wwPDB X-ray Structure Validation Summary Report (i)

Aug 21, 2020 – 02:31 PM BST

PDB ID	:	4Z61
Title	:	The plant peptide hormone receptor complex
Authors	:	Chai, J.; Wang, J.
Deposited on	:	2015-04-03
Resolution	:	2.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

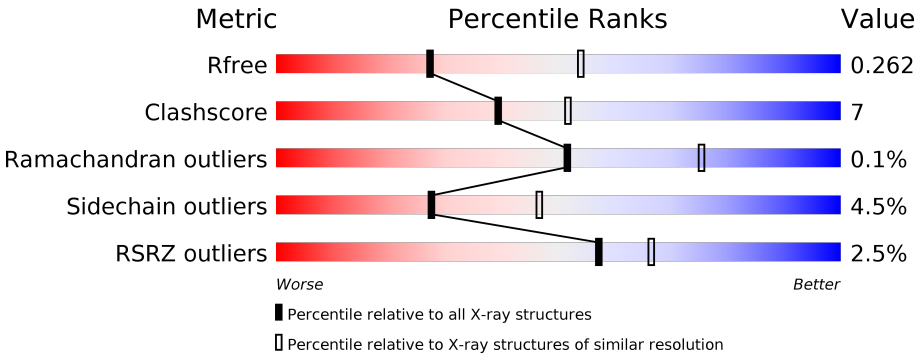
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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 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	642	2% 80% 14% • 5%
1	B	642	3% 71% 21% • 6%
2	C	222	% 65% 18% 17%
2	D	222	% 66% 16% • 17%
3	P	5	40% 40% 20%
3	Q	5	20% 40% 40%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12670 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 Phytosulfokine receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	610	Total	C	N	O	S	0	0	0
			4678	2964	789	907	18			
1	B	603	Total	C	N	O	S	0	0	0
			4631	2937	780	897	17			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	660	HIS	-	expression tag	UNP Q8LPB4
A	661	HIS	-	expression tag	UNP Q8LPB4
A	662	HIS	-	expression tag	UNP Q8LPB4
A	663	HIS	-	expression tag	UNP Q8LPB4
A	664	HIS	-	expression tag	UNP Q8LPB4
A	665	HIS	-	expression tag	UNP Q8LPB4
B	660	HIS	-	expression tag	UNP Q8LPB4
B	661	HIS	-	expression tag	UNP Q8LPB4
B	662	HIS	-	expression tag	UNP Q8LPB4
B	663	HIS	-	expression tag	UNP Q8LPB4
B	664	HIS	-	expression tag	UNP Q8LPB4
B	665	HIS	-	expression tag	UNP Q8LPB4

- Molecule 2 is a protein called Somatic embryogenesis receptor kinase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	185	Total	C	N	O	S	0	0	0
			1402	883	240	272	7			
2	D	185	Total	C	N	O	S	0	0	0
			1402	883	240	272	7			

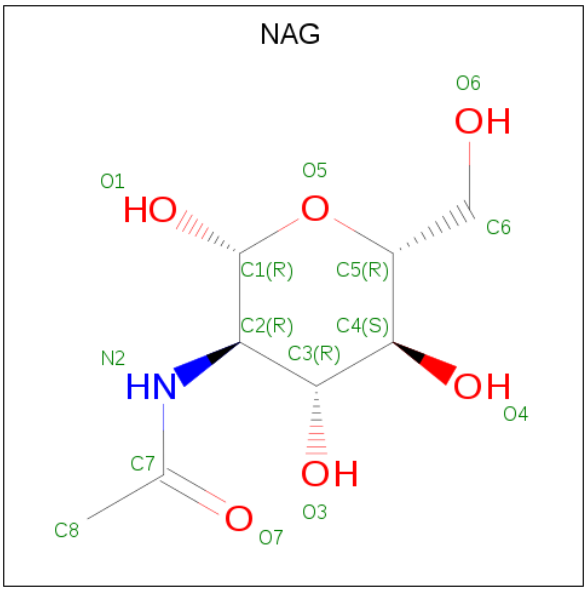
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	217	HIS	-	expression tag	UNP Q9XIC7
C	218	HIS	-	expression tag	UNP Q9XIC7
C	219	HIS	-	expression tag	UNP Q9XIC7
C	220	HIS	-	expression tag	UNP Q9XIC7
C	221	HIS	-	expression tag	UNP Q9XIC7
C	222	HIS	-	expression tag	UNP Q9XIC7
D	217	HIS	-	expression tag	UNP Q9XIC7
D	218	HIS	-	expression tag	UNP Q9XIC7
D	219	HIS	-	expression tag	UNP Q9XIC7
D	220	HIS	-	expression tag	UNP Q9XIC7
D	221	HIS	-	expression tag	UNP Q9XIC7
D	222	HIS	-	expression tag	UNP Q9XIC7

- Molecule 3 is a protein called PTR-ILE-PTR-THR-GLN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	5	Total	C	N	O	S	0	0	0
			57	33	6	16	2			
3	Q	5	Total	C	N	O	S	0	0	0
			57	33	6	16	2			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	B	1	Total C N O 14 8 1 5	0	0
4	B	1	Total C N O 14 8 1 5	0	0
4	B	1	Total C N O 14 8 1 5	0	0
4	B	1	Total C N O 14 8 1 5	0	0
4	B	1	Total C N O 14 8 1 5	0	0
4	B	1	Total C N O 14 8 1 5	0	0
4	C	1	Total C N O 14 8 1 5	0	0
4	D	1	Total C N O 14 8 1 5	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	103	Total O 103 103	0	0
5	B	60	Total O 60 60	0	0
5	C	25	Total O 25 25	0	0

Continued on next page...

Continued from previous page...

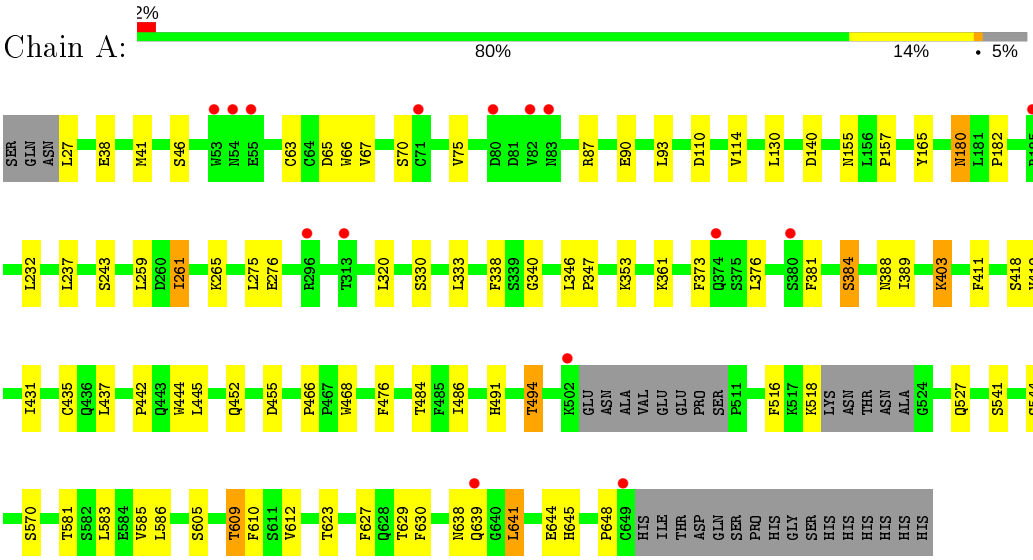
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	16	Total O 16 16	0	0
5	Q	1	Total O 1 1	0	0

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.

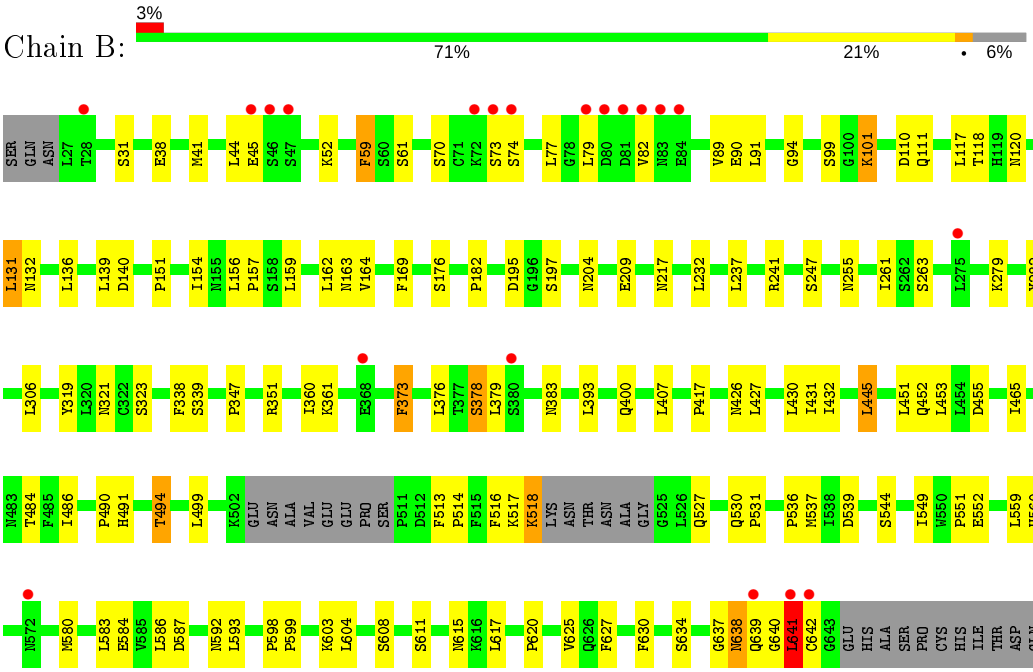
- Molecule 1: Phytosulfokine receptor 1

Chain A:



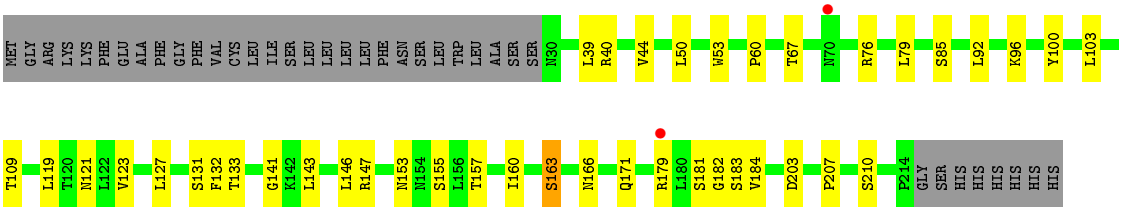
- Molecule 1: Phytosulfokine receptor 1

Chain B:



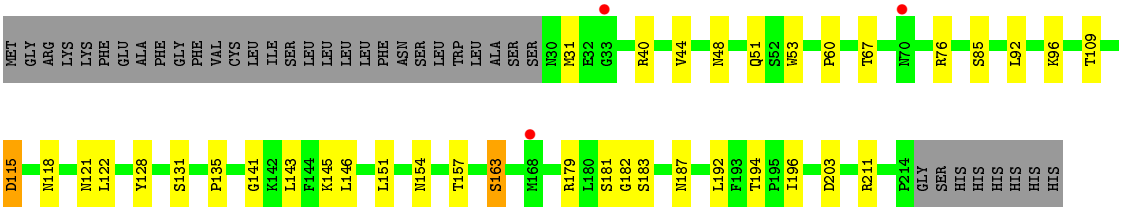
• Molecule 2: Somatic embryogenesis receptor kinase 2

Chain C:



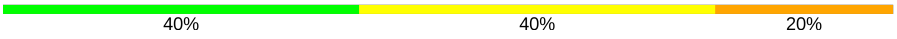
• Molecule 2: Somatic embryogenesis receptor kinase 2

Chain D:



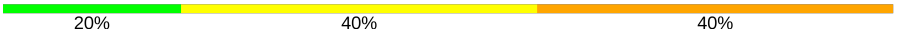
• Molecule 3: PTR-ILE-PTR-THR-GLN

Chain P:



• Molecule 3: PTR-ILE-PTR-THR-GLN

Chain Q:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	486.19Å 73.50Å 67.33Å 90.00° 95.84° 90.00°	Depositor
Resolution (Å)	29.87 – 2.75 29.87 – 2.75	Depositor EDS
% Data completeness (in resolution range)	87.7 (29.87-2.75) 87.6 (29.87-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.99 (at 2.76Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, R_{free}	0.196 , 0.262 0.199 , 0.262	Depositor DCC
R_{free} test set	2770 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	40.9	Xtriage
Anisotropy	0.332	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 39.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.028 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	12670	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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

5.1 Standard geometry

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

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	0.46	0/4769	0.66	0/6469
1	B	0.42	0/4720	0.64	1/6402 (0.0%)
2	C	0.42	0/1432	0.66	0/1963
2	D	0.44	0/1432	0.65	0/1963
3	P	1.40	0/23	1.17	0/27
3	Q	1.78	0/23	1.16	0/27
All	All	0.45	0/12399	0.65	1/16851 (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	B	0	1

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	B	91	LEU	CA-CB-CG	5.45	127.83	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	641	LEU	Peptide

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	4678	0	4669	52	0
1	B	4631	0	4637	86	0
2	C	1402	0	1368	23	0
2	D	1402	0	1368	24	0
3	P	57	0	42	4	0
3	Q	57	0	42	2	0
4	A	126	0	117	2	0
4	B	84	0	78	2	0
4	C	14	0	13	0	0
4	D	14	0	13	0	0
5	A	103	0	0	5	0
5	B	60	0	0	1	0
5	C	25	0	0	1	0
5	D	16	0	0	3	0
5	Q	1	0	0	0	0
All	All	12670	0	12347	183	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 7.

The worst 5 of 183 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:640:GLY:O	5:B:801:HOH:O	1.78	1.02
1:B:641:LEU:HD12	1:B:642:CYS:H	1.28	0.96
2:C:147:ARG:NH1	2:C:171:GLN:OE1	1.99	0.95
2:D:118:ASN:ND2	5:D:1601:HOH:O	2.01	0.93
1:B:637:GLY:C	1:B:638:ASN:HD22	1.71	0.93

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	604/642 (94%)	580 (96%)	24 (4%)	0	100 100
1	B	597/642 (93%)	577 (97%)	20 (3%)	0	100 100
2	C	183/222 (82%)	179 (98%)	3 (2%)	1 (0%)	29 47
2	D	183/222 (82%)	179 (98%)	3 (2%)	1 (0%)	29 47
3	P	2/5 (40%)	2 (100%)	0	0	100 100
3	Q	2/5 (40%)	2 (100%)	0	0	100 100
All	All	1571/1738 (90%)	1519 (97%)	50 (3%)	2 (0%)	51 75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	60	PRO
2	D	60	PRO

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	552/581 (95%)	528 (96%)	24 (4%)	29 48
1	B	547/581 (94%)	516 (94%)	31 (6%)	20 36
2	C	164/201 (82%)	161 (98%)	3 (2%)	59 75
2	D	164/201 (82%)	159 (97%)	5 (3%)	41 61
3	P	3/3 (100%)	3 (100%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	Q	3/3 (100%)	2 (67%)	1 (33%)	0 0
All	All	1433/1570 (91%)	1369 (96%)	64 (4%)	27 46

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	101	LYS
1	B	197	SER
2	D	115	ASP
1	B	110	ASP
1	B	132	ASN

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

Mol	Chain	Res	Type
1	B	482	ASN
1	B	638	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

4 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	$\#\|Z\| > 2$
3	TYS	P	28	3	15,16,17	1.99	3 (20%)	18,22,24	1.63	3 (16%)
3	TYS	Q	28	3	15,16,17	2.42	5 (33%)	18,22,24	1.60	3 (16%)
3	TYS	Q	30	3	15,16,17	2.96	6 (40%)	18,22,24	1.27	2 (11%)
3	TYS	P	30	3	15,16,17	1.56	3 (20%)	18,22,24	1.20	2 (11%)

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
3	TYS	P	28	3	-	2/10/11/13	0/1/1/1
3	TYS	Q	28	3	-	2/10/11/13	0/1/1/1
3	TYS	Q	30	3	-	3/10/11/13	0/1/1/1
3	TYS	P	30	3	-	3/10/11/13	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Q	30	TYS	CE1-CD1	-6.45	1.27	1.38
3	Q	30	TYS	CE2-CD2	-5.55	1.28	1.38
3	Q	28	TYS	CE1-CD1	-5.12	1.29	1.38
3	Q	30	TYS	OH-CZ	-4.67	1.35	1.42
3	P	28	TYS	CE1-CD1	-4.55	1.30	1.38

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	Q	28	TYS	O3-S-OH	5.21	118.37	105.83
3	P	28	TYS	OH-CZ-CE2	4.66	127.80	118.64
3	Q	30	TYS	O3-S-OH	4.11	115.73	105.83
3	P	30	TYS	O3-S-OH	3.56	114.39	105.83
3	Q	28	TYS	OH-CZ-CE2	3.23	124.98	118.64

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	Q	28	TYS	CE1-CZ-OH-S
3	Q	28	TYS	CE2-CZ-OH-S
3	Q	30	TYS	CZ-OH-S-O2
3	Q	30	TYS	CZ-OH-S-O3
3	P	30	TYS	CZ-OH-S-O1

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	Q	28	TYS	1	0
3	Q	30	TYS	1	0
3	P	30	TYS	3	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

17 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	$\#\|Z\| > 2$
4	NAG	A	706	1	14,14,15	0.58	0	17,19,21	1.18	2 (11%)
4	NAG	C	301	2	14,14,15	0.53	0	17,19,21	1.32	2 (11%)
4	NAG	A	702	1	14,14,15	0.53	0	17,19,21	0.90	0
4	NAG	A	709	1	14,14,15	0.49	0	17,19,21	1.39	2 (11%)
4	NAG	A	703	1	14,14,15	0.59	0	17,19,21	2.23	6 (35%)
4	NAG	B	703	1	14,14,15	0.44	0	17,19,21	1.86	2 (11%)
4	NAG	B	704	1	14,14,15	0.63	0	17,19,21	2.51	8 (47%)
4	NAG	A	704	1	14,14,15	0.49	0	17,19,21	1.07	2 (11%)
4	NAG	B	706	-	14,14,15	0.69	0	17,19,21	1.26	3 (17%)
4	NAG	A	707	1	14,14,15	0.74	0	17,19,21	1.22	3 (17%)
4	NAG	D	1501	2	14,14,15	0.40	0	17,19,21	1.85	2 (11%)
4	NAG	B	702	1	14,14,15	0.55	0	17,19,21	1.94	6 (35%)
4	NAG	B	705	1	14,14,15	0.49	0	17,19,21	1.44	1 (5%)
4	NAG	A	705	1	14,14,15	0.60	0	17,19,21	2.02	4 (23%)
4	NAG	A	708	1	14,14,15	0.35	0	17,19,21	2.00	2 (11%)
4	NAG	B	701	1	14,14,15	0.59	0	17,19,21	1.06	2 (11%)
4	NAG	A	701	1	14,14,15	0.61	0	17,19,21	1.05	1 (5%)

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
4	NAG	A	706	1	-	0/6/23/26	0/1/1/1
4	NAG	C	301	2	-	0/6/23/26	0/1/1/1
4	NAG	A	702	1	-	3/6/23/26	0/1/1/1
4	NAG	A	709	1	-	4/6/23/26	0/1/1/1
4	NAG	A	703	1	-	2/6/23/26	0/1/1/1
4	NAG	B	703	1	-	3/6/23/26	0/1/1/1
4	NAG	B	704	1	-	4/6/23/26	0/1/1/1
4	NAG	A	704	1	-	0/6/23/26	0/1/1/1
4	NAG	B	706	-	-	2/6/23/26	0/1/1/1
4	NAG	A	707	1	-	0/6/23/26	0/1/1/1
4	NAG	D	1501	2	-	2/6/23/26	0/1/1/1
4	NAG	B	702	1	-	3/6/23/26	0/1/1/1
4	NAG	B	705	1	-	0/6/23/26	0/1/1/1
4	NAG	A	705	1	-	1/6/23/26	0/1/1/1
4	NAG	A	708	1	-	2/6/23/26	0/1/1/1
4	NAG	B	701	1	-	0/6/23/26	0/1/1/1
4	NAG	A	701	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	708	NAG	C1-O5-C5	7.08	121.78	112.19
4	D	1501	NAG	C1-O5-C5	6.63	121.18	112.19
4	A	703	NAG	C1-O5-C5	6.27	120.69	112.19
4	B	704	NAG	C4-C3-C2	-5.03	103.65	111.02
4	B	705	NAG	O5-C5-C6	5.01	115.06	107.20

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	703	NAG	C3-C2-N2-C7
4	B	703	NAG	C8-C7-N2-C2
4	B	703	NAG	O7-C7-N2-C2
4	B	702	NAG	C1-C2-N2-C7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	B	702	NAG	C8-C7-N2-C2

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	706	NAG	1	0
4	A	705	NAG	1	0
4	B	701	NAG	1	0
4	A	701	NAG	1	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

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, 95^{th} 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	610/642 (95%)	-0.39	15 (2%) 57 66	8, 18, 41, 97	0
1	B	603/642 (93%)	-0.18	20 (3%) 46 54	14, 29, 53, 117	0
2	C	185/222 (83%)	-0.27	2 (1%) 80 86	12, 26, 41, 51	0
2	D	185/222 (83%)	-0.22	3 (1%) 72 79	18, 29, 44, 57	0
3	P	3/5 (60%)	-0.59	0 100 100	19, 19, 19, 20	0
3	Q	3/5 (60%)	-0.70	0 100 100	10, 10, 11, 14	0
All	All	1589/1738 (91%)	-0.28	40 (2%) 57 66	8, 25, 46, 117	0

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	82	VAL	7.0
1	B	82	VAL	5.6
1	B	83	ASN	4.5
1	A	80	ASP	4.3
1	B	28	THR	4.2

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

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, 95^{th} 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
3	TYS	P	30	16/17	0.93	0.16	14,23,32,34	0
3	TYS	P	28	16/17	0.95	0.14	17,22,43,44	0
3	TYS	Q	30	16/17	0.96	0.10	9,11,22,28	0
3	TYS	Q	28	16/17	0.96	0.14	11,15,31,35	0

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, 95^{th} 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
4	NAG	A	709	14/15	0.84	0.20	41,53,60,63	0
4	NAG	A	703	14/15	0.90	0.36	38,45,50,53	0
4	NAG	B	703	14/15	0.90	0.27	38,43,60,64	0
4	NAG	D	1501	14/15	0.90	0.37	34,40,48,49	0
4	NAG	B	706	14/15	0.91	0.16	28,36,39,41	0
4	NAG	B	702	14/15	0.91	0.13	15,31,35,40	0
4	NAG	B	704	14/15	0.92	0.18	19,25,30,40	0
4	NAG	A	702	14/15	0.93	0.20	29,44,56,57	0
4	NAG	B	705	14/15	0.93	0.16	16,24,30,34	0
4	NAG	C	301	14/15	0.94	0.12	32,34,39,40	0
4	NAG	A	708	14/15	0.94	0.16	14,16,19,19	0
4	NAG	B	701	14/15	0.94	0.16	15,23,33,36	0
4	NAG	A	704	14/15	0.95	0.20	13,20,27,30	0
4	NAG	A	705	14/15	0.95	0.14	11,16,21,27	0
4	NAG	A	706	14/15	0.96	0.23	18,23,30,34	0
4	NAG	A	707	14/15	0.96	0.17	13,19,23,26	0
4	NAG	A	701	14/15	0.97	0.16	10,20,27,29	0

6.5 Other polymers (i)

There are no such residues in this entry.