



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 25, 2021 – 06:02 PM EST

PDB ID : 7LL9
Title : D-Protein RFX-V2 Bound to the VEGFR1 Domain 3 Site on VEGF-A
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Zhao, Y.; Petriello, A.; Deshayes, K.; Kent, S.B.H.; Ault-Riche, D.; Sidhu,
S.S.
Deposited on : 2021-02-03
Resolution : 2.90 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.17.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.17.1

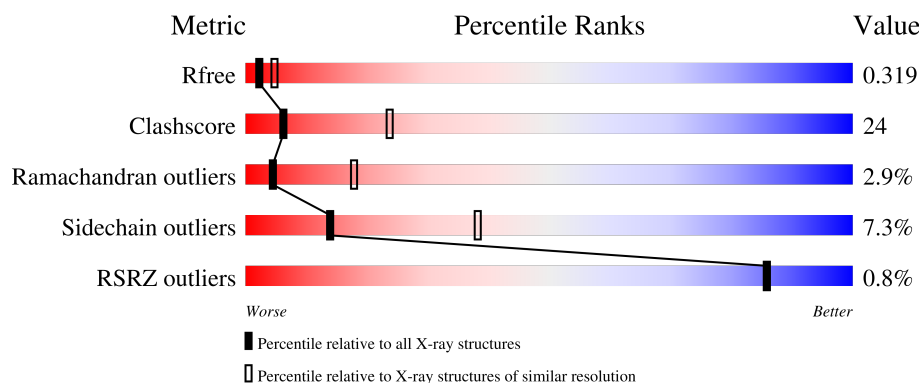
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	103	
1	B	103	
1	E	103	
1	F	103	
2	C	58	

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Mol	Chain	Length	Quality of chain
2	D	58	
2	G	58	
2	H	58	

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	DAR	C	17	-	-	X	-
2	DAS	D	37	-	-	X	-
2	DPR	D	38	-	-	X	-
2	DSN	D	39	-	-	X	-
2	DAL	D	56	-	-	X	-
2	DPR	D	57	-	-	X	-
2	DAR	G	17	-	-	X	-
2	DPR	H	38	-	-	X	-
2	DAL	H	56	-	-	X	-
2	DPR	H	57	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4909 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 Isoform L-VEGF189 of Vascular endothelial growth factor A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	96	Total	C	N	O	S	0	0	0
			779	489	131	146	13			
1	B	99	Total	C	N	O	S	0	0	0
			808	505	138	152	13			
1	E	96	Total	C	N	O	S	0	0	0
			779	489	131	146	13			
1	F	98	Total	C	N	O	S	0	0	0
			799	501	137	148	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	SER	-	expression tag	UNP P15692
B	33	SER	-	expression tag	UNP P15692
E	33	SER	-	expression tag	UNP P15692
F	33	SER	-	expression tag	UNP P15692

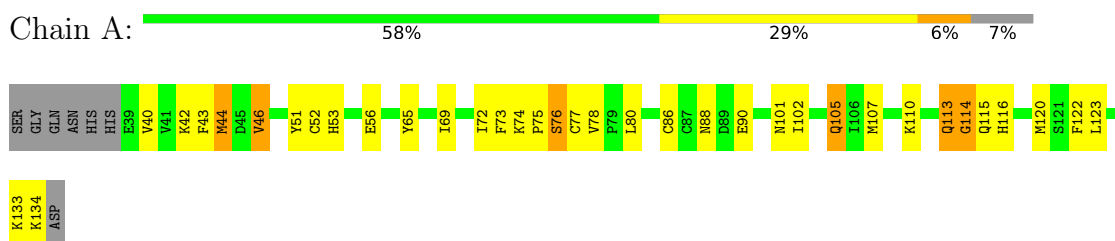
- Molecule 2 is a protein (with D amino acids) called RFX-V2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	53	Total	C	N	O	0	0	0
			436	274	79	83			
2	D	53	Total	C	N	O	0	0	0
			436	274	79	83			
2	G	53	Total	C	N	O	0	0	0
			436	274	79	83			
2	H	53	Total	C	N	O	0	0	0
			436	274	79	83			

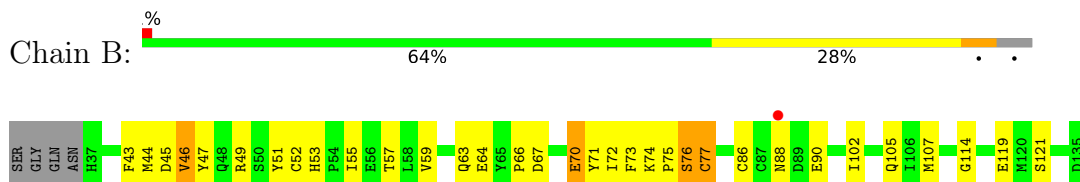
3 Residue-property plots

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.

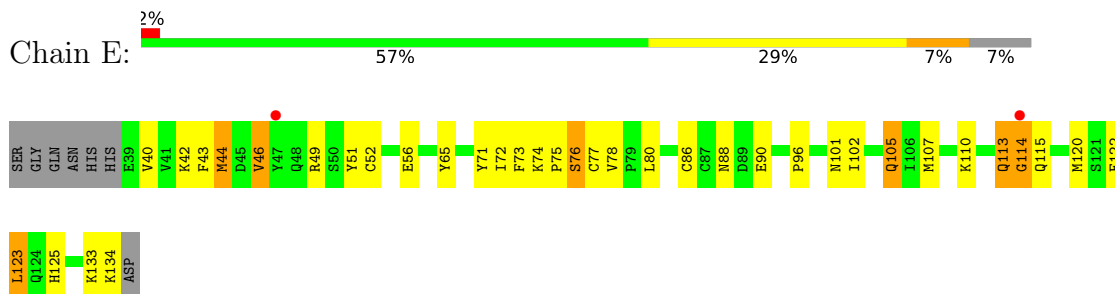
- Molecule 1: Isoform L-VEGF189 of Vascular endothelial growth factor A



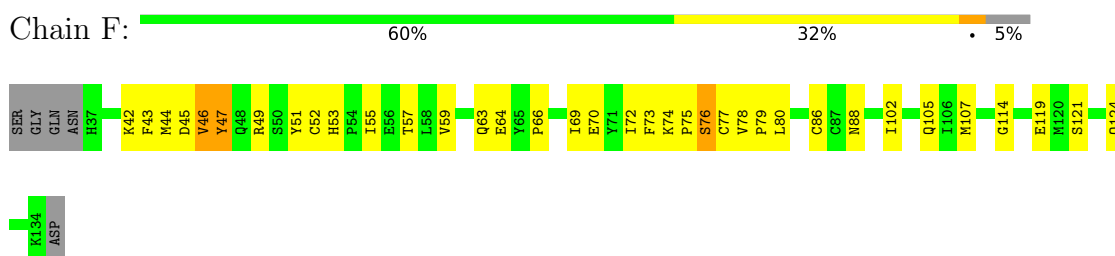
- Molecule 1: Isoform L-VEGF189 of Vascular endothelial growth factor A



- Molecule 1: Isoform L-VEGF189 of Vascular endothelial growth factor A

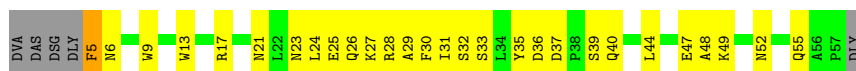


- Molecule 1: Isoform L-VEGF189 of Vascular endothelial growth factor A



- Molecule 2: RFX-V2

Chain C:  43% 47% 9%



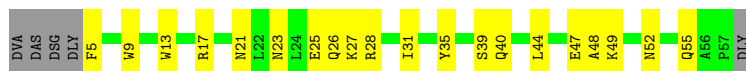
• Molecule 2: RFX-V2

Chain D:  36% 53% 9%



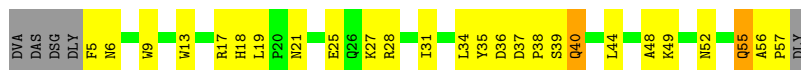
• Molecule 2: RFX-V2

Chain G:  57% 34% 9%



• Molecule 2: RFX-V2

Chain H:  47% 41% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.85Å 120.44Å 120.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.52 – 2.90 58.45 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (58.52-2.90) 99.8 (58.45-2.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.263 , 0.315 0.265 , 0.319	Depositor DCC
R_{free} test set	1033 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	95.7	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 64.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.488 for -h,l,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4909	wwPDB-VP
Average B, all atoms (Å ²)	137.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.76% 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: DPN, DLE, DHI, DAS, DGN, DAL, DTR, DSN, DGL, DAR, DIL, DLY, DSG, DTY, DPR

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	0.74	0/797	1.00	0/1073
1	B	0.76	0/828	1.00	0/1114
1	E	0.77	0/797	0.99	0/1073
1	F	0.80	0/819	1.01	1/1103 (0.1%)
All	All	0.77	0/3241	1.00	1/4363 (0.0%)

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	1
1	B	0	2
1	E	0	1
1	F	0	2
2	C	0	1
2	D	0	2
2	H	0	3
All	All	0	12

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	47	TYR	CB-CG-CD1	5.21	124.13	121.00

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	76	SER	Peptide
1	B	114	GLY	Peptide
1	B	76	SER	Peptide
2	C	5	DPN	Peptide
2	D	6	DSG	Peptide

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	779	0	747	37	0
1	B	808	0	765	28	0
1	E	779	0	747	51	0
1	F	799	0	761	30	0
2	C	436	0	386	31	0
2	D	436	0	385	45	0
2	G	436	0	388	20	0
2	H	436	0	386	34	0
All	All	4909	0	4565	231	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 24.

The worst 5 of 231 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:E:74:LYS:HE2	1:F:88:ASN:O	1.41	1.17
1:E:105:GLN:OE1	1:F:43:PHE:N	1.87	1.08
2:C:33:DSN:O	2:C:36:DAS:O	1.77	1.03
1:A:105:GLN:OE1	1:B:43:PHE:N	1.94	1.00
2:C:27:DLY:O	2:C:31:DIL:HG13	1.64	0.98

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	94/103 (91%)	82 (87%)	9 (10%)	3 (3%)	4	16
1	B	97/103 (94%)	82 (84%)	12 (12%)	3 (3%)	4	16
1	E	94/103 (91%)	82 (87%)	9 (10%)	3 (3%)	4	16
1	F	96/103 (93%)	81 (84%)	13 (14%)	2 (2%)	7	26
All	All	381/412 (92%)	327 (86%)	43 (11%)	11 (3%)	4	18

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	46	VAL
1	A	52	CYS
1	B	46	VAL
1	B	52	CYS
1	E	46	VAL

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	91/97 (94%)	84 (92%)	7 (8%)	13	35
1	B	94/97 (97%)	87 (93%)	7 (7%)	13	38
1	E	91/97 (94%)	84 (92%)	7 (8%)	13	35
1	F	93/97 (96%)	87 (94%)	6 (6%)	17	45
All	All	369/388 (95%)	342 (93%)	27 (7%)	14	38

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	44	MET
1	E	105	GLN
1	F	76	SER
1	E	77	CYS
1	E	110	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	88	ASN
1	F	113	GLN
1	B	88	ASN
1	B	112	HIS
1	B	113	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

212 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	DHI	C	18	2	5,10,11	0.58	0	3,12,14	1.16	0
2	DHI	G	18	2	5,10,11	0.59	0	3,12,14	1.09	0
2	DHI	D	18	2	5,10,11	0.63	0	3,12,14	1.89	1 (33%)
2	DHI	H	18	2	5,10,11	0.61	0	3,12,14	1.35	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	DHI	C	18	2	-	2/5/6/8	0/1/1/1
2	DHI	G	18	2	-	2/5/6/8	0/1/1/1
2	DHI	D	18	2	-	3/5/6/8	0/1/1/1
2	DHI	H	18	2	-	4/5/6/8	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	18	DHI	CB-CA-C	-2.71	106.38	111.47

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	18	DHI	C-CA-CB-CG
2	D	18	DHI	N-CA-CB-CG
2	D	18	DHI	C-CA-CB-CG
2	G	18	DHI	C-CA-CB-CG
2	H	18	DHI	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	18	DHI	2	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	96/103 (93%)	0.17	0 100 100	110, 125, 171, 190	0
1	B	99/103 (96%)	-0.08	1 (1%) 82 82	100, 129, 184, 201	0
1	E	96/103 (93%)	0.15	2 (2%) 63 61	97, 115, 160, 180	0
1	F	98/103 (95%)	0.04	0 100 100	97, 126, 186, 205	0
2	C	0/58	-	-	-	-
2	D	0/58	-	-	-	-
2	G	0/58	-	-	-	-
2	H	0/58	-	-	-	-
All	All	389/644 (60%)	0.07	3 (0%) 86 86	97, 124, 180, 205	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	114	GLY	3.2
1	E	47	TYR	2.4
1	B	88	ASN	2.4

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	DPR	H	38	7/8	0.56	0.26	230,233,239,247	0
2	DPR	D	38	7/8	0.64	0.28	218,220,225,231	0
2	DSN	D	39	6/7	0.64	0.32	215,222,225,229	0
2	DSG	D	6	8/9	0.67	0.20	194,208,215,216	0
2	DSG	H	6	8/9	0.68	0.19	176,197,209,216	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	DPR	D	57	7/8	0.69	0.15	162,171,177,178	0
2	DAS	D	37	8/9	0.70	0.16	172,182,194,202	0
2	DPN	C	5	11/12	0.73	0.22	164,174,183,185	0
2	DSG	D	43	8/9	0.74	0.20	215,221,225,226	0
2	DSN	D	41	6/7	0.74	0.20	206,211,217,217	0
2	DPN	H	5	11/12	0.76	0.12	204,207,224,229	0
2	DPN	D	5	11/12	0.76	0.15	201,203,220,222	0
2	DSN	H	39	6/7	0.77	0.32	235,236,238,241	0
2	DAS	D	36	8/9	0.78	0.36	189,197,199,202	0
2	DTR	H	9	14/15	0.80	0.21	155,189,195,196	0
2	DGL	G	8	9/10	0.81	0.27	126,149,168,169	0
2	DAR	D	17	11/12	0.82	0.17	125,137,160,163	0
2	DTR	H	13	14/15	0.82	0.28	142,154,159,160	0
2	DPR	H	57	7/8	0.82	0.14	155,169,176,177	0
2	DAS	H	36	8/9	0.83	0.35	184,192,194,201	0
2	DSG	D	11	8/9	0.84	0.27	178,181,184,185	0
2	DSG	C	6	8/9	0.84	0.25	162,177,196,207	0
2	DAS	H	10	8/9	0.84	0.14	157,167,173,178	0
2	DAS	H	37	8/9	0.84	0.12	175,188,201,210	0
2	DAL	H	42	5/6	0.85	0.21	212,218,222,222	0
2	DTR	D	9	14/15	0.85	0.19	167,189,193,193	0
2	DSG	D	52	8/9	0.85	0.13	213,214,220,221	0
2	DSG	H	11	8/9	0.85	0.27	171,177,182,185	0
2	DHI	D	18	10/11	0.85	0.31	171,190,204,205	0
2	DTR	D	13	14/15	0.86	0.28	146,151,163,164	0
2	DSG	G	6	8/9	0.86	0.15	167,175,186,191	0
2	DSG	H	23	8/9	0.86	0.17	194,200,206,208	0
2	DTY	H	35	12/13	0.86	0.30	161,174,176,178	0
2	DSG	H	52	8/9	0.86	0.12	197,207,210,210	0
2	DAS	H	53	8/9	0.86	0.10	194,200,210,218	0
2	DGN	D	55	9/10	0.86	0.22	179,185,191,194	0
2	DAL	D	56	5/6	0.86	0.21	183,185,186,187	0
2	DAR	D	14	11/12	0.86	0.17	151,159,167,170	0
2	DAR	H	14	11/12	0.86	0.15	138,155,163,171	0
2	DGN	H	40	9/10	0.87	0.14	187,198,227,230	0
2	DLE	D	22	8/9	0.87	0.21	186,189,192,194	0
2	DGN	C	55	9/10	0.87	0.16	108,118,122,124	0
2	DSN	H	41	6/7	0.87	0.19	209,219,221,222	0
2	DSG	D	23	8/9	0.87	0.27	203,210,220,221	0
2	DGL	H	8	9/10	0.87	0.18	175,192,203,204	0
2	DHI	H	18	10/11	0.87	0.24	157,176,186,187	0
2	DLY	C	7	9/10	0.88	0.33	127,159,167,170	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	DGL	H	25	9/10	0.88	0.28	193,202,219,226	0
2	DTY	D	35	12/13	0.88	0.30	161,174,181,183	0
2	DLY	H	7	9/10	0.88	0.28	170,183,202,207	0
2	DGN	G	55	9/10	0.88	0.14	97,112,115,116	0
2	DGN	H	55	9/10	0.88	0.20	162,182,187,189	0
2	DGL	C	8	9/10	0.88	0.31	135,154,169,174	0
2	DSG	H	43	8/9	0.88	0.20	207,214,218,227	0
2	DGL	D	8	9/10	0.88	0.24	180,190,199,201	0
2	DGL	H	47	9/10	0.89	0.29	221,225,232,247	0
2	DSN	D	33	6/7	0.89	0.17	188,192,194,197	0
2	DSN	H	33	6/7	0.89	0.18	188,190,195,206	0
2	DAS	D	53	8/9	0.89	0.09	204,209,216,221	0
2	DSG	D	21	8/9	0.89	0.15	168,174,182,195	0
2	DAS	D	10	8/9	0.89	0.14	168,172,175,179	0
2	DLY	D	7	9/10	0.89	0.31	177,187,193,193	0
2	DSG	G	23	8/9	0.89	0.21	93,100,104,108	0
2	DSG	C	11	8/9	0.89	0.23	111,130,143,146	0
2	DPN	G	5	11/12	0.89	0.17	167,175,184,187	0
2	DGN	D	26	9/10	0.89	0.35	210,216,237,246	0
2	DGL	D	47	9/10	0.89	0.18	186,196,218,227	0
2	DGN	G	40	9/10	0.90	0.21	103,125,153,158	0
2	DAR	H	28	11/12	0.90	0.34	177,192,199,201	0
2	DAS	C	53	8/9	0.90	0.16	93,105,109,110	0
2	DGL	G	15	9/10	0.90	0.33	107,111,123,130	0
2	DAR	G	14	11/12	0.90	0.25	97,109,133,139	0
2	DAR	H	17	11/12	0.90	0.14	121,128,154,159	0
2	DSG	C	43	8/9	0.90	0.18	93,104,108,110	0
2	DTR	C	9	14/15	0.90	0.24	117,133,145,147	0
2	DSG	G	43	8/9	0.90	0.16	89,103,111,114	0
2	DLY	C	27	9/10	0.90	0.22	78,82,87,89	0
2	DAS	G	36	8/9	0.90	0.14	109,119,133,145	0
2	DGN	D	40	9/10	0.90	0.16	194,201,222,225	0
2	DGL	H	15	9/10	0.91	0.36	152,170,201,207	0
2	DPR	D	20	7/8	0.91	0.12	164,165,166,167	0
2	DAL	D	29	5/6	0.91	0.15	179,183,190,192	0
2	DSN	C	32	6/7	0.91	0.13	84,89,95,100	0
2	DPR	H	20	7/8	0.91	0.11	169,169,172,175	0
2	DAS	G	53	8/9	0.91	0.16	92,105,113,121	0
2	DSG	C	21	8/9	0.91	0.15	96,101,120,121	0
2	DAL	D	54	5/6	0.91	0.15	206,206,213,220	0
2	DGL	D	25	9/10	0.91	0.33	202,208,229,229	0
2	DTR	G	9	14/15	0.91	0.23	110,126,140,142	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	DGN	C	40	9/10	0.91	0.15	106,128,146,150	0
2	DLE	D	44	8/9	0.91	0.35	203,216,222,223	0
2	DLE	H	44	8/9	0.91	0.33	201,211,214,216	0
2	DGL	C	47	9/10	0.91	0.19	85,94,101,107	0
2	DSG	H	21	8/9	0.91	0.15	177,181,182,183	0
2	DGL	C	15	9/10	0.92	0.32	106,109,121,123	0
2	DGL	D	15	9/10	0.92	0.31	165,173,207,207	0
2	DLE	C	22	8/9	0.92	0.30	86,88,98,99	0
2	DLY	D	27	9/10	0.92	0.24	172,178,187,196	0
2	DAS	G	37	8/9	0.92	0.23	125,134,165,174	0
2	DLY	H	27	9/10	0.92	0.18	163,167,176,188	0
2	DLY	G	50	9/10	0.92	0.24	83,88,115,118	0
2	DAR	C	28	11/12	0.92	0.20	81,83,87,87	0
2	DSG	G	52	8/9	0.92	0.12	83,89,91,92	0
2	DAR	D	28	11/12	0.92	0.34	189,201,208,211	0
2	DAR	G	28	11/12	0.92	0.21	82,85,87,87	0
2	DHI	G	18	10/11	0.92	0.16	111,126,146,149	0
2	DLE	H	22	8/9	0.92	0.32	179,191,207,211	0
2	DAL	H	29	5/6	0.92	0.16	175,181,188,201	0
2	DIL	D	31	8/9	0.92	0.30	193,194,196,196	0
2	DSG	G	11	8/9	0.92	0.26	104,124,138,141	0
2	DSN	H	32	6/7	0.92	0.12	169,178,184,190	0
2	DAL	D	12	5/6	0.92	0.18	169,173,173,177	0
2	DAR	C	14	11/12	0.92	0.25	100,112,134,144	0
2	DLE	H	24	8/9	0.92	0.34	155,173,190,191	0
2	DPR	C	57	7/8	0.92	0.19	110,111,112,115	0
2	DAR	G	17	11/12	0.92	0.24	95,100,105,106	0
2	DAS	C	36	8/9	0.92	0.10	111,120,135,141	0
2	DLE	H	45	8/9	0.93	0.28	197,213,221,223	0
2	DAL	G	46	5/6	0.93	0.17	93,96,99,101	0
2	DLE	D	19	8/9	0.93	0.21	166,171,173,174	0
2	DAS	C	37	8/9	0.93	0.18	134,146,171,191	0
2	DGL	G	47	9/10	0.93	0.19	81,94,102,107	0
2	DAR	C	17	11/12	0.93	0.20	99,102,105,105	0
2	DLY	C	50	9/10	0.93	0.23	86,90,113,114	0
2	DLY	G	27	9/10	0.93	0.16	80,85,88,90	0
2	DLE	C	51	8/9	0.93	0.22	83,87,94,96	0
2	DLE	H	51	8/9	0.93	0.17	187,194,201,205	0
2	DAL	G	56	5/6	0.93	0.13	108,109,111,111	0
2	DAL	H	56	5/6	0.93	0.18	179,180,184,187	0
2	DGN	H	26	9/10	0.93	0.34	192,203,209,216	0
2	DAL	C	42	5/6	0.93	0.18	110,111,111,113	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	DPR	G	57	7/8	0.93	0.15	112,112,114,115	0
2	DAL	D	42	5/6	0.93	0.29	218,220,224,227	0
2	DSG	G	21	8/9	0.94	0.12	92,98,109,117	0
2	DSN	D	32	6/7	0.94	0.12	177,185,188,190	0
2	DLY	G	49	9/10	0.94	0.27	83,89,109,114	0
2	DLY	G	7	9/10	0.94	0.30	125,162,176,181	0
2	DSN	C	33	6/7	0.94	0.18	91,93,94,98	0
2	DLY	H	50	9/10	0.94	0.27	206,208,213,213	0
2	DHI	C	18	10/11	0.94	0.13	109,122,143,144	0
2	DAL	C	56	5/6	0.94	0.07	109,112,113,115	0
2	DLE	D	24	8/9	0.94	0.28	175,193,200,203	0
2	DSG	C	52	8/9	0.94	0.12	85,91,94,95	0
2	DLE	G	24	8/9	0.94	0.34	96,100,103,103	0
2	DTY	G	35	12/13	0.94	0.20	93,95,109,110	0
2	DAL	H	46	5/6	0.94	0.20	220,220,224,226	0
2	DAS	C	10	8/9	0.94	0.19	103,126,131,132	0
2	DPR	C	20	7/8	0.94	0.17	102,104,109,110	0
2	DIL	D	16	8/9	0.95	0.22	168,171,174,175	0
2	DIL	H	31	8/9	0.95	0.34	185,187,189,190	0
2	DGL	G	25	9/10	0.95	0.15	89,93,105,112	0
2	DTR	C	13	14/15	0.95	0.29	90,111,117,121	0
2	DSN	G	32	6/7	0.95	0.11	81,86,92,92	0
2	DGN	C	26	9/10	0.95	0.17	82,86,88,89	0
2	DAS	G	10	8/9	0.95	0.19	95,118,124,130	0
2	DTR	G	13	14/15	0.95	0.26	89,106,113,116	0
2	DLE	C	45	8/9	0.95	0.28	91,95,96,96	0
2	DLE	G	45	8/9	0.95	0.21	85,88,91,93	0
2	DSN	G	33	6/7	0.95	0.19	89,90,91,91	0
2	DAL	C	46	5/6	0.95	0.16	97,98,102,103	0
2	DAL	G	54	5/6	0.95	0.14	94,95,98,102	0
2	DAL	H	54	5/6	0.95	0.22	204,205,208,229	0
2	DAL	H	12	5/6	0.95	0.17	166,170,174,175	0
2	DLE	D	34	8/9	0.95	0.27	175,186,191,192	0
2	DTY	C	35	12/13	0.95	0.16	92,93,106,109	0
2	DAL	G	29	5/6	0.95	0.17	86,90,93,94	0
2	DSG	C	23	8/9	0.95	0.18	89,95,100,105	0
2	DPN	D	30	11/12	0.95	0.50	189,207,218,221	0
2	DAL	H	48	5/6	0.95	0.17	224,226,229,232	0
2	DLY	C	49	9/10	0.95	0.24	89,92,112,115	0
2	DLY	D	49	9/10	0.95	0.27	207,211,224,225	0
2	DSN	G	41	6/7	0.95	0.16	90,104,108,113	0
2	DPN	H	30	11/12	0.95	0.47	179,194,206,206	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	DIL	C	31	8/9	0.95	0.26	84,88,88,90	0
2	DLE	C	34	8/9	0.96	0.17	92,95,100,103	0
2	DAL	D	48	5/6	0.96	0.23	225,225,225,226	0
2	DAL	G	12	5/6	0.96	0.18	97,98,100,102	0
2	DLE	C	44	8/9	0.96	0.20	83,91,94,98	0
2	DLE	H	34	8/9	0.96	0.23	169,176,179,188	0
2	DSN	C	41	6/7	0.96	0.13	99,109,113,115	0
2	DLY	H	49	9/10	0.96	0.22	192,198,213,216	0
2	DLE	C	19	8/9	0.96	0.28	102,108,116,118	0
2	DLY	D	50	9/10	0.96	0.23	209,214,222,222	0
2	DPR	G	20	7/8	0.96	0.20	102,104,109,110	0
2	DPN	G	30	11/12	0.96	0.33	81,88,89,90	0
2	DPR	G	38	7/8	0.96	0.17	104,119,127,128	0
2	DAL	D	46	5/6	0.96	0.21	220,220,221,225	0
2	DGN	G	26	9/10	0.96	0.19	79,85,87,90	0
2	DAL	G	42	5/6	0.96	0.14	104,104,105,105	0
2	DGL	C	25	9/10	0.96	0.16	90,95,106,116	0
2	DAL	C	12	5/6	0.96	0.17	101,101,102,106	0
2	DLE	H	19	8/9	0.96	0.21	168,176,179,187	0
2	DLE	D	51	8/9	0.97	0.17	205,208,215,218	0
2	DLE	G	51	8/9	0.97	0.17	79,84,92,94	0
2	DLE	D	45	8/9	0.97	0.28	209,219,225,231	0
2	DPR	C	38	7/8	0.97	0.16	112,124,131,131	0
2	DLE	G	34	8/9	0.97	0.21	88,93,96,99	0
2	DLE	G	19	8/9	0.97	0.28	100,106,111,113	0
2	DPN	C	30	11/12	0.97	0.30	82,85,89,89	0
2	DIL	H	16	8/9	0.97	0.24	161,162,165,165	0
2	DSN	G	39	6/7	0.97	0.16	116,118,126,133	0
2	DAL	C	29	5/6	0.97	0.16	85,88,90,91	0
2	DLE	G	44	8/9	0.97	0.21	80,91,94,94	0
2	DLE	C	24	8/9	0.97	0.25	97,99,100,102	0
2	DLE	G	22	8/9	0.97	0.29	86,88,96,100	0
2	DSN	C	39	6/7	0.98	0.20	115,122,129,136	0
2	DAL	G	48	5/6	0.98	0.21	79,83,85,87	0
2	DIL	G	31	8/9	0.98	0.25	82,85,87,88	0
2	DIL	G	16	8/9	0.98	0.34	93,97,98,100	0
2	DIL	C	16	8/9	0.98	0.39	90,99,102,105	0
2	DAL	C	54	5/6	0.98	0.12	99,102,109,111	0
2	DAL	C	48	5/6	0.98	0.18	82,87,87,91	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.