PHE:HB2	1:A:504:ARG:NH1	2.30	0.46
1:A:93:LYS:HG2	1:A:96:TRP:CZ2	2.51	0.46
1:A:87:LYS:HB3	1:A:200:ARG:CG	2.46	0.45
1:A:130:THR:O	1:A:133:GLN:N	2.49	0.45
1:A:110:PHE:HA	1:A:113:ARG:CD	2.46	0.45
1:A:227:LEU:HD22	1:A:549:ALA:HA	1.97	0.45
1:A:127:ARG:NH2	1:A:150:GLU:OE2	2.44	0.45
1:A:84:ALA:HA	1:A:144:GLY:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:LYS:CD	1:A:526:GLU:OE1	2.55	0.45
1:A:293:GLY:CA	1:A:408:GLY:HA3	2.46	0.45
1:A:249:LEU:HA	1:A:521:VAL:O	2.16	0.45
1:A:117:ASN:CG	1:A:123:ILE:CD1	2.88	0.45
1:A:88:GLU:OE2	1:A:146:TYR:OH	2.27	0.44
1:A:207:VAL:O	1:A:208:GLN:CG	2.64	0.44
1:A:405:LEU:HD13	1:A:411:LEU:CD1	2.28	0.44
1:A:195:VAL:HA	1:A:205:LYS:O	2.17	0.44
1:A:480:HIS:O	1:A:513:ALA:N	2.50	0.44
1:A:196:LEU:CD1	1:A:205:LYS:CE	2.78	0.43
1:A:252:MET:HE2	1:A:252:MET:HB3	1.80	0.43
1:A:510:PHE:HA	1:A:518:ILE:O	2.18	0.43
1:A:130:THR:O	1:A:131:PRO:C	2.60	0.43
1:A:312:PRO:HD2	3:A:1207:HOH:O	2.18	0.43
1:A:122:PHE:C	1:A:123:ILE:HG13	2.44	0.43
1:A:153:ARG:HG2	1:A:155:TYR:CZ	2.54	0.43
1:A:251:ILE:HG23	1:A:518:ILE:HG23	2.00	0.42
1:A:427:ASN:O	1:A:429:GLY:N	2.52	0.42
1:A:283:ASN:HD22	1:A:383:PHE:HE2	1.67	0.42
1:A:198:ASP:CB	1:A:202:ARG:HB2	2.46	0.42
1:A:89:LEU:HD12	1:A:114:ILE:HD12	2.02	0.41
1:A:473:ARG:HE	1:A:540:PRO:HD3	1.85	0.41
1:A:62:ARG:HG2	1:A:153:ARG:NH2	2.36	0.41
1:A:66:THR:HA	1:A:71:GLU:O	2.19	0.41
1:A:372:GLN:HB3	1:A:448:VAL:HB	2.02	0.41
1:A:52:SER:H	1:A:197:LYS:HB3	1.84	0.41
1:A:198:ASP:OD2	1:A:204:ILE:CG1	2.69	0.40
1:A:117:ASN:HD22	1:A:123:ILE:CD1	2.24	0.40
1:A:219:LEU:HD12	1:A:219:LEU:HA	1.86	0.40
1:A:52:SER:N	1:A:197:LYS:HB3	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	487/535 (91%)	465 (96%)	21 (4%)	1 (0%)	43 62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	471	VAL

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	395/423 (93%)	391 (99%)	4 (1%)	68 85

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	VAL
1	A	121	GLU
1	A	371	GLN
1	A	475	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	GLN
1	A	264	ASN

5.3.3 RNA ⓘ

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](#)

1 ligand is 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	NEF	A	1101	1	34,37,38	1.34	5 (14%)	35,51,53	1.89	6 (17%)

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	NEF	A	1101	1	-	9/21/44/46	0/2/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	NEF	O18-C16	-4.11	1.19	1.30
2	A	1101	NEF	C13-S19	-2.42	1.76	1.82
2	A	1101	NEF	C15-C16	2.41	1.52	1.48
2	A	1101	NEF	O2-C1	2.15	1.28	1.20
2	A	1101	NEF	O24-N22	-2.14	1.20	1.35

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	NEF	C6-C4-C15	6.94	127.56	122.02
2	A	1101	NEF	O2-C1-C3	-4.83	112.07	124.86
2	A	1101	NEF	C17-C14-C21	-3.26	115.20	118.92
2	A	1101	NEF	C13-C3-N4	3.12	116.53	109.93
2	A	1101	NEF	O17-C16-C15	-2.73	115.45	120.20
2	A	1101	NEF	C2-C4-C6	-2.15	117.94	120.39

There are no chirality outliers.

All (9) torsion outliers are listed below:

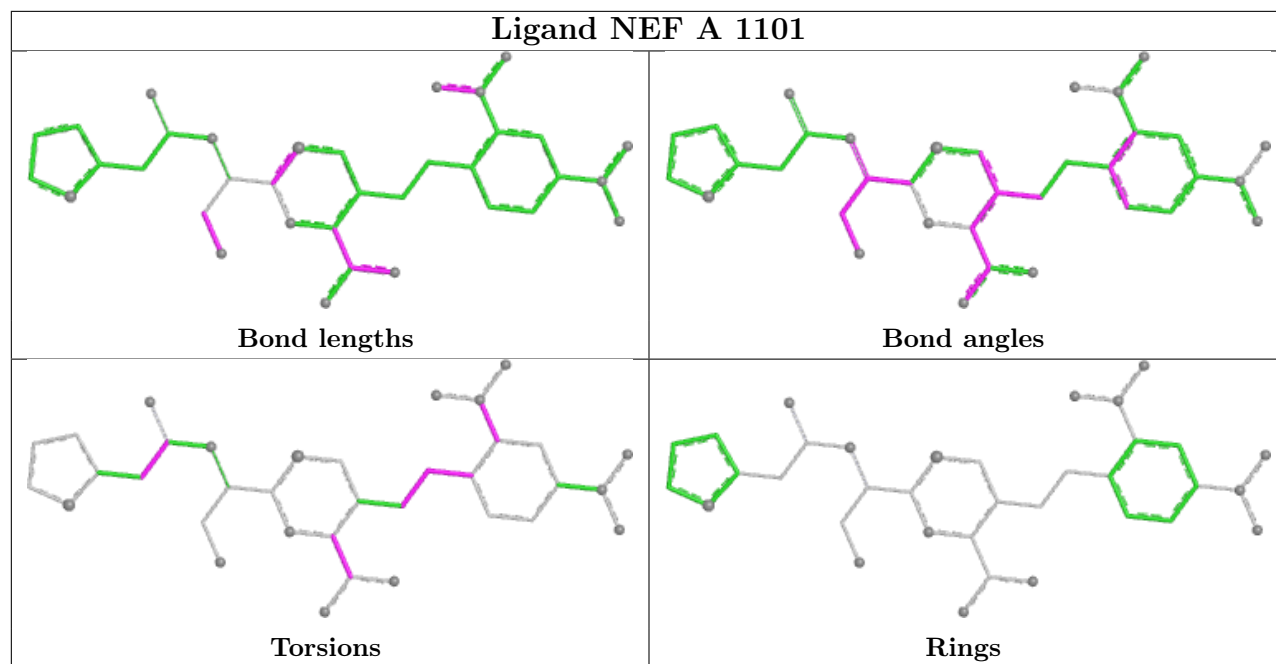
Mol	Chain	Res	Type	Atoms
2	A	1101	NEF	C14-C12-C6-C4
2	A	1101	NEF	C6-C12-C14-C21
2	A	1101	NEF	N14-C15-C16-O18
2	A	1101	NEF	C14-C21-N22-O25
2	A	1101	NEF	C20-C21-N22-O25
2	A	1101	NEF	N4-C5-C7-C8
2	A	1101	NEF	C6-C12-C14-C17
2	A	1101	NEF	O6-C5-C7-C8
2	A	1101	NEF	N14-C15-C16-O17

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	NEF	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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, 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	492/535 (91%)	0.75	56 (11%) 10 8	27, 48, 108, 134	1 (0%)

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	207	VAL	5.8
1	A	488	ALA	5.3
1	A	472	PHE	5.2
1	A	122	PHE	4.9
1	A	195	VAL	4.6
1	A	468	GLN	4.5
1	A	471	VAL	4.4
1	A	473	ARG	4.3
1	A	175	ARG	4.3
1	A	210	THR	4.1
1	A	198	ASP	3.9
1	A	503	TYR	3.7
1	A	55	HIS	3.7
1	A	56	ILE	3.7
1	A	148	ILE	3.7
1	A	276	LEU	3.7
1	A	411	LEU	3.7
1	A	502	ALA	3.6
1	A	194	GLN	3.6
1	A	113	ARG	3.6
1	A	206	ASP	3.6
1	A	203	VAL	3.6
1	A	469	GLY	3.6
1	A	196	LEU	3.6
1	A	489	ARG	3.5
1	A	131	PRO	3.4
1	A	204	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	277	GLN	3.1
1	A	137	VAL	3.0
1	A	123	ILE	3.0
1	A	54	ARG	2.9
1	A	561	PRO	2.9
1	A	209	VAL	2.9
1	A	200	ARG	2.7
1	A	476	VAL	2.7
1	A	136	GLY	2.7
1	A	126	VAL	2.6
1	A	135	GLU	2.6
1	A	208	GLN	2.6
1	A	328	TYR	2.6
1	A	128	GLY	2.6
1	A	430	LYS	2.6
1	A	53	VAL	2.5
1	A	470	GLY	2.3
1	A	199	ARG	2.3
1	A	124	TYR	2.3
1	A	121	GLU	2.3
1	A	528	SER	2.3
1	A	52	SER	2.3
1	A	132	GLU	2.3
1	A	197	LYS	2.2
1	A	138	ILE	2.2
1	A	119	GLU	2.2
1	A	202	ARG	2.1
1	A	50	ALA	2.0
1	A	238	ALA	2.0

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

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

6.3 Carbohydrates ⓘ

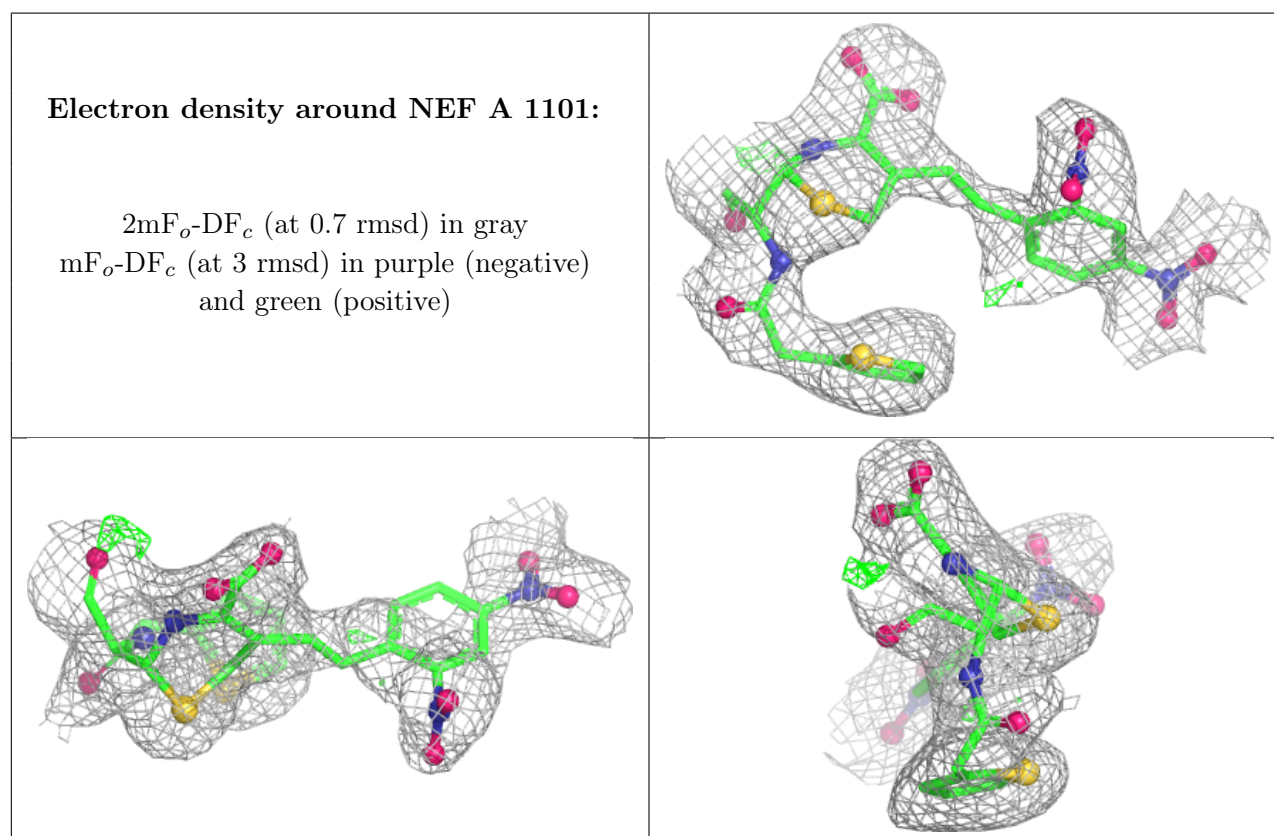
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
2	NEF	A	1101	35/36	0.82	0.13	46,64,105,107	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.