



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 12, 2017 – 08:24 pm GMT

PDB ID : 1FEL
Title : CRYSTALLOGRAPHIC STUDIES ON COMPLEXES BETWEEN
RETINOIDS AND PLASMA RETINOL-BINDING PROTEIN
Authors : Zanotti, G.; Marcello, M.; Malpeli, G.; Sartori, G.; Berni, R.
Deposited on : 1994-08-29
Resolution : 1.80 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

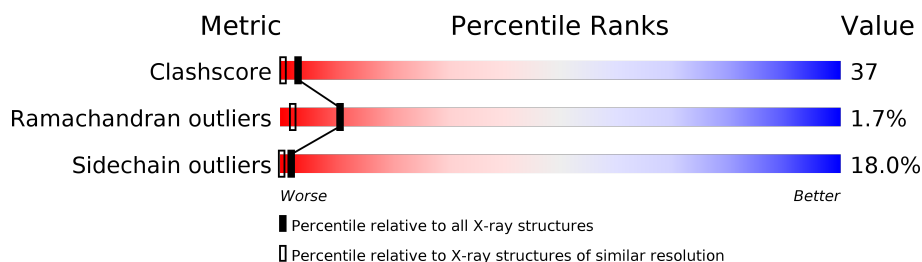
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
Clashscore	112137	5742 (1.80-1.80)
Ramachandran outliers	110173	5676 (1.80-1.80)
Sidechain outliers	110143	5675 (1.80-1.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	183	

2 Entry composition [i](#)

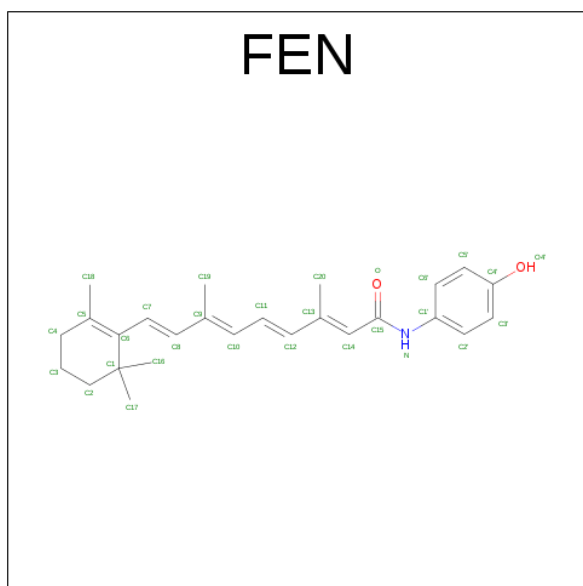
There are 3 unique types of molecules in this entry. The entry contains 1603 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 RETINOL BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	175	Total	C	N	O	S	0	0	1
			1411	889	246	266	10			

- Molecule 2 is N-(4-HYDROXYPHENYL)ALL-TRANS RETINAMIDE (three-letter code: FEN) (formula: C₂₆H₃₃NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			29	26	1	2		

- Molecule 3 is water.

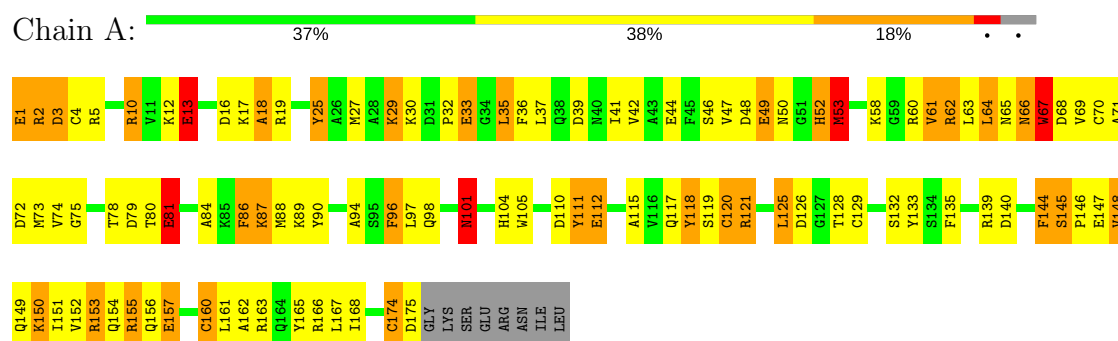
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	163	Total	O	0	0
			163	163		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

Note EDS was not executed.

• Molecule 1: RETINOL BINDING PROTEIN



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	46.63Å 49.26Å 76.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	9.00 – 1.80	Depositor
% Data completeness (in resolution range)	(Not available) (9.00-1.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.204 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1603	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	1.10	8/1445 (0.6%)	2.17	56/1952 (2.9%)

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	1	0

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	147	GLU	CD-OE2	7.86	1.34	1.25
1	A	33	GLU	CD-OE2	6.68	1.32	1.25
1	A	13	GLU	CD-OE2	6.48	1.32	1.25
1	A	1	GLU	CD-OE2	6.41	1.32	1.25
1	A	81	GLU	CD-OE1	6.38	1.32	1.25
1	A	112	GLU	CD-OE1	6.23	1.32	1.25
1	A	49	GLU	CD-OE2	6.05	1.32	1.25
1	A	157	GLU	CD-OE1	5.03	1.31	1.25

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	155	ARG	NE-CZ-NH1	20.55	130.57	120.30
1	A	140	ASP	CB-CG-OD2	12.16	129.25	118.30
1	A	121	ARG	NE-CZ-NH1	11.52	126.06	120.30
1	A	126	ASP	CB-CG-OD2	-11.17	108.25	118.30
1	A	160	CYS	CB-CA-C	10.37	131.14	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	119	SER	N-CA-CB	10.16	125.74	110.50
1	A	144	PHE	CB-CA-C	-9.54	91.32	110.40
1	A	121	ARG	NE-CZ-NH2	-9.35	115.63	120.30
1	A	140	ASP	CB-CG-OD1	-9.30	109.93	118.30
1	A	155	ARG	NE-CZ-NH2	-8.96	115.82	120.30
1	A	126	ASP	CB-CG-OD1	8.66	126.10	118.30
1	A	111	TYR	CB-CG-CD1	-8.59	115.84	121.00
1	A	39	ASP	CB-CG-OD1	-8.39	110.75	118.30
1	A	155	ARG	CD-NE-CZ	8.24	135.13	123.60
1	A	133	TYR	N-CA-CB	8.17	125.31	110.60
1	A	86	PHE	CB-CG-CD1	-8.07	115.15	120.80
1	A	160	CYS	CA-CB-SG	-7.88	99.81	114.00
1	A	60	ARG	NE-CZ-NH2	-7.67	116.46	120.30
1	A	78	THR	CA-CB-CG2	-7.67	101.65	112.40
1	A	121	ARG	CD-NE-CZ	7.06	133.48	123.60
1	A	49	GLU	N-CA-CB	6.91	123.04	110.60
1	A	128	THR	CA-CB-CG2	-6.89	102.75	112.40
1	A	3	ASP	CB-CG-OD2	-6.82	112.16	118.30
1	A	165	TYR	CB-CG-CD2	6.79	125.07	121.00
1	A	163	ARG	NE-CZ-NH1	6.73	123.67	120.30
1	A	145	SER	N-CA-CB	-6.49	100.77	110.50
1	A	3	ASP	N-CA-CB	-6.48	98.94	110.60
1	A	64	LEU	N-CA-CB	6.17	122.75	110.40
1	A	18	ALA	N-CA-CB	6.05	118.57	110.10
1	A	118	TYR	CB-CG-CD1	-5.98	117.41	121.00
1	A	48	ASP	CB-CG-OD1	-5.87	113.02	118.30
1	A	96	PHE	CB-CG-CD2	-5.82	116.72	120.80
1	A	115	ALA	N-CA-CB	5.78	118.20	110.10
1	A	67	TRP	CB-CA-C	-5.71	98.97	110.40
1	A	81	GLU	C-N-CA	-5.59	107.72	121.70
1	A	53	MET	N-CA-CB	5.57	120.62	110.60
1	A	139	ARG	NE-CZ-NH2	5.52	123.06	120.30
1	A	84	ALA	N-CA-CB	-5.51	102.39	110.10
1	A	67	TRP	CA-CB-CG	5.40	123.97	113.70
1	A	25	TYR	CB-CG-CD1	-5.36	117.78	121.00
1	A	135	PHE	CB-CG-CD1	5.33	124.53	120.80
1	A	154	GLN	O-C-N	-5.32	114.19	122.70
1	A	64	LEU	CB-CA-C	5.31	120.30	110.20
1	A	155	ARG	NH1-CZ-NH2	-5.27	113.61	119.40
1	A	174	CYS	N-CA-CB	5.21	119.98	110.60
1	A	61	VAL	CA-CB-CG2	-5.20	103.10	110.90
1	A	166	ARG	NE-CZ-NH1	5.19	122.89	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	72	ASP	CB-CG-OD2	-5.18	113.64	118.30
1	A	13	GLU	CG-CD-OE2	-5.13	108.04	118.30
1	A	60	ARG	NE-CZ-NH1	5.13	122.86	120.30
1	A	81	GLU	CA-CB-CG	5.09	124.59	113.40
1	A	101	ASN	N-CA-CB	-5.07	101.47	110.60
1	A	32	PRO	CB-CA-C	-5.06	99.35	112.00
1	A	67	TRP	N-CA-CB	5.04	119.68	110.60
1	A	120	CYS	CA-CB-SG	-5.04	104.94	114.00
1	A	42	VAL	CB-CA-C	-5.03	101.84	111.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	49	GLU	CA

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	1411	0	1339	100	0
2	A	29	0	32	11	0
3	A	163	0	0	18	0
All	All	1603	0	1371	102	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 37.

All (102) 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:150:LYS:HE2	1:A:151:ILE:HG13	1.37	1.04
1:A:144:PHE:HB3	1:A:148:VAL:HG13	1.42	0.98
1:A:120:CYS:HG	1:A:129:CYS:HG	1.13	0.90
1:A:150:LYS:HE2	1:A:151:ILE:CG1	2.03	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:LEU:HD13	1:A:67:TRP:HB2	1.56	0.88
1:A:73:MET:CE	1:A:97:LEU:HD13	2.04	0.87
1:A:94:ALA:HB1	1:A:96:PHE:CE1	2.09	0.87
1:A:144:PHE:HB3	1:A:148:VAL:CG1	2.04	0.86
1:A:63:LEU:HD13	1:A:67:TRP:CB	2.05	0.86
1:A:71:ALA:HB1	1:A:73:MET:CE	2.06	0.86
1:A:36:PHE:HA	2:A:184:FEN:H203	1.57	0.85
1:A:73:MET:HE1	1:A:97:LEU:HD13	1.61	0.82
1:A:58:LYS:NZ	1:A:175:ASP:N	2.29	0.80
1:A:13:GLU:HB2	3:A:319:HOH:O	1.82	0.80
1:A:71:ALA:HB1	1:A:73:MET:HE2	1.64	0.78
1:A:112:GLU:HG3	3:A:322:HOH:O	1.83	0.77
1:A:61:VAL:HG11	2:A:184:FEN:N	2.02	0.74
1:A:27:MET:HB2	3:A:193:HOH:O	1.88	0.73
1:A:58:LYS:HD2	3:A:238:HOH:O	1.89	0.72
1:A:35:LEU:HB2	3:A:220:HOH:O	1.88	0.71
1:A:63:LEU:N	1:A:63:LEU:HD12	2.06	0.71
1:A:63:LEU:HA	2:A:184:FEN:C3'	2.20	0.71
1:A:53:MET:N	3:A:314:HOH:O	2.24	0.70
1:A:58:LYS:HZ1	1:A:175:ASP:N	1.89	0.70
1:A:71:ALA:HB1	1:A:73:MET:HE3	1.75	0.69
1:A:63:LEU:O	1:A:66:ASN:N	2.22	0.68
1:A:70:CYS:HB3	1:A:174:CYS:SG	2.33	0.68
1:A:63:LEU:HD12	1:A:63:LEU:H	1.59	0.67
1:A:41:ILE:HA	1:A:58:LYS:O	1.94	0.67
1:A:61:VAL:HG11	2:A:184:FEN:HN	1.58	0.67
1:A:73:MET:HE1	1:A:97:LEU:HB3	1.76	0.65
1:A:150:LYS:HA	1:A:153:ARG:HG2	1.79	0.64
1:A:129:CYS:SG	1:A:132:SER:HB3	2.38	0.64
1:A:150:LYS:O	1:A:153:ARG:HG3	1.97	0.64
1:A:63:LEU:HD13	1:A:67:TRP:HB3	1.78	0.64
1:A:73:MET:HE2	1:A:97:LEU:HD13	1.77	0.64
1:A:12:LYS:NZ	3:A:271:HOH:O	2.26	0.63
1:A:145:SER:OG	1:A:148:VAL:HG12	1.99	0.62
1:A:17:LYS:HG3	3:A:344:HOH:O	2.00	0.62
1:A:150:LYS:HA	1:A:153:ARG:CG	2.29	0.62
1:A:37:LEU:HD23	1:A:61:VAL:HG22	1.82	0.62
1:A:125:LEU:HD13	3:A:298:HOH:O	2.00	0.60
1:A:63:LEU:HA	2:A:184:FEN:H3'	1.83	0.60
1:A:64:LEU:H	2:A:184:FEN:H3'	1.65	0.60
1:A:47:VAL:HG23	1:A:52:HIS:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:GLU:HG2	1:A:81:GLU:O	2.02	0.57
1:A:61:VAL:CG1	2:A:184:FEN:HN	2.18	0.57
1:A:73:MET:CE	1:A:97:LEU:HD22	2.35	0.57
1:A:152:VAL:O	1:A:156:GLN:HG3	2.05	0.56
1:A:80:THR:HB	3:A:280:HOH:O	2.04	0.56
1:A:150:LYS:CE	1:A:151:ILE:HG13	2.25	0.56
1:A:86:PHE:O	1:A:104:HIS:N	2.35	0.55
1:A:129:CYS:O	3:A:223:HOH:O	2.17	0.54
1:A:70:CYS:HB3	1:A:174:CYS:HB3	1.89	0.54
1:A:64:LEU:N	2:A:184:FEN:H3'	2.23	0.54
1:A:63:LEU:HB2	1:A:67:TRP:HB2	1.90	0.54
1:A:36:PHE:HA	2:A:184:FEN:C20	2.34	0.53
1:A:73:MET:HE1	1:A:97:LEU:HD22	1.89	0.53
1:A:16:ASP:OD2	1:A:19:ARG:HD2	2.08	0.53
1:A:4:CYS:SG	1:A:160:CYS:CB	2.98	0.52
2:A:184:FEN:H181	2:A:184:FEN:C8	2.41	0.51
1:A:37:LEU:HD23	1:A:61:VAL:CG2	2.40	0.51
1:A:145:SER:O	1:A:149:GLN:HG3	2.10	0.51
1:A:13:GLU:CD	1:A:13:GLU:H	2.15	0.50
1:A:35:LEU:HD13	1:A:35:LEU:N	2.26	0.50
1:A:29:LYS:HB3	1:A:168:ILE:HD11	1.94	0.50
1:A:125:LEU:HA	3:A:298:HOH:O	2.11	0.50
1:A:63:LEU:N	1:A:67:TRP:O	2.44	0.50
1:A:73:MET:HE1	1:A:97:LEU:CD1	2.38	0.49
2:A:184:FEN:H181	2:A:184:FEN:H8	1.95	0.49
1:A:2:ARG:HB2	3:A:199:HOH:O	2.13	0.48
1:A:75:GLY:HA2	1:A:89:LYS:O	2.14	0.48
1:A:110:ASP:C	1:A:112:GLU:H	2.17	0.47
1:A:64:LEU:O	1:A:64:LEU:HD12	2.14	0.47
1:A:94:ALA:HA	3:A:197:HOH:O	2.15	0.47
1:A:58:LYS:CE	1:A:175:ASP:N	2.77	0.47
1:A:90:TYR:OH	1:A:98:GLN:NE2	2.47	0.47
1:A:3:ASP:OD2	1:A:5:ARG:NH2	2.33	0.47
1:A:63:LEU:CD1	1:A:63:LEU:N	2.78	0.46
1:A:25:TYR:HE2	3:A:207:HOH:O	1.98	0.46
1:A:30:LYS:HD3	1:A:30:LYS:C	2.36	0.46
1:A:18:ALA:HB2	1:A:47:VAL:HG11	1.97	0.46
1:A:87:LYS:HE3	1:A:87:LYS:HA	1.98	0.46
1:A:63:LEU:O	1:A:64:LEU:C	2.54	0.46
1:A:50:ASN:ND2	3:A:235:HOH:O	2.37	0.45
1:A:88:MET:O	1:A:101:ASN:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:ARG:HG2	3:A:272:HOH:O	2.16	0.45
1:A:70:CYS:HB3	1:A:174:CYS:CB	2.46	0.45
1:A:58:LYS:HZ2	1:A:175:ASP:N	2.15	0.44
1:A:74:VAL:O	1:A:90:TYR:HA	2.17	0.44
1:A:145:SER:HB2	1:A:146:PRO:HD2	1.99	0.44
1:A:73:MET:HE1	1:A:97:LEU:CB	2.44	0.44
1:A:117:GLN:HG2	1:A:118:TYR:N	2.34	0.43
1:A:63:LEU:CD1	1:A:63:LEU:H	2.28	0.42
1:A:105:TRP:CD1	1:A:105:TRP:N	2.83	0.42
1:A:87:LYS:HE2	3:A:321:HOH:O	2.19	0.42
1:A:161:LEU:HD23	1:A:161:LEU:HA	1.86	0.41
1:A:58:LYS:HE3	1:A:175:ASP:N	2.35	0.41
1:A:150:LYS:HE2	1:A:151:ILE:HG12	1.96	0.41
1:A:62:ARG:HH11	1:A:62:ARG:HD3	1.74	0.41
1:A:157:GLU:HA	1:A:162:ALA:HB2	2.03	0.40
1:A:37:LEU:HA	1:A:37:LEU:HD23	1.92	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	173/183 (94%)	161 (93%)	9 (5%)	3 (2%)	11 2

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	HIS
1	A	53	MET
1	A	111	TYR

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	150/158 (95%)	123 (82%)	27 (18%)	2 0

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	GLU
1	A	2	ARG
1	A	10	ARG
1	A	13	GLU
1	A	29	LYS
1	A	33	GLU
1	A	35	LEU
1	A	44	GLU
1	A	46	SER
1	A	49	GLU
1	A	62	ARG
1	A	65	ASN
1	A	66	ASN
1	A	67	TRP
1	A	68	ASP
1	A	69	VAL
1	A	79	ASP
1	A	81	GLU
1	A	87	LYS
1	A	101	ASN
1	A	121	ARG
1	A	125	LEU
1	A	148	VAL
1	A	150	LYS
1	A	153	ARG
1	A	155	ARG
1	A	167	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	ASN
1	A	66	ASN
1	A	98	GLN
1	A	170	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 carbohydrates 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	FEN	A	184	-	30,30,30	1.75	6 (20%)	40,41,41	5.43	16 (40%)

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	FEN	A	184	-	-	0/19/36/36	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	184	FEN	C19-C9	2.03	1.55	1.50
2	A	184	FEN	C18-C5	2.10	1.54	1.51
2	A	184	FEN	C6'-C5'	2.13	1.42	1.38
2	A	184	FEN	C1-C6	2.38	1.57	1.53
2	A	184	FEN	C14-C13	3.55	1.40	1.35
2	A	184	FEN	O-C15	6.10	1.36	1.24

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	184	FEN	O-C15-C14	-25.01	88.56	124.65
2	A	184	FEN	C1'-N-C15	-6.22	118.77	128.27
2	A	184	FEN	C18-C5-C6	-5.48	118.37	124.51
2	A	184	FEN	C1-C6-C5	-4.17	116.73	122.59
2	A	184	FEN	C4-C5-C6	-3.85	117.09	122.74
2	A	184	FEN	C3-C4-C5	-3.80	107.24	113.78
2	A	184	FEN	C17-C1-C6	-3.60	104.47	110.31
2	A	184	FEN	C2-C3-C4	-3.41	103.21	111.34
2	A	184	FEN	C6'-C1'-C2'	-2.91	114.98	119.04
2	A	184	FEN	C17-C1-C16	-2.87	99.70	108.50
2	A	184	FEN	C8-C9-C10	-2.78	114.67	118.94
2	A	184	FEN	C3'-C2'-C1'	2.64	123.38	120.30
2	A	184	FEN	C16-C1-C2	2.79	119.82	108.80
2	A	184	FEN	C16-C1-C6	4.61	117.78	110.31
2	A	184	FEN	C14-C15-N	12.44	131.65	112.33
2	A	184	FEN	O-C15-N	13.13	138.59	122.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	184	FEN	11	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.