Full wwPDB X-ray Structure Validation Report (i)

Jun 11, 2024 – 11:47 PM EDT

PDB ID	:	2D4Q
Title	:	Crystal structure of the Sec-PH domain of the human neurofibromatosis type 1 protein
Authors	:	D'angelo, I.; Welti, S.; Bonneau, F.; Scheffzek, K.
Deposited on	:	2005-10-22
Resolution	:	2.30 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 (i) 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 (i)) were used in the production of this report:

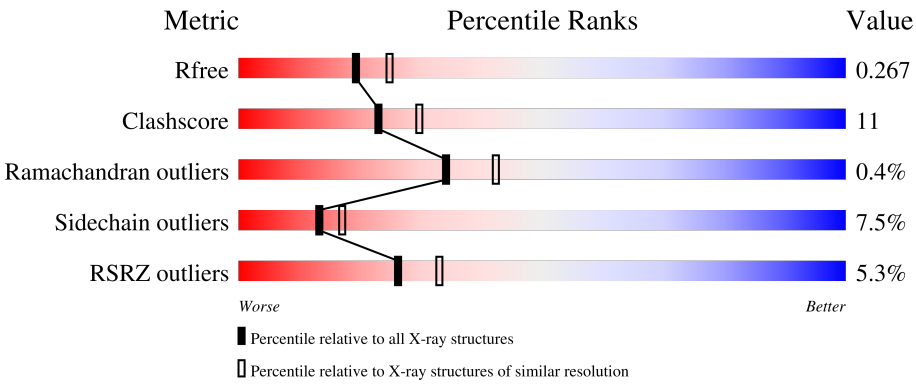
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	257	5% 79% 18% •
1	B	257	5% 69% 26% • •

2 Entry composition (i)

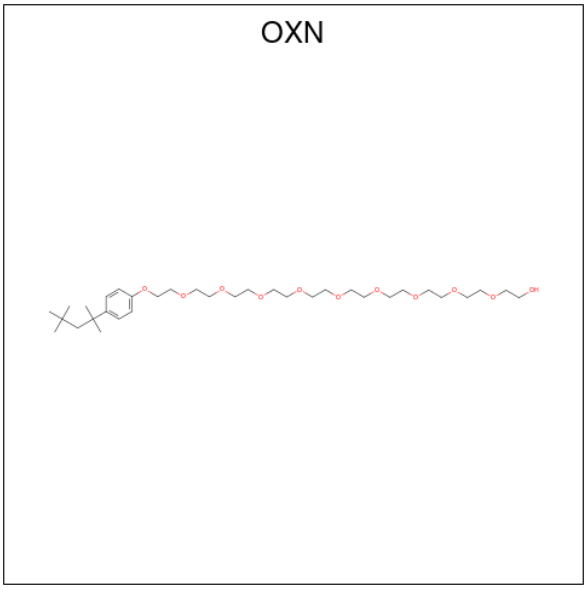
There are 4 unique types of molecules in this entry. The entry contains 4320 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Neurofibromin.

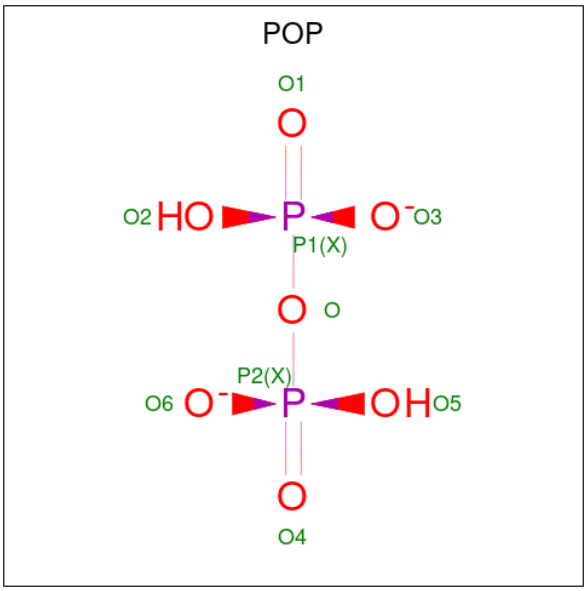
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	257	2082	1349	346	382	5	89	0	0
1	B	255	2059	1336	340	378	5	73	0	0

- Molecule 2 is OXTOXYNOL-10 (three-letter code: OXN) (formula: $C_{34}H_{62}O_{11}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	24	20	4	0	0
2	B	1	24	20	4	0	0

- Molecule 3 is PYROPHOSPHATE 2- (three-letter code: POP) (formula: $H_2O_7P_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O P 9 7 2	0	0
3	B	1	Total O P 9 7 2	0	0

- Molecule 4 is water.

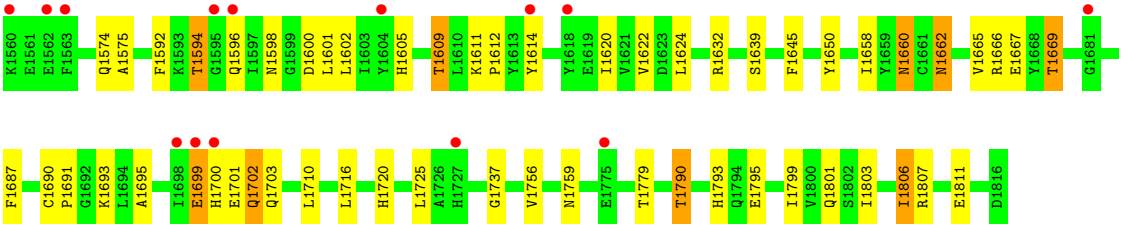
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	58	Total O 58 58	0	0
4	B	55	Total O 55 55	0	0

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.

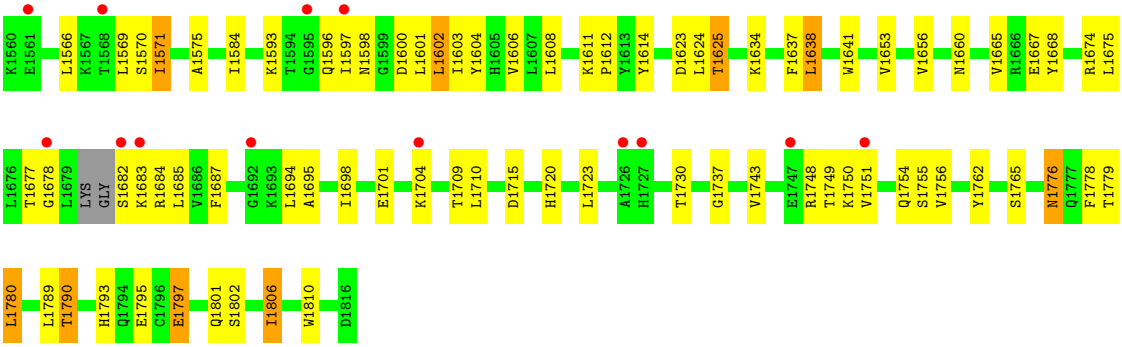
- Molecule 1: Neurofibromin

Chain A:



- Molecule 1: Neurofibromin

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	113.50Å 113.50Å 125.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.30 14.99 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.5 (15.00-2.30) 100.0 (14.99-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	4.48 (at 2.34Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.240 , 0.280 0.219 , 0.267	Depositor DCC
R_{free} test set	1720 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å^2)	41.4	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 49.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4320	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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 (i)

5.1 Standard geometry (i)

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

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	0.55	0/2133	0.73	1/2892 (0.0%)
1	B	0.59	0/2109	0.77	0/2861
All	All	0.57	0/4242	0.75	1/5753 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1720	HIS	N-CA-C	7.57	131.44	111.00

There are no chirality outliers.

There are no planarity outliers.

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	2082	0	2082	39	1
1	B	2059	0	2050	52	1
2	A	24	0	30	1	0
2	B	24	0	30	1	0
3	B	18	0	0	2	0
4	A	58	0	0	4	0
4	B	55	0	0	4	0
All	All	4320	0	4192	91	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 11.

All (91) 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:1575:ALA:HB1	1:B:1704:LYS:HD2	1.09	1.06
1:A:1605:HIS:O	1:A:1609:THR:HG22	1.54	1.06
1:B:1793:HIS:HD2	1:B:1795:GLU:H	1.18	0.90
1:B:1623:ASP:OD2	1:B:1625:THR:HG23	1.72	0.88
1:B:1793:HIS:CD2	1:B:1795:GLU:H	1.98	0.81
1:B:1575:ALA:CB	1:B:1704:LYS:HD2	2.04	0.80
1:A:1611:LYS:HB3	1:A:1612:PRO:HD3	1.65	0.78
1:B:1625:THR:HG21	1:B:1709:THR:HG23	1.66	0.77
1:A:1793:HIS:HD2	1:A:1795:GLU:H	1.33	0.76
1:B:1751:VAL:O	4:B:88:HOH:O	2.05	0.72
1:A:1662:ASN:ND2	1:A:1665:VAL:H	1.90	0.69
1:B:1604:TYR:CZ	1:B:1608:LEU:HD11	2.30	0.66
1:A:1662:ASN:C	1:A:1662:ASN:HD22	1.98	0.66
1:B:1566:LEU:O	1:B:1571:ILE:HD11	1.96	0.65
1:B:1687:PHE:CG	1:B:1756:VAL:HG11	2.32	0.65
1:B:1737:GLY:O	1:B:1806:ILE:HG12	1.97	0.64
1:B:1779:THR:HG22	1:B:1790:THR:HB	1.80	0.63
1:A:1598:ASN:HD21	1:A:1600:ASP:HB2	1.65	0.62
1:A:1666:ARG:O	1:A:1669:THR:HG22	2.01	0.61
1:B:1634:LYS:HA	3:B:602:POP:O2	2.02	0.60
1:A:1669:THR:HG23	4:A:81:HOH:O	2.02	0.59
1:B:1695:ALA:HA	1:B:1698:ILE:O	2.02	0.59
1:B:1720:HIS:O	1:B:1793:HIS:HE1	1.86	0.59
1:A:1695:ALA:O	1:A:1701:GLU:HA	2.03	0.59
1:A:1790:THR:HG23	4:A:29:HOH:O	2.02	0.59
1:B:1806:ILE:HD13	4:B:42:HOH:O	2.04	0.57
1:B:1584:ILE:HD13	1:B:1698:ILE:HD13	1.88	0.56
1:B:1623:ASP:OD2	1:B:1625:THR:CG2	2.50	0.56
1:A:1687:PHE:CG	1:A:1756:VAL:HG11	2.41	0.55
1:B:1569:LEU:O	1:B:1570:SER:HB2	2.07	0.55
1:A:1793:HIS:CD2	1:A:1795:GLU:H	2.21	0.55
1:B:1793:HIS:HD2	1:B:1795:GLU:N	1.98	0.55
1:A:1737:GLY:O	1:A:1806:ILE:HG12	2.06	0.55
1:B:1598:ASN:HD22	1:B:1601:LEU:H	1.55	0.55
1:A:1605:HIS:O	1:A:1609:THR:CG2	2.43	0.54
1:A:1669:THR:CG2	4:A:81:HOH:O	2.54	0.54
1:A:1592:PHE:CD1	1:A:1602:LEU:HD22	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1656:VAL:HB	1:B:1685:LEU:HD23	1.90	0.54
1:B:1682:SER:C	1:B:1684:ARG:H	2.12	0.54
1:A:1598:ASN:ND2	1:A:1601:LEU:H	2.06	0.53
1:B:1750:LYS:HA	1:B:1754:GLN:O	2.08	0.53
1:A:1624:LEU:HD13	1:A:1665:VAL:HG11	1.92	0.51
1:A:1695:ALA:HB1	1:A:1701:GLU:HA	1.92	0.51
1:A:1695:ALA:HB1	1:A:1701:GLU:CA	2.41	0.51
1:B:1593:LYS:HB3	1:B:1596:GLN:HG2	1.93	0.51
1:B:1606:VAL:HG21	1:B:1641:TRP:HH2	1.76	0.51
1:B:1778:PHE:HE1	1:B:1780:LEU:HD13	1.76	0.51
1:B:1748:ARG:HD3	1:B:1755:SER:HB3	1.92	0.51
1:A:1598:ASN:HD22	1:A:1601:LEU:H	1.59	0.51
1:A:1807:ARG:O	1:A:1811:GLU:HG3	2.11	0.51
1:B:1571:ILE:HD12	4:B:16:HOH:O	2.11	0.50
1:A:1574:GLN:HG2	1:A:1575:ALA:N	2.26	0.50
1:B:1598:ASN:HD21	1:B:1600:ASP:HB2	1.75	0.50
1:A:1622:VAL:HG13	1:A:1658:ILE:HA	1.93	0.50
1:B:1776:ASN:HA	1:B:1793:HIS:O	2.10	0.50
1:B:1598:ASN:HD22	1:B:1601:LEU:HG	1.76	0.49
1:A:1702:GLN:HE21	1:A:1702:GLN:HA	1.75	0.49
1:B:1797:GLU:O	1:B:1801:GLN:HG2	2.13	0.48
1:A:1594:THR:HG21	1:A:1632:ARG:HG2	1.95	0.48
1:B:1598:ASN:ND2	1:B:1601:LEU:H	2.12	0.48
1:B:1778:PHE:CE1	1:B:1780:LEU:HD13	2.49	0.48
1:B:1634:LYS:HG2	3:B:602:POP:O2	2.15	0.47
1:B:1604:TYR:CE1	1:B:1608:LEU:HD21	2.50	0.47
1:B:1604:TYR:CE2	1:B:1608:LEU:HD11	2.50	0.47
1:A:1691:PRO:HB3	1:A:1703:GLN:NE2	2.29	0.47
1:B:1674:ARG:HG3	4:B:11:HOH:O	2.16	0.46
1:A:1645:PHE:HB2	1:A:1650:TYR:CZ	2.51	0.46
1:B:1603:ILE:HD11	1:B:1637:PHE:CE1	2.50	0.46
1:A:1702:GLN:O	1:A:1702:GLN:HG3	2.15	0.46
1:B:1677:THR:HG23	1:B:1678:GLY:N	2.31	0.45
1:B:1611:LYS:HB3	1:B:1612:PRO:HD3	1.98	0.45
1:B:1720:HIS:O	1:B:1793:HIS:CE1	2.70	0.44
1:A:1799:ILE:O	1:A:1803:ILE:HG13	2.18	0.44
1:A:1660:ASN:ND2	1:A:1759:ASN:HD22	2.15	0.44
1:A:1662:ASN:HD21	1:A:1665:VAL:H	1.60	0.44
1:B:1638:LEU:HG	1:B:1668:TYR:OH	2.18	0.44
1:B:1624:LEU:HD13	1:B:1665:VAL:HG11	2.00	0.43
1:A:1620:ILE:HD13	2:A:701:OXN:H191	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1645:PHE:HB2	1:A:1650:TYR:CE1	2.53	0.43
1:A:1690:CYS:SG	1:A:1693:LYS:HG2	2.59	0.42
1:B:1602:LEU:HD13	1:B:1641:TRP:HZ2	1.84	0.42
1:A:1662:ASN:ND2	1:A:1662:ASN:C	2.71	0.42
1:B:1593:LYS:H	1:B:1597:ILE:HD12	1.84	0.42
1:A:1703:GLN:HE22	1:A:1710:LEU:HD21	1.85	0.42
1:B:1743:VAL:HG13	1:B:1762:TYR:HE1	1.85	0.41
1:B:1653:VAL:HG21	2:B:702:OXN:H221	2.01	0.41
1:A:1699:GLU:O	1:A:1700:HIS:C	2.58	0.41
1:B:1675:LEU:C	1:B:1675:LEU:HD23	2.40	0.41
1:B:1765:SER:HB2	1:B:1810:TRP:CZ2	2.55	0.41
1:A:1779:THR:HG22	4:A:48:HOH:O	2.21	0.40
1:B:1566:LEU:O	1:B:1571:ILE:CD1	2.69	0.40

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:A:1667:GLU:OE1	1:B:1667:GLU:OE2[3_455]	2.11	0.09

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	255/257 (99%)	239 (94%)	15 (6%)	1 (0%)	34	42
1	B	251/257 (98%)	240 (96%)	10 (4%)	1 (0%)	34	42
All	All	506/514 (98%)	479 (95%)	25 (5%)	2 (0%)	34	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1596	GLN
1	B	1683	LYS

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	227/227 (100%)	213 (94%)	14 (6%)	18 25
1	B	224/227 (99%)	204 (91%)	20 (9%)	9 11
All	All	451/454 (99%)	417 (92%)	34 (8%)	13 17

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1594	THR
1	A	1609	THR
1	A	1614	TYR
1	A	1639	SER
1	A	1660	ASN
1	A	1662	ASN
1	A	1669	THR
1	A	1699	GLU
1	A	1702	GLN
1	A	1716	LEU
1	A	1725	LEU
1	A	1790	THR
1	A	1801	GLN
1	A	1806	ILE
1	B	1571	ILE
1	B	1602	LEU
1	B	1614	TYR
1	B	1625	THR
1	B	1638	LEU
1	B	1660	ASN
1	B	1694	LEU
1	B	1701	GLU

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Mol	Chain	Res	Type
1	B	1710	LEU
1	B	1715	ASP
1	B	1723	LEU
1	B	1730	THR
1	B	1749	THR
1	B	1776	ASN
1	B	1780	LEU
1	B	1789	LEU
1	B	1790	THR
1	B	1797	GLU
1	B	1802	SER
1	B	1806	ILE

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

Mol	Chain	Res	Type
1	A	1596	GLN
1	A	1598	ASN
1	A	1660	ASN
1	A	1662	ASN
1	A	1672	HIS
1	A	1702	GLN
1	A	1785	GLN
1	A	1793	HIS
1	A	1801	GLN
1	B	1598	ASN
1	B	1672	HIS
1	B	1754	GLN
1	B	1759	ASN
1	B	1777	GLN
1	B	1793	HIS
1	B	1801	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

4 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	OXN	A	701	-	23,24,45	1.82	5 (21%)	29,30,53	2.10	6 (20%)
3	POP	B	602	-	6,8,8	0.92	0	12,13,13	1.77	3 (25%)
3	POP	B	601	-	6,8,8	0.90	0	12,13,13	1.80	3 (25%)
2	OXN	B	702	-	23,24,45	2.03	8 (34%)	29,30,53	2.07	6 (20%)

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	OXN	A	701	-	-	9/22/22/43	0/1/1/1
3	POP	B	602	-	-	0/6/6/6	-
3	POP	B	601	-	-	0/6/6/6	-
2	OXN	B	702	-	-	8/22/22/43	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	702	OXN	C10-C9	4.03	1.46	1.39
2	B	702	OXN	C5-C1	3.60	1.65	1.53
2	A	701	OXN	C10-C9	3.57	1.45	1.39
2	A	701	OXN	C14-C9	3.18	1.44	1.39
2	B	702	OXN	C6-C9	3.12	1.58	1.53
2	A	701	OXN	C5-C1	3.09	1.64	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	702	OXN	C14-C9	2.86	1.44	1.39
2	B	702	OXN	C23-C22	2.82	1.63	1.49
2	A	701	OXN	C23-C22	2.68	1.62	1.49
2	B	702	OXN	C11-C10	2.50	1.42	1.38
2	B	702	OXN	C14-C13	2.16	1.42	1.38
2	B	702	OXN	O24-C23	2.14	1.52	1.40
2	A	701	OXN	C14-C13	2.12	1.42	1.38

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	701	OXN	C16-O15-C12	7.87	138.38	117.93
2	B	702	OXN	C16-O15-C12	7.80	138.22	117.93
2	A	701	OXN	C7-C6-C9	-3.84	100.48	110.18
3	B	602	POP	O5-P2-O4	-3.72	96.34	110.83
3	B	601	POP	O5-P2-O4	-3.58	96.90	110.83
3	B	601	POP	O5-P2-O	3.19	115.33	104.64
2	B	702	OXN	C7-C6-C9	-2.87	102.93	110.18
2	B	702	OXN	C22-O21-C20	2.82	125.59	113.26
2	B	702	OXN	O21-C22-C23	2.81	123.16	110.35
2	A	701	OXN	C22-O21-C20	2.72	125.15	113.26
2	A	701	OXN	O21-C22-C23	2.67	122.54	110.35
3	B	602	POP	O5-P2-O	2.58	113.29	104.64
3	B	602	POP	O6-P2-O	2.56	113.23	104.64
2	B	702	OXN	C2-C1-C4	-2.36	100.01	110.53
2	A	701	OXN	C2-C1-C4	-2.29	100.33	110.53
2	B	702	OXN	C25-O24-C23	2.08	125.44	112.90
2	A	701	OXN	C25-O24-C23	2.02	125.06	112.90
3	B	601	POP	O6-P2-O4	2.01	118.67	110.83

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	OXN	O18-C19-C20-O21
2	A	701	OXN	O15-C16-C17-O18
2	B	702	OXN	O15-C16-C17-O18
2	A	701	OXN	C13-C12-O15-C16
2	A	701	OXN	C11-C12-O15-C16
2	B	702	OXN	O18-C19-C20-O21
2	B	702	OXN	C4-C1-C5-C6
2	A	701	OXN	O21-C22-C23-O24

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Mol	Chain	Res	Type	Atoms
2	B	702	OXN	O21-C22-C23-O24
2	B	702	OXN	C11-C12-O15-C16
2	B	702	OXN	C13-C12-O15-C16
2	B	702	OXN	C19-C20-O21-C22
2	A	701	OXN	C20-C19-O18-C17
2	A	701	OXN	C4-C1-C5-C6
2	A	701	OXN	C19-C20-O21-C22
2	B	702	OXN	C16-C17-O18-C19
2	A	701	OXN	C7-C6-C9-C10

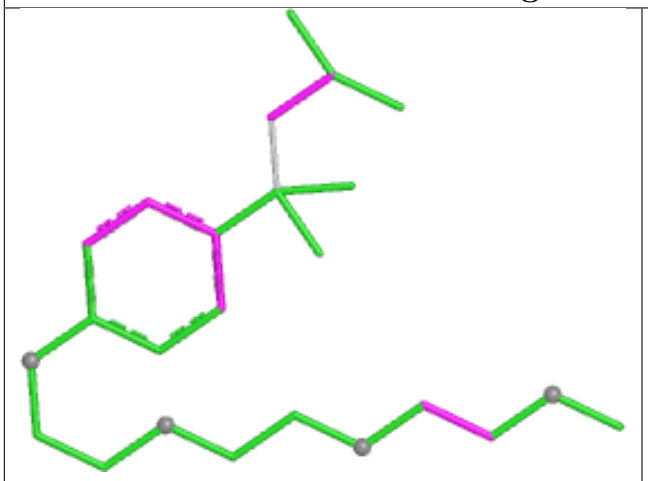
There are no ring outliers.

3 monomers are involved in 4 short contacts:

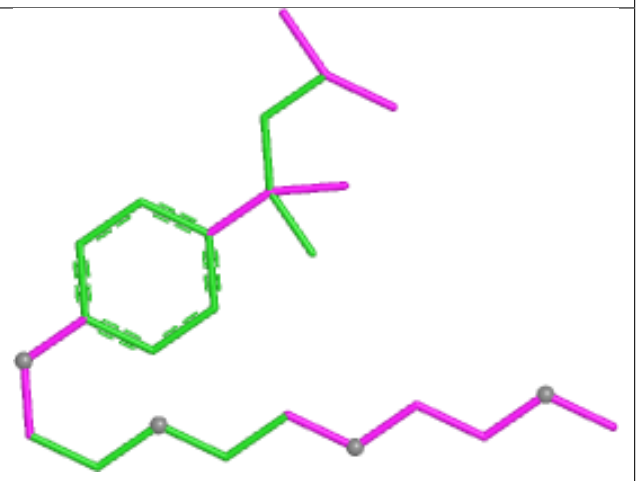
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	OXN	1	0
3	B	602	POP	2	0
2	B	702	OXN	1	0

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 then 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.

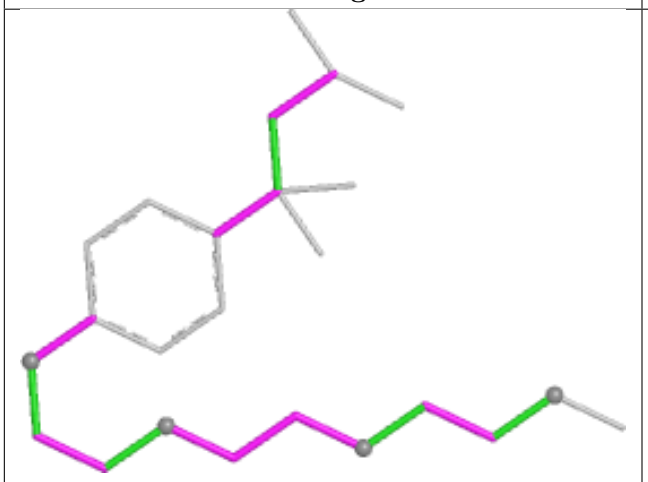
Ligand OXN A 701



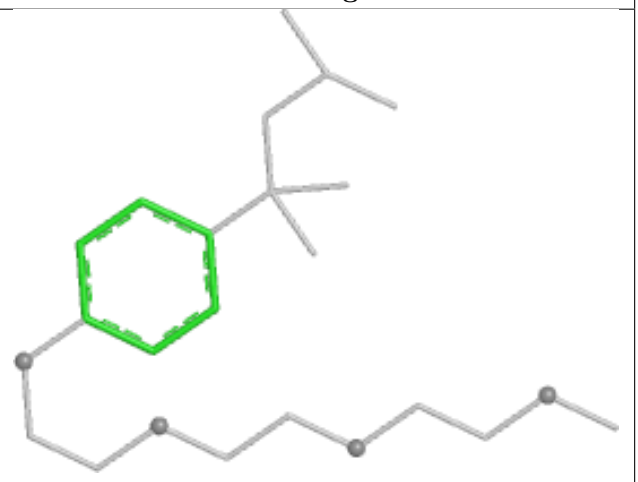
Bond lengths



Bond angles

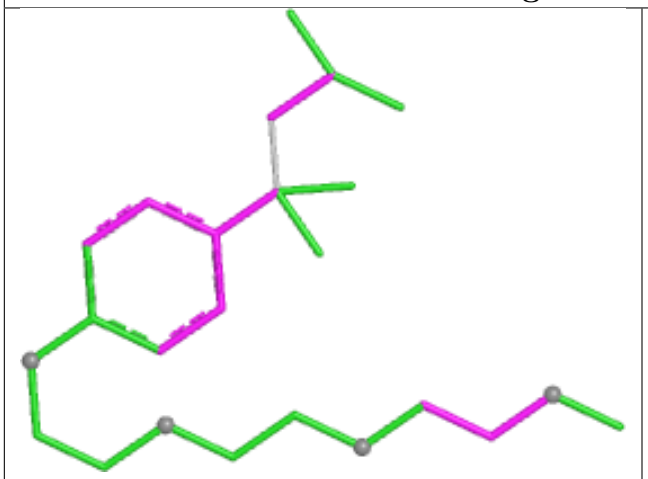


Torsions

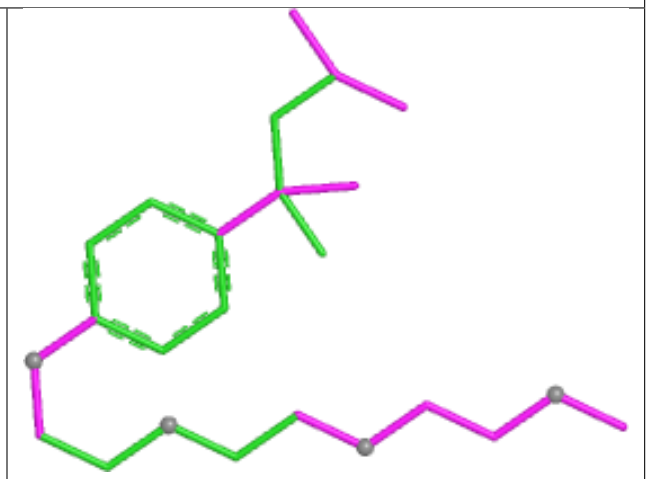


Rings

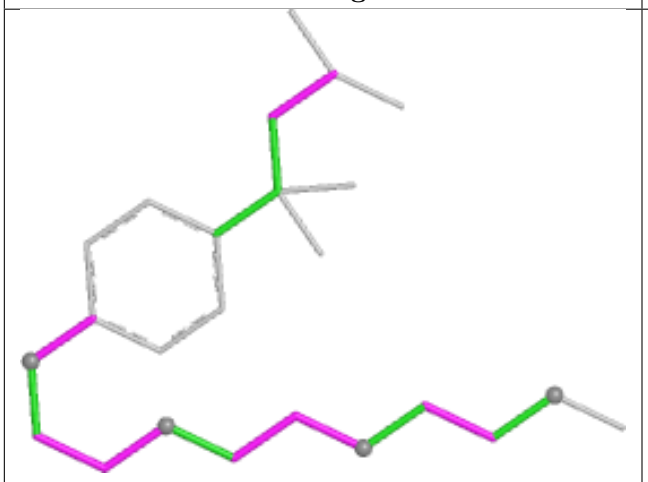
Ligand OXN B 702



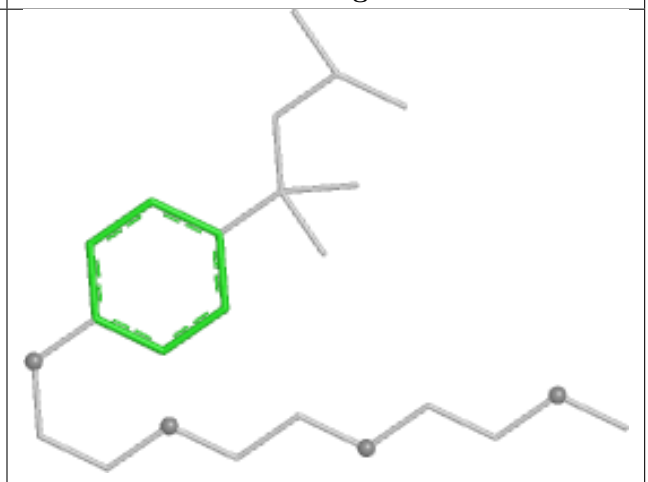
Bond lengths



Bond angles



Torsions



Rings

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 (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	257/257 (100%)	0.20	14 (5%)	25	32	24, 43, 79, 99	25 (9%)
1	B	255/257 (99%)	0.08	13 (5%)	28	35	21, 37, 72, 92	19 (7%)
All	All	512/514 (99%)	0.14	27 (5%)	26	33	21, 41, 76, 99	44 (8%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1562	GLU	4.8
1	A	1681	GLY	4.6
1	B	1727	HIS	4.1
1	A	1698	ILE	4.0
1	A	1563	PHE	3.9
1	A	1775	GLU	3.8
1	A	1604	TYR	3.7
1	B	1678	GLY	3.6
1	A	1595	GLY	3.4
1	A	1700	HIS	3.3
1	B	1595	GLY	3.0
1	B	1692	GLY	3.0
1	B	1597	ILE	2.9
1	B	1747	GLU	2.9
1	B	1683	LYS	2.8
1	A	1727	HIS	2.8
1	A	1699	GLU	2.8
1	A	1618	TYR	2.4
1	B	1682	SER	2.4
1	B	1751	VAL	2.3
1	B	1561	GLU	2.3
1	B	1726	ALA	2.2
1	A	1614	TYR	2.1
1	A	1596	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	1568	THR	2.0
1	B	1704	LYS	2.0
1	A	1560	LYS	2.0

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)

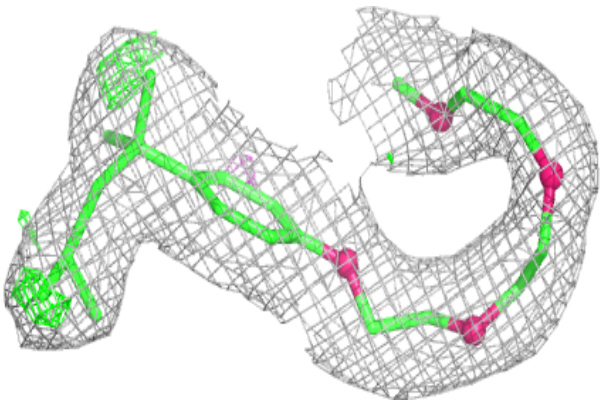
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

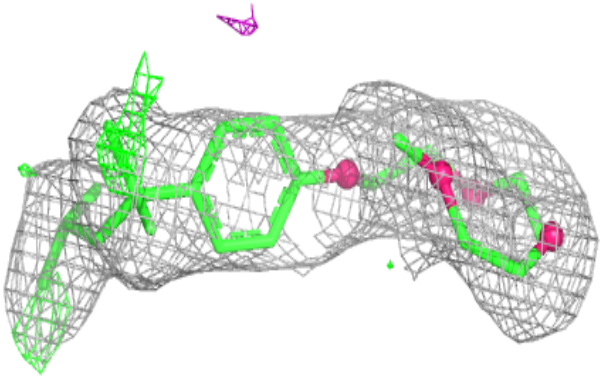
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	OXN	A	701	24/45	0.72	0.23	58,78,88,89	0
2	OXN	B	702	24/45	0.74	0.21	37,66,83,86	0
3	POP	B	601	9/9	0.84	0.19	68,92,93,96	0
3	POP	B	602	9/9	0.91	0.24	55,76,86,95	0

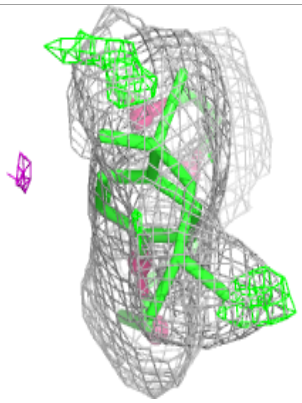
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around OXN A 701:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

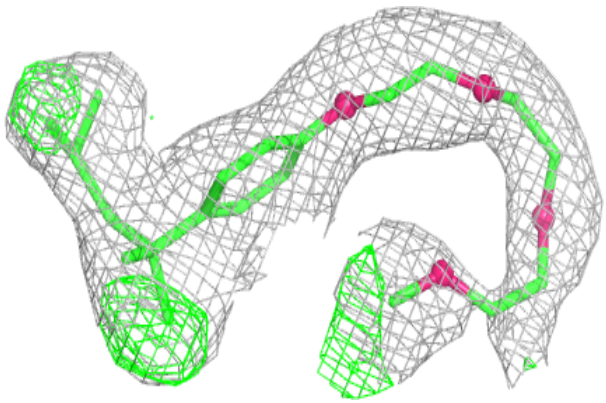


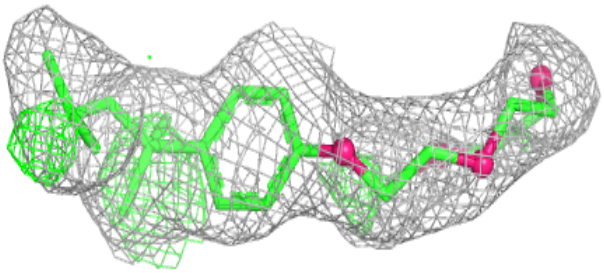


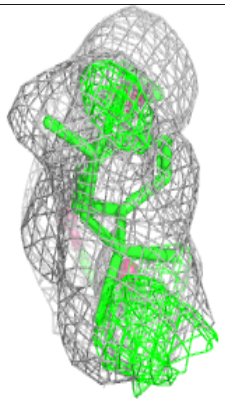


Electron density around OXN B 702:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.